International Symposium on

SUSTAINABLE MANAGEMENT OF ANIMAL GENETIC RESOURCES FOR LIVELIHOOD SECURITY IN DEVELOPING COUNTRIES

&

XII ANNUAL CONVENTION OF SOCIETY FOR CONSERVATION OF DOMESTIC ANIMAL BIODIVERSITY (SOCDAB)

COMPENDIUM OF
INVITED LECTURES AND ABSTRACTS

Madras Veterinary College
Chennai

February
13-14, 2015

Organized by

Tamilnadu Veterinary and Animal Sciences University (TANUVAS), Chennai, India
&
Society for Conservation of Domestic
Animal Biodiversity (SOCDAB), NBAGR, Karnal, India

Society for Conservation of Domestic Animal Biodiversity (SOCDAB)

India is the pride possessor of the world's most varied forms of fauna and flora. The presence of more than 140 breeds of various livestock species is unparalleled worldwide. These farm animal genetic resources have remained the backbone of Indian agrarian economy through the production of milk, meat, eggs, fibers and manure. More recently, modern breeders have applied the science of genetics and breeding to produce more efficient, high producing farm animals mainly through crossbreeding with exotic germplasm. In the process, the populations and genetic base of several valuable indigenous breeds and strains of animals are shrinking rapidly. We need to consider the conservation of farm animal genetic resources as insurance that our generation and future generations have a healthy and adequate food supply. The animal genetic resources are regarded today as being important to efforts that are designed to maintain and enhance the competitiveness of Indian agriculture on domestic and international markets. Realising the growing concern that urgent action is needed on the issue of conservation of farm animal genetic resources, a group of concerned professionals met, discussed and resolved to provide a platform to dedicated and enthusiastic conservationists. The establishment of the Society for Conservation of Domestic Animal Biodiversity (SOCDAB) with its headquarters at National Bureau of Animal Genetic Resources in June, 1998 is the culmination of dedicated efforts of such professionals.

The chief motto behind the establishment of SOCDAB has been,

"Let's not take our future food needs for granted. Let's bank on our native farm animal genetic resources"

OBJECTIVES

1. To create awareness in all sections of society about Domestic Animal Diversity and need for conservation.
2. To undertake such activities which foster sustainable management of domestic animals.
3. To emphasize the importance of judicious use of animal wealth.
4. To generate programmes and suggest measures to various agencies for conserving the endangered species and breeds of the animals.
5. To provide a forum for the amateurs and professionals to undertake activities directed towards conservation.
6. To promote research, education and development of domestic animals which would result in their profitable utilization.
7. To undertake programmes for monitoring the loss of domestic animal biodiversity and forecasting their status.

ACTIVITIES

- ❖ Organization of National / International Seminars / Symposia / Workshops/ group meetings on characterization and conservation of indigenous animal genetic resources.
- ❖ Creation of mass awareness about the domestic animal biodiversity in the scientific community as well as in general public through activities of the society.
- ❖ Creation of awareness among the general public about torture and abuses to the indigenous animal genetic resources which they roam about after completing their useful and productive life span.
- ❖ Dissemination of knowledge and technologies about sustainable management and economics of animals through published literature or other mss media.
- ❖ Listing of endangered / threatened indigenous animal genetic resources and forecasting their status for their conservation.

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राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो
ICAR - NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES
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KARNAL - 132 001 (Haryana)

डा. आर्जव शर्मा
निदेशक
Dr. Arjava Sharma
Director

MESSAGE

I am pleased to know that Tamil Nadu Veterinary and Animal Sciences University (TANUVAS), Chennai in association with Society for Conservation of Domestic Animal Biodiversity (SOCDAB) is organising International Symposium on "Sustainable Management of Animal Genetic Resources for Livelihood Security in Developing Countries alongwith XII Annual convention of the SOCDAB at Madras Veterinary College, Chennai during February 13-14, 2015.

Our country is bestowed with rich animal genetic biodiversity and their contribution to the National GDP is highly significant. NBAGR is a unique organization of ICAR which is actively involved in identification, evaluation, characterization, conservation and policy for utilization of these animal genetic resources for the country. Bureau with the help of other organizations has taken lead to register different breeds of livestock and poultry. The total number of indigenous registered breeds in the country now stands at 151, which include 39 cattle, 13 buffalo, 24 goat, 40 sheep, 6 horses& ponies, 9 camel, 3 pig, 1 donkey and 16 chicken.

Conservation is a complex and costly proposition which needs exchange of knowledge and information in systematic ways. Realising these and other related issues of characterization and conservation of farm animal genetic resources, a group of professionals met, discussed and resolved to provide a platform to dedicated and enthusiastic conservationists. The establishment of the Society for Conservation of Domestic Animal Biodiversity (SOCDAB) with its headquarters at National Bureau of Animal Genetic Resources in June, 1998 was the culmination of these. SOCDAB has been instrumental in organising number of symposium and seminars specifically on conservation and sustainable management of native farm animal breeds and creating awareness on *in situ* and *ex situ* conservation of these livestock biodiversity.

I am sure that the present International Symposium on "Sustainable Management of Animal Genetic Resources for Livelihood Security in Developing Countries and XII Annual convention of the SOCDAB will come out with very useful strategies for further improving the productivity of the livestock genetic resources.

I wish the International symposium a grand success!

10/II/15
[ARJAVA SHARMA]

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TAMIL NADU VETERINARY AND ANIMAL SCIENCES UNIVERSITY

Dr. S. THILAGAR
VICE-CHANCELLOR

Madhavaram Milk Colony
Chennai - 600 051

MESSAGE

It is a matter of great pleasure that Tamil Nadu Veterinary and Animal Sciences University (TANUVAS) is organising the XII International Symposium on **"Sustainable Management of Animal Genetic Resources for Livelihood Security in Developing Countries"** at Madras Veterinary College, Chennai-7 during February 13-14, 2015 in collaboration with Society for Conservation of Domestic Animal Biodiversity (SOCDAB) & National Bureau of Animal Genetic Resources (NBAGR), Karnal during its silver jubilee year.

TANUVAS is the premier institute concentrating on conservation of valuable native germplasm by *in situ* and *ex situ* means through organised farms and well sophisticated laboratories. The issues of the farmers in the field are addressed appropriately through extension machineries and research wings of TANUVAS for the sustainable management of livestock and poultry genetic resources. The research stations of TANUVAS supplies superior germplasm to the needy farmers for genetic improvement of their livestock, thereby improving their livelihood.

This compendium has a good collection of invited lectures from eminent scientists and research abstracts on recent developments and thrust areas in the field of characterization, conservation and management of livestock biodiversity. It is an appropriate platform wherein the constraints and limitations faced by the farmers in rearing the native germplasm will be discussed and suitable strategies would be formulated to ease out their predicament, along with the international scientists.

I extend my best wishes for the grand success of the symposium.

11/2/15
(Dr.S.THILAGAR)

11th February 2015
Chennai

TAMIL NADU VETERINARY AND ANIMAL SCIENCES UNIVERSITY

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Dated: 10.02.2015

MESSAGE

It is indeed a great pleasure to know that the International Symposium on "Sustainable Management of Animal Genetic Resources for Livelihood Security in Developing Countries and XII Annual convention of the SOCDAB" is being jointly organised by Tamil Nadu Veterinary and Animal Sciences University (TANUVAS), Chennai, Society for Conservation of Domestic Animal Biodiversity (SOCDAB) & National Bureau of Animal Genetic Resources (NBAGR), Karnal at Madras Veterinary College, Chennai during February 13-14, 2015.

The Madras Veterinary College (MVC), the first of the four constituent veterinary colleges of TANUVAS, was started as an equine treatment school with five students in a temporary structure at Saidapet, Chennai in 1903. It is one of the oldest veterinary schools in the country. Since inception, the college started growing in stature and is now recognized as a premier veterinary institute in the country and world over known for working conservation and management of AnGR of this country. I welcome all the delegates to this premier institution.

The livestock genetic resources of our country is a national heritage that needs to be conserved, protected and further improved to meet the ever growing needs of the human population. The strategies for sustainable management of these domestic biodiversity in light of advancing genomics will be of great importance for providing livelihood security. The theme of the symposium on sustainable management and conservation of farm animal genetic resources is need of the hour.

I assure that the symposium will provide an opportunity to scientists, academicians, Animal Husbandry officials, policy planners, farmers and other stakeholders to share their experiences and technical know-how with the younger generation, inspiring them to use their talents for harnessing more scientific knowledge which can be a way forward for the effective and sustainable management of indigenous farm animal diversity. I hope you will enjoy the stay in Chennai and gain knowledge in this memorable event.

I wish that recommendations emerging through the deliberations will help in sustainable management of livestock subsequently upliftment of rural masses.

(C.BALACHANDRAN)

TAMIL NADU VETERINARY AND ANIMAL SCIENCES UNIVERSITY

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FOREWARD

Date: 11.02.2015

I am immensely pleased to welcome all the delegates and dignitaries from India and abroad to the International Symposium on "**SUSTAINABLE MANAGEMENT OF ANIMAL GENETIC RESOURCES FOR LIVELIHOOD SECURITY IN DEVELOPING COUNTRIES**" and XII Annual convention of the SOCDAB during February 13-14, 2015 at Madras Veterinary College, TANUVAS, Chennai, Tamil Nadu, India.

The theme of the International Symposium is to eradicate hunger, poverty and malnutrition from this world by means of improvement and conservation of domestic animal biodiversity. Diversity of farm animal species is key factor to efficient production systems in rural areas. The Indigenous breeds have been endowed with thermo-tolerance, resistance against diseases, ability to use poor quality biomass, and survive under adverse conditions with assured production of milk, wool, meat, eggs and draft power to feed exploding populations in the developing countries.

The two day International Symposium is an attempt to showcase advancement in the field of characterization, conservation and improvement of indigenous animals achieved by the participating delegates and dignitaries out of their research work. Eminent scientists and professionals with wide experience have been invited to share their knowledge and experiences. The overwhelming response from different parts of country and abroad for oral and poster presentations is really heartening. The compendium brought out during this event is of invited lectures and research abstracts contributed by the researchers of national and international repute.

I am highly indebted to the President, and EC Members of SOCDAB, Karnal for nominating TANUVAS to organize this International symposium. My special thanks to all the International Scientist from Brazil, USA, Denmark, Iran, Thailand, Zambia, UAE and Egypt for their efforts to attend this mega event. I acknowledge with thanks for the support and guidance given by the organising committee members, Directorate of Centre for Animal Production Studies, Dean, Madras Veterinary College, TANUVAS, Chennai. I also offer my sincere thanks to all the sponsors of this symposium. The invitees and participants deserve special mention in making this international symposium in a grand success. Best wishes to all.

11/02/2015.
(P.KUMARASAMY)

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INVITED PAPERS

1. PRESENT STATUS AND FUTURE PROSPECTS OF INDIAN CATTLE AND BUFFALOES IN BRAZIL AND THEIR CONTRIBUTION TO LIVELIHOOD SECURITY IN DEVELOPING COUNTRIES

"Situação atual e perspectivas futuras de bovinos e búfalos indianos no Brasil e sua contribuição para a segurança da subsistência nos países em desenvolvimento."

José Otávio Lemos

Technical Adviser, ABCZ - Brazilian Association of Zebu Breeders, Brazil

Humans, in ancient times, and well before the written word, felt protected inside a cave, and sat around a campfire. Each would tell his deeds to the others.

Storytelling has always been one of the main pastimes of men and women. Even today, films and computer games are reflections of these practices. A symposium is that same thing, with the proper dressing of contemporaneity of today.

And the stories of the Indian people are, probably, the oldest in the world. They date back, perhaps, 8,000 years, and were born in a region which now belongs to Pakistan, the Indus Valley.

And among the many things that were said at that time, religion was one of them. The belief in something greater.

Despite the undeniable multiplicity, Hinduism is not as polytheistic as it looks. Many westerners think about it that way, and this is as frivolous as implying, looking at the Christian saints, that Christianity is a religion with many gods.

Adhinatha, a maximum divinity, is manifested in the trinity Brahma, Vishnu and Shiva, unity in diversity.

The faith of the Hindus; has a philosophical basis divided into dharshanas (points of view), and the determination of where the logic ends and the imaginary begins is difficult.

But when we leave our eyes open to every opportunity that the universe opens up for us, we find very beautiful coincidences and truths.

Within the theme, a first evocation to the Kamadhenu, also known as Surabhi. Described in the Hindu religion as the mother of all cows. She is the miraculous "cow of abundance", which provides its owner everything he wants, and is often portrayed as the mother of other bovines. In iconography, a white cow with a head, a torso and arms of a woman on the trunk and legs of a bovine; or as a white cow containing various deities within its body. All cows are revered in Hinduism as the earthly incarnation of it.

Science has made amazing discoveries, and Richard Dawkins makes a very significant question: "What historian could have dared to hope for a world in which every individual of each species brings in his/her body, a long and detailed text - a written document passed from generation to generation through the ages?"

Dressed with significant armor today, the best technology, scientists of our recent time made discoveries that simply with eyes and a group of fossils cannot be determined. They've entered the innermost of the beings, the DNA, at the beginning of the 90's, with the use of molecular biology. Based on the analysis of the sequences of the mitochondrial DNA of six European, three Indian and four African cattle breeds, scientists annexed the African and European in the same group, separating the Indian. Thus, they've described the possibility of two different domestication processes occurring. Yes, because the three groups (Indian, European and African) descend from a common ancestor, the Uro or Aurochs. Aside from the Bali and Mithan cattle, all Bos have the Bos primigenius, the Uro, as initial ascendant.

And the origin of the Bos primigenius is in Asia, the continent of India.

Studies indicate that the evolution center of the Bos primigenius was in Asia, but the first group to be domesticated was from Europe, approximately 10 thousand years ago.

The estimated time of separation between the Bos primigenius primigenius (taurus) and the Bos primigenius namandicus (indicus) was 210 thousand years.

Another group of scientists, D. G. Bradley, D.E. MacHugh and P. Cunningham, in 1996, also analyzing mitochondrial DNA sequences from 13 cattle breeds, confirmed that there are differences between Indian-origin animals with European/African-origin ones, and the time estimated for it was between 117 and 275 years; and 22 to 26 thousand years between European and African breeds.

By religion or mythology, or by science, the first cow, the mother of all others, is Indian.

Questions arise about the origin of the African cattle. It features phenotypic characteristics of zebu breeds from India and classic taurus haplotypes. But the association of mitochondrial DNA analysis and polymorphisms on the Y chromosome indicate that the initial distribution of African cattle was of European origin (indicated by mitochondrial DNA analysis). However, over time, there were some uses of Zebu male (found in the studies of polymorphism of the Y chromosome), probably because they are animals which are more resistant to parasites.

And resistance to parasites and diseases is one of the characteristics that led the Bos primigenius namandicus (Bos taurus indicus or Bos indicus) to take the post of most important bovine species, and their crossings, in food production in tropical and even subtropical areas of the planet. And this portion of the continents is considered, more each day, the barn to the world. Also an area where developing countries have been declaring their importance for humanity.

There are several characteristics of zebu that, together, make it a successful tropical ecotype. And two more are very strong: the melanin protecting the skin from the sun's strong rays, and the blood system working at the refraction of the sunlight, which taurus do not possess.

The rising of the environmental temperature and consequently the animal's temperature, triggers a cascade of physiological changes in order to minimize the effects caused by thermal stress. This can be proven by a lower feed efficiency, decreased milk production, a worse reproductive performance, a lower reproductive output and in the secretion of important hormones for the homeostasis in taurus compared to the Zebu, when under stress. Above the comfort zone, the major heat losses are through evaporation from the skin, followed by the increase in the sweating rate and respiratory movements. When the ambient temperature exceeds 30° C, the skin evaporation is responsible for 85% of the heat loss to the environment, whereas the remaining 15% are due to losses by respiratory evaporation.

And another species, Bubalus bubalis, with Indian breeds scattered by many countries is another of enormous contribution to the world's livestock.

Made the way to Kamadhenu, we found buffaloes connected to the deities of Hinduism. Pashupati ("Lord of the Animals", from pashu, animals, and pati, "lord") is one of the first representations of Shiva. Emerged in the neolithic, around 6,000 years ago. It is represented with three faces, looking over time (past-present-future). The crown shaped like buffalo horns shows Shiva's proximity to this animal which represents the strengths of earth and virility.

All bovines and buffaloes are very important for humanity in their various functions; but the Indian breed ones are impregnated with an adhesive glue between them and humans around them. And as most of the world where you can produce food is of adverse climate, soil, vegetation, hydrography and rainfall conditions (difficult for the taurus, first domesticated Bos), they have become irreplaceable, with their genetic built in the thousands of years of their establishment as a participant being of a whole ecosystem of very demanding biomass for food-producing organisms on a commercial scale - the tropical.

India has the largest cattle and buffalo herd in the world. It is the country of the highest milk production in the world. For religious reasons, cattle meat production is not within their objectives. However, a large portion of what is produced of red protein in the world today is with Bos indicus genetics.

The world's largest exporter of beef, and owner of the largest commercial herd, with 200 million heads, Brazil, has over 80% of its cattle effective composed of zebu or its crossbreds. And the buffaloes, with blood of Murrah and Jaffarabadi breeds, are also representative in production of beef and other products of interest in food, medicine and clothing, among others.

Also Australia, one of the world's three largest meat exporters, has in its herd basis the largest share of Zebu genetics, and is the country that gets paid more for the quality of this product.

Completing the trio of most exporters, the United States, which also has in the zebu, crossbred or pure, a great builder of this result. And Mexico is a supplier of steers that are slaughtered in the United States, and the Bos indicus is indispensable there.

The British, during the time they dominated India, were the great responsible for the world to know the cattle descendent from Kamadhenu and Indian buffalo. They've sent specimens of the two species to zoos and farmers in various parts of the world. And these animals showed they were not purely curious species, but highly productive.

But we need to keep the racial groups that nature evolved in India.

In September 2014, a workshop in SGVP, Ahmedabad (Gujarat), with a theme also on the conservation of native Zebu breeds discussed the matter and indicated approaches to maintain and increase the genuine Indian breeds. A number of crossings, especially in the last 40 years, extinguished some excellent Indian native breeds, and others are practically on the verge of extinction. Today, animal scientists that research cattle in India are in agreement that the cattle crossbred with the taurus has not rendered much to the country.

In 1910, the Holstein cows had lactations of 1,320 kg. Currently, this cattle has reached 10,000 kg. On the other hand, if the Zebu cow yields between 2,000 – 3,000 kg, a lot more than the Dutch back then, we are able to increase, through selective breeding of our buffalo and zebu species, the milk production from 3,000 kg to 10,000 kg for our cattle.

Brazil has been successfully managing to have a livestock of higher productivity per area and, each time, with fewer animals. Each individual, buffalo or zebu, with higher yield in the production of meat and milk, with increased fertility, number one feature to be selected in any species sorted by man. Buffalo and zebu need to be fertile, well conformed to the function we want for them, stiffer so we can have uniformity in production and with good angulation, base that helps a lot in longevity. Under these optics, the results will be better every day.

The first Indian zebu cattle and buffalo arrived in Brazil just over 100 years ago, and made the country the owner of the largest commercial herd in the world, without having any native breed of cattle or buffalo. Everything was imported and multiplied.

Records in weight gain and milk production are repeatedly beat in Brazil, and a steady growth in product quality, features for which the market pays better. Cows that produce lactation for several months, with a milk of high percentage of total solids and characteristics the Bos taurus cattle cannot produce. Beef cattle quick at building a volume carcass, with tender meat and correct amount of fat.

And such genetics did not only stay in Brazil, which has become a breeding and irradiation center of Indian zebu breeds (Ongole, Gyr, Kankrej, Red Sindhi, Kangayan), and others made with them (Indubrasil, Polled Red Sindhi, Polled Gyr, Polled Ongole, Tabapuã and Brahman - produced by the Americans, and whose main initial breeders of the breed were Brazilian bulls), also the Murrah and Jaffarabadi buffalo. It expanded to other countries, and became a treasure for them, with considerable percentage of the GDP of each of them. Today, for example, Bolivia has 90% of their herd with pure or crossbred Zebu breeds. Colombia, Mexico, Paraguay, Panama, South Africa... So many countries that, fortunately, increase the production thanks to the Indian-origin cattle.

An example of how the native cattle of India can be effective in its multiplication. In 1962, an import to Brazil took several specimens of many breeds. From the Jaffarabadi breed, Palitana variety, two females and one male. Today there are thousands of heads with the blood of those imported in Brazil and in many other countries. Much is due to the correct reproduction biotechnologies, but without the fertility of the species, such thing would not have happened.

Although still more timid, the buffalo raising is developing in the country as a profitable and healthy alternative. This is because the Buffalo adapts easily to any environment. The production and consumption of buffalo milk has been increasing due to the demand for food such as cheese and butter. The high level of fat and total solids in buffalo milk increase the yield in the manufacture of the derivatives compared to cow milk. The meat of such animals is also appreciated, for it contains lower levels of fat, cholesterol, calories and more protein and minerals than that of the bovines.

The Brazilian buffalo herd is estimated at around 1.15 million buffaloes, and the North, having 720,000 animals, the largest producer in the country, especially in Pará, which accounts for 39% of the national herd. Then come the Northeast and the Southeast, with 135 and 104 thousand heads, respectively.

Nandi, the mount of Shiva in his travels by the Earth. Another reference to Hinduism, and a good symbolism that, through the livestock with Indian genetic, peoples are blessed, and developing countries will reach better levels so that the wealth reaches the populations of each of the several that use Indian breeds, which are more efficient since the utilization of food, with less requirements. They digest more roughage, and don't have their rumination disturbed in high temperature environments, as occurs with the European cattle, that has their rumination paralyzed when the temperature exceeds 32,2º C. It appears that the Indian cattle require 25% less protein and about 20% fewer calories to maintain themselves. This is very significant when you do the math of the production cost versus the value determined by the animal kilo produced per area.

It is quite possible that this extraordinary plasticity of the buffalo and zebu breeds in such different environments is connected to the variety of conditions in which they formed their hereditary assets, in the succession of millennia.

This was only possible thanks to two types of selection that the breed had on it: the natural and the artificial.

Charles Darwin, regarding the evolution of species, did not talk, in his time, about adaptive value as it is used today, but his whole theory is based on the same concept: maximum adaptation to a particular environment and preservation of the population.

Adaptive value, also called *fitness* or aptitude, is the ability of the animal to survive and reproduce. It is manifested through the phenotype. The phenotype is the result of the genotype, the environment and the genotype-environment interaction on the individual.

So it is important that all the countries that are users of such genetic have their eyes on the continued preservation and enhancement of the best individuals of each breed for the continued progression, animal improvement, which will enable humanity to benefit well from the species, with the respect they deserve for being part of the whole of life, continued in each and every being, as tiny as it may be, simple truth: there is nothing permanent in a mutant Universe, a strong teaching of Buddha, with which he began his way of preaching to the good people he met on his way.

** José Otávio Lemos is a Brazilian animal scientist, graduated from Faculdade de Zootecnia de Uberaba, and has several specializations, through courses at major universities. He has a professional career with performances in animal improvement and production, recognized by organizations and governments, which have awarded him medals and titles. Participatory in many breeders' associations, having held various positions at boards and councils, and currently occupying the position of technical adviser at ABCZ - Brazilian Association of Zebu Breeders. He is the author of books on Indian cattle breeds. Judge in hundreds of exhibitions with zebu and buffalo breeds in his country of birth and in so many others (effective Judge for ABCZ and ACBB - Brazilian Association of Buffalo Breeders). He has also presented many lectures on buffalo and zebu cattle in symposia, seminars and international conferences in Brazil and countries of America and Africa. He lives with his family in the city of Uberaba/MG - Brazil.*

2. DEFINING THE UNDEFINED ANIMAL GENETIC RESOURCES TO COMPLETE THE NATIONAL INVENTORY OF INDIA

Arjava Sharma and P.K.Vij
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Proper management of animal genetic resource (AnGR) is vital for food security, sustainable development and in providing livelihood security to ever growing human population. The diversity of AnGR in form of domesticated livestock and poultry breeds is developed through evolution within specific ecological niche during last thousands of years. Several complex and interactive factors like human needs, adaptability of a species, agro-climatic conditions, animal husbandry practices along with combined results of both natural selection and directed selections by the livestock keepers ultimately culminated in the emergence of such animal diversity. Each animal population is specific combinations of alleles forming specific genepool, which serves a particular purpose in its native tract. Importance of existing animal diversity can be appreciated by the following statement by Food and Agriculture Organization of the United Nations (FAO). *"Understanding the diversity, distribution, basic characteristics, comparative performance and the current status of each country's animal genetic resources is essential for their efficient and sustainable use, development and conservation. Complete national inventories, supported by periodic monitoring of trends and associated risks, are a basic requirement for the effective management of animal genetic resources. Without such information, some breed population and unique characteristics they contain may decline significantly, or be lost, before their value is recognized and measures taken to conserve them"*.

India is a globally acknowledged as one of the largest livestock diversity center. India possesses huge as well as diverse livestock population distributed over a large range of geographical, ecological and climatic regions. Farm animal population comprises of 512 million of livestock and 729 million of poultry (Livestock Census, 2012). Only 20 percent of this population belongs to well defined 151 registered indigenous breeds in the country and remaining 80 percent belong to many animal populations that are not assigned to any recognized breed. The populations which have not been characterized and accredited so far, are commonly referred to as "non-descript" or "traditional". Even though parts of these "non-descript" populations are known to be multiple crosses of recognized breeds, some animals may belong to homogenous groups distinguishable from other populations on the basis of identifiable and stable phenotypic characteristics that warrant their being distinguished as separate breeds.

"A domestic animal population may be regarded as a breed, if the animals fulfil the criteria of (i) being subjected to a common utilization pattern, (ii) sharing a common habitat/distribution area, (iii) representing largely a closed gene pool, and (iv) being regarded as distinct by their keepers/breeders". A particular community may claim to maintain a distinct AnGR population in a specific environment and subject to a common pattern of breeding and utilization. Characterization studies of these populations are needed which will serve as a mean to identify and register the distinct breeds possessing unique niche products. The process will facilitate in developing the inventory of farm animal breeds.

Characterization also aims at enhancing sustainable utilization while describing the broad set of breed's unique attributes beyond simple production traits, including aspects such as the quality of products, efficiency of resource utilization, adaptation to local agro-climatic conditions, and resistance to parasites and diseases. Characterization of a population should be done both at the phenotypic (phenotypic characterization) as well as molecular level (genetic characterization). Both are complementary to each other. To give population a breed status, phenotypic characterization is essential. However, genetic characterization can supplement or validate the phenotypic characterization.

Phenotypic Characterization

Phenotypic characterization of AnGR generally refers to the process of identifying distinct populations and describing their external and production characteristics within a given production environment.

The first step of identification and characterization of a population is the primary assessment or *baseline survey*, which should include identification of distinct populations using information on their geographic and ecological isolation, traditional nomenclatures (traditionally recognized populations), etc. and generating information on their qualitative and quantitative description, geographic and demographic distribution, native habitats and production systems including management practices and socio-economic profile, indigenous traditional knowledge etc. The process also includes studying its historical development, status, trends and the associated risks that a population is exposed to.

Preliminary information for a population can be gathered from different sources, like livestock census, literature, reports and direct interaction with individuals, community etc. Before, starting the phenotypic characterization, it should be sufficiently clear that population have homogenous features and seems to be distinct and found in sufficiently larger geographical area. Phenotypic resemblance; morphological, physiological and behavioral may be fundamental step to delineate a population for characterization.

Objectives of phenotypic characterization

- To identify new breeds
- To know the geographical distributions of the breeds
- To know status of breeds in terms of population, characteristics, etc. in native environments
- To document unique characteristics of the breed
- To identify elite animals to be used in improvement programmes
- To develop monitoring mechanism for conservation and sustainable use of the genetic resources.
- To create public awareness regarding the importance of AnGR
- To document animal genetic resources.

Constituents of phenotypic characterization

A phenotypic characterization excercise will involve collecting a number of different kinds of data, which includes:

- Demographical and geographical distribution of the population.
- Native environment
- Socio-economic status of the communities rearing those animals.
- Qualitative and quantitative characterization w.r.t. morphological traits, production potential and reproductive status etc.
- Management practices and utility
- Images of typical adult males and females, as well as herds or flocks in their typical production environments.
- Relevant indigenous knowledge (including gender-specific knowledge) of management strategies used by communities to utilize the genetic diversity in their livestock.

While most of these data elements can be collected directly during field work, valuable information may also be obtained from secondary sources in the published and unpublished literature. Most of the elements listed can be collected during primary characterization studies (single visits to field sites); others require advanced characterization studies (repeated measurements and observations). The latter group includes variables that describe economic performance traits (e.g. growth, milk production, egg production, wool production), adaptation (levels of resistance and tolerance to stressors) and trends (e.g. in population size and structure, and phenotypic performance). The data collected in a single visit can only provide indicative information on economically important quantitative traits. Repeated and more structured data collection is required for systematic characterization of such traits. Indicative data on average performance levels can be collected through one-time measurements, interviews with livestock keepers or from available records.

Survey for phenotypic characterization

Survey is a systematic exercise in data collection, processing and dissemination. It includes any structured activities used to obtain data and information on AnGR, their production environments, uses, management and the traits affecting them.

Rapid appraisal may be conducted before surveying for the breed, which involves interaction with livestock keepers and other stakeholders a little bit in informal way. Then *household surveys* should be conducted formally for collecting data from random sample of households chosen from among all households. The larger the samples, the more accurate the survey will be as estimator of the target population.

Survey should target key informants, who are an important source of information. They may be community leaders, personnel involved in veterinary services, NGOs, breeders organizations, breed societies, researchers working on animal production system.

Questionnaires for interviews: Structured questionnaires can be developed to capture data systematically through interviews. Interviews can be conducted with individuals or selected groups of individuals. Apart from livestock keepers, individual interviews may be conducted with government officials, service providers, livestock traders, community leaders or development/extension agents. Focus-group discussions can be held with livestock keepers, community representatives or other stakeholders.

Survey Plan: On the assumption that the breeding tract of a breed is spread over adjoining/contiguous districts in one or more states, stratified two stage sampling design would be adopted. Different zones within a district would be identified which would constitute the different strata. Villages within the stratum would constitute the first unit and houses within the village, the second unit. Totally, 3 districts and within each district *4 strata* would be randomly selected. From each stratum, *5 villages* would be randomly selected. First quarter, would be devoted to determining demographical and geographical distribution of the breeds. Subsequently, recording information on morphological characteristics, performance and utility traits would continue.

Demographical and Geographical Distribution

Complete enumeration of selected villages would be done for the purpose of deriving demographic distribution of the breed. This study would cover the following information:

- Agewise and sexwise distribution
- Group-wise enumeration
- Geographical distribution of the breed.

When the complete information is obtained by stratified survey, the groupwise, sexwise and breedwise total population in the breeding tract would be estimatedted by superimposing the proportion obtained through survey on the livestock census data.

Native Environments

The field work phase of a phenotypic characterization study is an opportunity both to directly collect data on the production environments of the targeted AnGR populations and to collect data on socio-economic profile of livestock keepers. This information can be related to datasets obtained from other sources like geographical distribution.

Breed Characterisation and Management Practices

Cattle and Buffalo**:** Information would be recorded on 3000 animals covering 3 districts of the breeding tract. In each district, 200 animals under each of the following group would be studied for aspects given against the group. Thus, there would be 1000 animals in a district, which would be randomly selected from 4 randomly selected zones. The group classification is given below:

Group	Study coverage
a. Calves (up to 1 year)	Physical traits, feeding, management practices and growth traits
b. Stock (1 - 3 years)	Physical traits, feeding, management practices and growth traits
c. Milking females	Physical traits and feeding and management practices, production, reproduction and growth traits.
d. Working males	Physical traits, and feeding and management practices, utility.
e. Breeding bulls	Physical and reproductive traits, and feeding and management practices.

Goat: Information would be recorded on *3000 animals* covering 3 districts of the breeding tract. In each district, 200 animals under each of the following groups would be studied for aspects given against the group. Thus, there would be *1000 animals in a district*, which would be randomly selected from 4 randomly selected zones. The group classification is given below:

Group	Study coverage
a. Kids (1-3 months)	Physical traits, feeding, management practices & growth traits.
b. Young Stock (6-12 months)	Physical traits, feeding, management practices, and growth traits
c. Yearlings	Physical and reproductive traits, and feeding management practices and growth traits.
d. Milking Does	Physical, productive and reproductive traits, feeding and management practices.
e. Stud Bucks	Physical and reproductive traits, and feeding and management practices.

Sheep: Information would be recorded on *3000 animals* covering 3 districts of the breeding tract. In each district, 250 animals under each of the following groups would be studied for aspects given against the group. Thus, there would be *1000 animals in a district* which would be randomly selected from 4 randomly selected zones. The group classification is given below:

Group	Study coverage
a. Lamb (1-3 months)	Physical traits, feeding, management practices & growth traits.
b. Young Stock (6-12 months)	Physical traits, feeding, management practices, and growth traits
c. Milking ewes	Physical, productive and reproductive traits, feeding and management practices.
d. Stud rams	Physical and reproductive traits, and feeding and management practices.

Equines: Information would be recorded on *1200 animals* covering 3 districts of the breeding tract. In each district, 100 animals under each of the following group would be studied for aspects given against the group. Thus, there would be *400 animals in a district*, which would be randomly selected from 4 randomly selected zones. The group classification is given below:

Group	Study coverage
a. Foal (up to 1 year)	Physical traits, feeding, management practices and growth traits.
b. Young stock (1 - 3 years)	Physical traits, feeding, management practices and growth traits.
c. Adult female (>3Year)	Physical traits and feeding and management practices, production, reproduction and growth traits.

d. Adult male (>3Year)	Physical traits, reproductive traits, and feeding and management practices, utility.

Camel: Information would be recorded on *1200 animals* covering 3 districts of the breeding tract. In each district, 100 animals under each of the following group would be studied for aspects given against the group. Thus, there would be *400 animals in a district*, which would be randomly selected from 4 randomly selected zones. The group classification is given below:

Group	Study coverage
a. Camel calves (up to 1 year)	Physical traits, feeding, management practices and growth traits.
b. Young stock (1 - 4 years)	Physical traits, feeding, management practices and growth traits.
c. Milking females	Physical traits, feeding and management practices, production, reproduction and growth traits.
d. Adult males	Physical traits, reproductive traits, and feeding and management practices, utility.

Pig: Information would be recorded on *3000 animals* covering 3 districts of the breeding tract. In each district, 250 animals under each of the following groups would be studied for aspects given against the group. Thus, there would be *1000 animals in a district* which would be randomly selected from 4 randomly selected zones. The group classification is given below:

Group	Study coverage
a. Piglets (0-2 months)	Physical traits, feeding, management practices & growth traits.
b. Young Stock (2-8 months)	Physical traits, feeding, management practices, and growth traits
c. Sows	Physical, productive and reproductive traits, feeding and management practices.
d. Boars	Physical and reproductive traits, and feeding and management practices.

Chicken: Information would be recorded on *3000 birds* covering 3 districts of the breeding tract. In each district, 250 birds under each of the following group would be studied for aspects given against the group. Thus, there would be *1000 birds in a district*, which would be randomly selected from 4 randomly selected zones. The group classification is given below:

Group	Study coverage
a. Cockerels (upto 5 months)	Physical traits, feeding, management practices and growth traits
b. Pullets (upto 5 months)	Physical traits, feeding, management practices and growth traits
c. Cock (above 5 months)	Physical and reproductive traits, feeding and management practices, growth traits
d. Hen (above 5 months)	Physical traits and feeding and management practices, utility, egg production traits, growth traits.

Genetic Characterisation

In the absence of information about the genetic attributes, development of local populations is often ignored in favour of the introduction of germplasm from exotic breeds, about which more information is generally available.Therefore, characterization of populations both at the level of phenotypes including their interaction with production systems and at the genetic level is most essential. Genetic characterization assesses the genetic constitution of a breed. It assesses the genetic uniformity, admixture or subdivisions, inbreeding, or introgression in the population. It is also helpful in providing insight into breed formation, informing about closest wild ancestral species and localization of the site of domestication. Further, these can be used in parentage testing.

So far, most molecular work was based on the use of neutral genetic marker data, which served as a proxy or estimate of the likelihood of important functional genetic variation within breeds or breed groups. The most frequently used markers in genetic diversity studies are the microsatellite markers. Dense marker panels of single nucleotide polymorphisms (SNP) are becoming available for most livestock species. In addition, whole genome sequencing has been completed or is under way for most major livestock species. These new tools are likely to substitute microsatellites in many applications. Models to link existing information on genetic diversity largely based on microsatellite markers to new information about to be generated with SNP markers may be needed.

Registration of Breeds

India is signatory to several international treaties like CBD, WTO, TRIPS, Interlaken Declaration on AnGR, etc. and is committed to

- protect the local animal genetic diversity
- provide recognition to the developers/breeders of animal breeds
- implement the *Global Plan of Action* on AnGR
- ensure that the livestock biodiversity is utilized to promote food security and remains available to future generations.

This can be achieved through a national documentation system of valuable sovereign genetic resources with well defined characteristics. Registration is nothing but a documentation of the knowledge, skills and techniques (KST) and, biological resources of local communities.

Recognising the need for an authentic national documentation system of valuable sovereign genetic resource with known characteristics, Indian Council of Agricultural Research (ICAR) initiated a mechanism for "Registration of Animal Germplasm" at National Bureau of Animal Genetic Resources (NBAGR), Karnal. This would empower India to

establish national sovereignty over genetic resources

control bio-piracy

claim ownership

conserve biodiversity

enhance value of AnGR

create a greater sense of pride among local communities over the knowledge they possess.

The registration of Indian livestock and poultry revolves around the concept of a breed. Populations of livestock and poultry, which are unique, stable and uniform, and has potential attributes of academic, scientific or commercial value can be registered as breeds. Any citizen of India / breed society registered as per constitution of India / NGO / Govt. agency can apply for registration of livestock and poultry breeds. All claims for registration should accompany scientific evidence for uniqueness, reproducibility and value of the material.

The applicant should submit 3 copies of the application to Director, ICAR-NBAGR, Karnal along with relevant documents, literature and photographs for the proper evaluation of the breed *(for details, please refer to guidelines for breed registration)*. The application must be signed by the applicant and countersigned by Director, Department of Animal Husbandry of the concerned state or his representative.

All breeds approved for registration are officially notified and published along with brief description in Indian Journal of Animal Sciences, NBAGR Newsletter, ICAR News, NBAGR Website and ICAR Website. Appeal for counter claim, if any, should reach the Breed Registration Committee within a period of three months of the publication of Notification.

3. INDIAN CATTLE –SOURCE OF SUSTAINABLE LIVELIHOOD SECURITY FOR SMALLHOLDERS

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Our countryhas its identity as rural India having about 70%itspopulation in villages and about 34% rural population is living below poverty line. Cattle rearing being supplementary to agriculture has been a part of social and cultural heritage of Indian civilization. Cattle have been the source of livelihood for landless and resource poor farmers, majority of them living below poverty line. Indigenous cattle have been instrumental in providing milk, milk products, draft power, bio-fertilizer and bio-fuel besides producing bio-molecules and other products beneficial for human health. The distribution of cattle amongst various categories of animal keepers revealed that marginal, small and semi-medium farmers on an average have about 89% of cattle. Majority of these smallholder farmers are below poverty line and livestock rearing including cattle has been the source of their livelihood, social and nutritional security. However,the innate production potential of cattle is not exploited to the fullest extent by these farmers due to lack of awareness about the improved resources, technologies and other inputs attributed to lower literacy of this stratum of the rural people.

Cattle Genetic Resources–Population Scenario and Dynamics

India possesses vast population of cattle (190.9 million), out of which 151.17 million are indigenous and 39.73 million crossbred/exotic cattle. Among the indigenous cattle, only 22.21 million heads (11.64%) have been described and categorized into 44different populations including 37 distinct/registered breeds.Majority of the Indian cattle breeds were initially developed for draft animal power. Indigenous cattle breeds are generally classified on the basis of their utility like milch breeds (Sahiwal, Red Sindhi, Gir and Rathi), draft breeds (Hallikar, Khillar, Nagauri, Kangayam, Red Kandhari etc.) and dual purpose breeds (Tharparkar, Hariana, Kankrej, Deoni, Ongole, Dangi, Kenkatha etc.). These unique breeds have been developed over a period of thousands of years through dedicated efforts of livestock keepers/pastoralists and other stake holders in different agro-climatic regions of the country (Table 1). Indian cattle appear to have many unique genes for higher thermo-tolerance, higher resistance to tropical diseases and better feed conversion efficiency under low or zero input system.However, majority of indigenous cattle are non-descript and low producers mainly attributed to the poor genetic make-up for milk production and inadequate availability of feed and fodder.

It is a matter of concern that the population of indigenous cattle over the years has declined, while the population of crossbred cattle has increased. The share of indigenous cattle to total cattle population has declined from 93% during 1992 to 79% during 2012. On the contrary the share of crossbred cattle has increased from meager 7% to 21% during the corresponding periods. The comparison of cattle population as per 19th Livestock Census (2012) with 18th Census (2007) revealed a decline of 4.1% in total cattle population. The decline in indigenous cattle population was -8.94%, while the exotic/crossbred cattle population increased by 20.2%. This is a matter of satisfaction that there was only slight decline (-0.01%) in indigenous female cattle population. The decline in indigenous males was -19.32% as compared to -12.75% decline in crossbred males (2007 versus 2012). As per 2012 census, out of 61.95 million males of indigenous cattle, 39.85 millions are used for draft work, 2.98 million used for both draft & breeding purpose and 2.08 million use for breeding only. This indicates that 44.91 million males (79.25%) have been used every year and about 17 indigenous males are still surplus in our country. Hence, the declining trend in male population of indigenous cattle should not be the matter of concern. Rather, efforts should be made to increase the population of female cattle by using sexed semen of indigenous bulls after perfecting the technique of semen sexing.

The distribution of indigenous female cattle under various categories of age revealed an increase of 7.83% in under one year of age category during 2012 versus 2007However, the decline in number of in milk indigenous cattle by 3.51% during the corresponding periods is a matter of concern and needs immediate necessary corrections. The number of dry cows during the corresponding periods has increased by 6.39%. Further, the significantly higher number of not calved once cows (6.03 million)constituting 10.88% of breedable population and 6.76% of total female population is a matter of worry, needs to be solved to enhance the milk production from indigenous cattle.

The distribution of indigenous cattle population over different states in India varies from 13948 heads in Sikkim to 18.76 million in Madya Pradesh. The second state having highest number of indigenous cattle (15.98 million) is UP followed by West Bengal, Maharashtra, Rajasthan, Odisha, Assam, Chattisgarh, Bihar and Jharkhand. Top 10 states having highest number of indigenous cattle possess 78.7% of total population of indigenous cattle (Table 2). As per 18th Livestock Census, there are about 22.2 million population of recognized indigenous breeds. Rajasthan tops all the states with a population of 5.29 million indigenous cattle, followed by Gujarat (4.29 million) and other states. First 10 states contribute 95.77% of total indigenous cattle population (Table 3). First three states of Rajasthan, Gujarat and Karnataka possess 13.48 million cattle, which constitutes 60.72% of total indigenous cattle population. The UP and MP has highest number of breeds (8 each), followed by Rajasthan and Bihar (7 each), Karnataka and TN (6 each), Odisha (5), Maharashtra (4), Gujarat and Haryana (3 each).

The comparison of breed-wise population in India reveals that Kankrej has highest population (38.8 lac) followed by Hariana (26.0 lac), Gir (21.3 lac), Rathi (9.2 lac), Tharparkar (5.6 lac), Red Sindhi (5.5 lac) and Sahiwal (4.6 lac). These 7 breeds constitute 50% of total recognized 37 indigenous breeds. Hariana breed has its spread in 11 states and 1 UT, followed by Sahiwal (8 states, 2 UT), Gir (6 states, 2 UT), Tharparkar and Red Sindhi (6 states each). On the contrary, Rathi was prominent only in Rajasthan.

Cattle Genetic Resources – Potential for Productivity

The distinct biodiversity of our cattle breeds have been diluted during last few decades due to use of only few improver breeds and neglect of the low producers. Besides this, crossbreeding of local cattle with exotic breeds has also contributed to the dilution of well-defined indigenous cattle breeds resulting in reduced herd sizes of these breeds at organized farms. Further, adoption of crossbreeding of native cattle with exotic breeds by farmers have also reduced the number of indigenous cattle under field conditions. It is obvious from the declining trend of indigenous cattle and ascending trend of crossbred cattle over the last two decades. This has attributed to lower milk production of only 2.37 kg/day of Indian cattle at the national level with a range of 0.76 kg/day (Meghalaya) to 6.52 kg/day (Panjab). Panjab is followed by Haryana (4.91 kg/day). This is due to availability of good breeds like Sahiwal and Hariana in these states and better management of indigenous cows. The indigenous cattle of Rajasthan and Gujarat are also having better milk production (3.54 & 3.85 kg/day) due to availability of good breeds like Gir, Kankrej, Rathi, Sahiwal and Tharparkar in these states. Other 4 states namely Bihar, J&K, TN and UP has per cow per day productivity higher than the national average (Table 4). Panjab and Haryana has only 0.24 and 0.54% of total cattle population as indigenous breeds.

The milk production scenario of the country from indigenous cattle indicates that UP was top producer followed by Rajasthan, MP, West Bengal, Bihar, Gujarat, Karnataka, Maharashtra, AP and Jharkhand (Table 5). Top 10 states contributed 22.49 million tonesof milkfrom indigenous cattle, which is 84.24% of total milk from indigenous cattle. First top 3 states contribution to indigenous cow milk pool was 41.82%. However, the ranking of top 10 milk producing states on the basis of milk yield/cow/day ranged from 3rd (Gujarat) to 18th (Maharashtra).

Though in majority of the states, Indian cattle breeds are draft in nature, yet a slight improvement in their productivity will considerably increase the total milk production of the country.Considering the importance of indigenous cattle, some of the breed improvement programs have been initiated to conserve and multiply these breeds. The associated herd progeny testing program has been going on at NDRI Karnal for the genetic improvement of Sahiwal cattle. All India Coordinated Research Project on Hariana and Ongole cattle has been undertaken at different centres by Project Directorate on Cattle, Meerut. Lately, three more breeds namely Sahiwal, Gir and Kankarej have been included in the indigenous breed improvement program (IBP) and different centres have been identified as germplasm units and data recording units for different breeds under the program.The conservation and genetic improvement of indigenous cattle has been undertaken partially under the National Project on Cattle and Buffalo Breeding by Ministry of Agriculture, Govt. of India. The National Project on Bovine Breeding and Dairy Development has been formulated with an integrated, holistic and scientific approach to improve and upgrade bovines for enhancing their production and productivity. A total of 31 cattle breeds and 7 buffalo breeds will be conserved and developed under this program. National Dairy Plan I (NDP-I) has been launched focusing on production of high genetic merit cattle through progeny testing and pedigree selection. Preservation and conservation of 6 indigenous breeds namely Gir, Sahiwal, Kankrej, Rathi, Tharparkar and Hariana is being undertaken under NDP-I. Recently, Govt. has taken initiative for the conservation and genetic improvement of the indigenous cattle under 'National Gokul Mission'. Under this Mission provision of rupees 500 crores has been made for improvement of indigenous cattle and dairy development. It is proposed to establish Gokul Grams in the outskirts of metropolitan cities under the program.

Indigenous Cattle –Production Performance

The breeding policy for improving the indigenous cattle is selective breeding in well-defined breeds and grading up of non-descript cattle with the indigenous breeds prevalent in the area or adjoining area. The performance of some important indigenous cattle breeds is given(Table 6).The perusal of the table indicated that the milk production of Indian cattle breeds ranged from low to medium and there is an ample scope to improve upon these breeds through selective breeding. However, some of the indigenous breeds like Sahiwal, Red Sindhi and Tharparkar in organized herds were almost as good as crossbred cattle under field conditions. The overall average 305-day lactation milk yield of elite Sahiwal cows was 2574 kg during 2010-11 at NDRI Karnal. Further, indigenous cattle are more economical in terms of cost of maintenance. This was attributed to lower feeding, management and veterinary costs in local breeds. However, the cost of milk production was lower in crossbred cattle as compared to indigenous cattle under intensive production system. Higher milk production in crossbred cattle was responsible for lower cost of milk production.

Fitness of Indigenous Cattle – An Edge over Crossbred Cattle

Indigenous cows have an edge over the crossbreds in terms of comparatively higher milk constituents, disease resistance and overall fitness. The incidences of reproductive disorders are generally higher in crossbred cows (Gandhi, 2014). Similarly, comparatively more young crossbred bulls are culled due to poor semen quality than Sahiwal young males (Gandhi, 2014). Rearing and maintaining crossbred cattle has been a costlier affair and needs lots of rich input resources. Further, there are many constraints of adopting crossbreeding under field conditions. The major constraints reported were repeat breeding, higher mortality in young calves, lower milk fat content, lower price of milk, higher cost of critical inputs and higher cost of veterinary services. Sustaining higher milk production due to non-availability of superior semen and higher incidence of health disorders in general and reproductive disorders in particular in crossbred cattle are other constraints for famers.

Chattels for Cattle Production:

- Vast indigenous cattle population with higher biodiversity (37 breeds) having innate potential to adapt to diverse changing climatic conditions of hot arid, humid tropical and temperate climates and better resistance to internal and external parasites and diseases.
- Diversified draft, milch and dual purpose cattle breeds contributing to milk and draft power besides providing bio-fuel and bio-fertilizer
- Massive rural population rearing cattle for livelihood security
- Higher demand and consumption of milk, milk products and other cattle by-products
- Higher innate potential to survive and produce on coarse, poor quality feed and fodder resources under zero input system (Acharya, 2011).

- Gigantic network of Research Institutes, State Agricultural/Animal Science/Veterinary Universities, State Animal Husbandry Departments, Livestock Development Boards and NGOs engaged in cattle development.
- Vast infrastructure in terms of 161 cattle farms, 4355 gaushalas, 54 semen production centres, 191 frozen semen banks, 77765 AI centres, 10217 veterinary hospitals/polyclinics, 22713 veterinary dispensaries and 24794 veterinary aid centres
- Availability of large amount of ITKs with cattle keepers/pastoralists for rearing and management of different species of livestock
- Seasonal migration of nomadic pastoralists to overcome adverse climatic conditions during summer, winter and rainy seasons to sustain and multiply the breed population of their choice.

Pragmatic Approach:

Keeping in view the reduction in number of animals of indigenous breeds due to crossbreeding at organized farms and under field conditions, there is need to increase the population size of well-defined breeds of cattle along with enhancing their productivity by generating and utilizing superior germplasm. Further, non-descript cattle has to be upgraded with these breeds to increase their milk production. The following action plan is suggested:

- Focus more on genetic up-gradation of indigenous/native cattle using superior semen from progeny tested/pedigree selected bulls and by expanding AI and natural service network to provide services at the farmers' doorstep. If 10% of non-descript indigenous cattle are graded up with milch breeds in a period of 5 years and assuming 4kg/cow/day milk production in next generation, additional 27.2 million kg milk/day would be produced adding about 10 million tons milk/annum to national average.
- National priority should be given to conservation of cattle to maintain genetic diversity of breeds and preserve those showing decline in numbers or facing extinction. Breeding policy for different breeds should be revised looking to their importance in present context of economic important traits. Breed association should be developed and strengthened for conservation of breeds.
- Creation/provision of national fund for conservation of cattle genetic resources.
- Allocate more funds for infrastructure development, cattle policy reforms and IPR issues.
- Provide economic advantage to cattle keepers for conservation and multiplication of endangered cattle breeds.
- Conduct breed-wise livestock census.
- Establish and/or strengthen nucleus farms in the breeding tract for each breed to produce genetically superior germplasm for genetic improvement and conservation. Declare all the cattle breeding farms as *in-situ* conservation and breeding centres.
- Effective use of more than 20 lac cows maintained in 4355 *gaushalas.*
- Registration of cattle keepers and identification of farmers having elite cattle of indigenous breeds
- Recognition of role model breeders for their contribution.
- Unravel the unique genes and bio-prospecting the special utility traits, biomolecules, products etc. of indigenous cattle for enhanced productivity using emerging biotechnological tools.
- Pasture development program with dual purpose of grass and seed production may be taken up to address the scarcity of fodder. Provision should be made for purchase of seed of pasture grasses at remunerative price by the farmers to establish pasture in dry areas on degraded land.

- Fodder depot in fodder deficient zones needs to be established along with infrastructure development for making compact feed blocks for effective storage for longer period ensuring fodder to livestock during scarcity. Production of hydroponic fodder needs to be encouraged for smallholder farmers.
- Effect of climate change on bovines has to be addressed judiciously. Suitable strategies and mitigation approaches should be developed by strengthening shelter, feed resources and disease surveillance and monitoring.
- Develop branded products from indigenous cattle and creation of niche markets for these products.
- Selection and use of bulls with A_2A_2 type beta-casein genes in cattle breeding programs.
- Producing more number of semen doses from bulls of indigenous breeds. According to an estimate to cover 40% population of 57 million breedable indigenous cows through AI, about 41 million semen doses per annum are required from indigenous bulls. For production of these semen doses about 6000 indigenous bulls of well-recognized breeds would be required. To cover remaining 60% population by natural service about 30000 superior bulls would be required.
- Enhance coverage of cattle population of the country through AI from 25 to 40% by 2030.
- Effective use of reproductive biotechnologies like ET, ONBS, Ovum Pick-up and IVF under farm and field conditions for multiplication of superior germplasm.
- Develop infrastructure for semen sexing of indigenous cattle breeds to save male wastage amounting to about rupees10000 crores annually.
- The disease diagnostic facilities needs to be further strengthened in various regions of the country. Besides this, cheap pen side diagnostic kits needs to be developed and vaccination schedule for various diseases needs to be followed religiously. Research on designing thermo-stable vaccines is an important key area and will help in effective delivery under field conditions.
- Food safety and quality enhancement of milk, milk products and other biomolecules has to be ensured.
- Evaluate the genetic potential of the animals and economic status of the livestock keepers for providing the necessary inputs for a sustainable program for higher milk production. The zero input production system (ZIP) for landless and small holders is suggested for rearing local non-descript cattle. The medium farmers having limited resources may follow the low input production system (LIP) rearing mostly cows of indigenous breeds/graded up cattle with indigenous breeds available in the area/ adjoining area. The intensive dairy production system i.e. high input production system (HIP) is advocated for the animal keepers having adequate input resources. Under this system rearing of high producing cattle is suggested (Acharya, 2011).
- Impart training and increase the number of awareness programs for smallholders especially women to ensure adoption of new technologies for enhancing productivity of cattle.
- Import elite semen of indigenous breeds from other countries having superior germplasm of indigenous breeds.
- Explore inter-country collaboration for breed improvement programs for indigenous cattle with neighboring countries.

Conclusions

India is endowed with large cattle population and cattle rearing has been source of livelihood security to farmers in the face of natural calamities. Smallholders have played a vital role in contribution to national economy as majority of cattle population is reared by them. The milk productivity of indigenous cattle needs to be enhanced using breeding, feeding and health management interventions. Further, mining of unique genes and bio-prospecting of special utility traits, biomolecules, products etc. of indigenous cattle would enhance the net economic worth of Indian cattle. Improving indigenous cattle and developing branded cow milk and other products using ITKs available with pastoralists & smallholders and creation of niche markets for these products would empower these stakeholders in general and rural women in particular to ensure livelihood security. Food safety and quality enhancement of milk and milk products has go a long way to narrow the gap between achieved and achievable. Conducting breed-wise livestock census, developing a roadmap for breeding & conservation of indigenous cattle and creation of national fund for conservation of cattle genetic resources should be given priority.

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Table 1 : Indigenous cattle breeds of various agro-climatic regions

Region	Agro-climatic Region	States	Breeds
I	Western Himalayan region	Himachal Pradesh, Jammu & Kashmir, Uttarakhand	Tarai, Kumauni
II	Eastern Himalayan region	Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim, Tripura, West Bengal	Siri, Tho-Tho
III	Lower Gangetic plain region	West Bengal	-
IV	Middle Gangetic plain region	Uttar Pradesh, Bihar	Bachaur, Purnea, Gangatiri
V	Upper Gangetic plain region	Uttar Pradesh	Ponwar, Kherigarh, Mewati

VI	Trans Gangetic plain region	Chandigarh, Delhi, Haryana, Punjab, Rajasthan	Sahiwal, Hariana, Rathi
VII	Eastern plateau and hills region	Chhattisgarh, Jharkhand, Madhya Pradesh, Maharashtra, Orissa, West Bengal	Gaolao, Motu, Ghumusari, Khariar, Binjharpuri, Kosali
VIII	Central plateau and hills region	Madhya Pradesh, Rajasthan, Uttar Pradesh	Mewati, Kenkatha, Gaolao
IX	Western plateau and hills region	Madhya Pradesh, Maharashtra	Malvi, Deoni, Dangi, Nimari, Red Kandhari, Krishna Valley, Khillari
X	Southern plateau and hills region	Andhra Pradesh, Karnataka, Tamil Nadu	Krishna Valley, Deoni, Khillari, Amritmahal, Hallikar, Ongole, Bargur, Kangayam, Punganur, Pulikulam
XI	East coast plains and hills region	Andhra Pradesh, Orissa, Puducherry, Tamil Nadu	Ongole, Umbalachery, Motu
XII	West coast plains and ghat region	Goa, Karnataka, Kerala, Maharashtra, Tamil Nadu	Amritmahal, Vechur, MalnadGidda, Khillari
XIII	Gujarat plains and hills region	Gujarat, Dadra & Nagar Haveli, Daman & Diu	Kankrej, Gir, Tharparkar
XIV	Western dry region	Rajasthan	Rathi, Nagori, Tharparkar, Kankrej
XV	Island region	Andaman & Nicobar Islands, Lakshdweep	-

(Source: NBAGR, Karnal)

Table 2 : Top ten States having higher cattle population (million)

Sl. No	**Exotic/crossbred**			**Indigenous**			**Total cattle**		
	State	**Number**	**% age**	**State**	**Number**	**% age**	**State**	**Number**	**% age**
1.	Tamil Nadu	6.35	15.98	M.P.	18.76	12.41	M.P.	19.60	10.27
2.	Maharashtra	3.65	9.19	U.P.	15.98	10.57	U.P.	19.56	10.25
3.	U.P.	3.58	9.01	W.B.	13.72	9.08	W.B.	16.51	8.65
4.	Bihar	3.48	8.76	Maharashtra	11.83	7.83	Maharashtra	15.48	8.11
5.	Karnataka	2.91	7.32	Rajasthan	11.59	7.67	Rajasthan	13.32	6.98

6.	W.B.	2.80	7.05	Odisha	10.31	6.82	Bihar	12.23	6.41
7.	A.P.	2.40	6.04	Assam	9.91	6.56	Odisha	11.62	6.09
8.	Punjab	2.06	5.18		9.64	6.38	Assam	10.31	5.40
9.	Gujarat	1.93	4.86	Bihar	8.76	5.79	Gujarat	9.98	5.23
10.	Rajasthan	1.74	4.37	Jharkhand	8.47	5.60		9.81	5.14
Total		30.90	77.77		118.97	78.70		138.42	72.51

Table 3 : Top 10 States having highest number of recognized indigenous cattle breeds

State	Population (million)	Ranking	Breeds
Rajasthan	5.29	1	Gir, Hariana, Kankrej, Malvi, Nagori, Rathi, Tharparkar
Gujarat	4.29	2	Dangi, Gir, Kankrej
Karnataka	3.90	3	Amritmahal, Deoni, Hallikar, Khilari, Krishna Valley, MalnadGidda
Uttar Pradesh	1.62	4	Gangahri, Hariana, Kenkatha, Kherigarh, Mewati, Ponwar, Sahiwal, Tharparkar
Odisha	1.34	5	Binjharpuri, Ghumusari, Hariana, Mottu, Red Sindhi
Madhya Pradesh	1.24	6	Gaolao, Gir, Hariana, Kenkatha, Malvi, Nimari, Sahiwal, Tarai
Maharashtra	1.23	7	Dangi, Gir, Khillari, Red Kandhari
Bihar	0.96	8	Bachaur, Gaolao, Hariana, Purnea, Red Sindhi, Sahiwal, Tharparkar
Tamil Nadu	0.72	9	Alambadi, Bargur, Jellicut, Kangayam, Manapari, Umbla Cherry
Haryana	0.67	10	Hariana, Sahiwal, Tharparkar
Total	21.26		

Table 4 : Top 10 States having highest milk yield/day from indigenous cattle (2011-12)

State	Milk Yield/cow/ day (kg)	Rank	Number of indigenous cattle (million)	% of State cattle population
Punjab	6.52	1	0.363	0.24
Haryana	4.91	2	0.812	0.54
Gujarat	3.85	3	8.06	5.33
Rajasthan	3.54	4	11.59	7.67
Bihar	2.86	5	8.76	5.79
Jammu & Kashmir	2.60	6	1.33	0.88
Tamil Nadu	2.58	7	2.46	1.63
Uttar Pradesh	2.57	8	15.98	10.57

Karnataka	2.30	9	6.60	4.37
Madhya Pradesh	2.15	10	18.76	12.41

Table 5: Top 10 milk producing States from indigenous cattle during 2011-12

State	Rank	Milk Production (mt)	In milk population (million)	Milk Yield/cow/day (kg)
Uttar Pradesh	1	4.104	4.369	2.57
Rajasthan	2	3.983	3.070	3.54
Madhya Pradesh	3	3.077	3.920	2.15
West Bengal	4	2.282	3.300	1.89
Bihar	5	2.246	2.143	2.86
Gujarat	6	2.059	1.463	3.85
Karnataka	7	1.369	1.625	2.30
Maharashtra	8	1.277	1.980	1.76
Andhra Pradesh	9	1.196	1.690	1.93
Jharkhand	10	0.894	1.376	1.77
Total		22.487	24.936	

Table 6. Average performance of indigenous cattle under organized herds

Breeds\ Traits	Age at First Calving (Mo)	First Lactation Total Milk Yield (kg)	First Lactation Length (days)	First Calving Interval (days)	Reference
Sahiwal	36.6	1942	295	430	Raja (2010)
Red Sindhi	44.1	1864	306	422	Gupta (1992)
Gir	51.0	1414	336	506	Joshi et al (2005)
Kankrej	53.2	1731	301	488	Shamlal (1989)
Rathi	47.0	1494	388	567	Joshi et al (2005)
Tharparkar	38.8	1823	321	437	Pirzada (2012)
Hariana	52.2	839	277	528	Joshi et al (2005)
Ongole	50.2	584	220	543	Joshi et al (2005)
Deoni	46.4	940	299	466	Joshi et al (2005)
Malvi	49.2	910	270	465	Joshi et al (2005)

4. GENETIC IMPROVEMENT OF CATTLE GENETIC RESOURCES OF INDIA: ISSUES AND CHALLENGES

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Introduction

India is bestowed with a rich cattle genetic diversity composed of 37 recognized breeds classified according to their utility as milch (4), dual (8) and draft (25).Majority of these cattle breeds have been evolved through natural selection and were mainly used for agricultural and draft purposes. So they have low genetic potential for milk production but are known for heat tolerance, disease resistance, hardiness, ability to survive under harsh climatic conditions and utilization of low quality roughages. These breeds constitute only 20-25 per cent of the total indigenouscattle population while the rest are classified as non-descript. The crossbreeding programme implemented in the past have resulted in dilution of the distinct biodiversity of our indigenous cattle breeds and majority are in the verge of extinction.

Cattle breeds of India: The cattle breeds classified based on their utility are listed in table -1. The best breeds are generally found in the drier parts of India, such as in Punjab, Haryana, Rajasthan, Gujarat and parts of Maharashtra and Karnataka while in most of the warmer and humid parts, such as in Assam, West Bengal, Orissa, Bihar, Tamil Nadu and Kerala, the animals are non-descript, of inferior quality and poor milk producers (Chakravarti, 1985). It is also reported that the cattle from drier regions are well built and those from heavy rainfall areas, coastal and hilly regions are of smaller build. The highest number of draught breeds (25) clearly indicates that the primary thrust in cattle had been on draught and might be the reason for the very few dairy breeds (4) with comparatively lower milk yield. But due to the changes in the agricultural and food pattern of the country, the utility of cattle has changed from non-food functions such as draught and dung to food functions especially milk production which led to the implementation of crossbreeding of indigenous cattle with high yielding exotic cattle.

Table-1 Classification of cattle breeds of India

Dairy breeds	Draught Breeds		Dual purpose breeds
1. Gir	1. AmritMahal	13. Kosali	1. Deoni
2. Rathi	2. Bachur	14. Krishna Valley	2. Gaolao
3. Red Sindhi	3. Bargur	15. Malanadgidda	3. Hariana
4. Sahiwal	4. Binjharpuri	16. Motu	4. Kankrej
	5. Dangi	17. Nagori	5. Malvi
	6. Ghumusari	18. Nimari	6. Mewati
	7. Hallikar	19. Ponwar	7. Ongole
	8. Kangayam	20. Pulikulam	8. Tharparkar
	9. Kenkatha	21. Punganur	
	10 Khariar	22. Red Kandhari	
	11. Kherigarh	23. Siri	
	12. Khillar	24. Umblachery	
	13. Kosali	25. Vechur	

Cattle production system in India: The cattle rearing in India is rural based small holding mixed farming system. Cattle have been maintained mainly for three purposes viz., draught power in agricultural operations, milk production for household consumption and dung as manure and fuel in that sequence. Generally dairying was considered as subsidiary to agriculture and not as a core enterprise. Due to no organized breeding and selection, the indigenous cattle were smaller in size, very low in milk production but resistant to various tropical diseases and well-adjusted to the adverse tropical climatic conditions (Mathur, 2000). The average herd size is very small with one or two cows per household which are mainly fed on grazing in the available agricultural/ barren land or the agricultural by-products. The male animals were mainly used for draft purposes in the agricultural field and selectively for breeding. Since the females were raised for multipurpose and not for milk production alone, most of the Indian cattle are poor milk producers, but efficient convertors of the low quality feed into milk and manure.

Cattle population: According to the 19th livestock census, India owns the largest cattle population of 190.904 million which contributes 37.28 per cent of the national livestock population and 13 per cent of world cattle population. The overall cattle population of the country increased from 185.18 million to 199.08 million (7.5%) during 2002 to 2007 but decreased by 4.10% during 2007-2012 (from 199.08 million to 190.90 million). This entire decrease in cattle population was due to decrease in the male population by 15.70 million (0.87 crossbred and 14.83 million indigenous cattle). In fact there was a net gain of 7.54 million heads in the female cattle population. An overall significant increase (24.69 million to 33.06 million) of 33.9 per cent was observed in the exotic/ crossbred population during 2002-2007 and 20.18% (33.06 million to 39.73 million) during 2007-2012 (Table-2).

Table-2.Population status of cattle during the year 2012

Category	Male	Female				
		In milk	Dry	Milch animals (In milk + Dry)	Total females	Total
Crossbred	**5972**	**14304**	**5115**	**19420**	**33759**	**39731**
Indigenous/ non-descript	**61949**	**29650**	**18475**	**48124**	**89224**	**151173**
Total	**67921**	**43954**	**23590**	**67544**	**122983**	**190904**

Milk production: India is the largest producer of milk and in 2012-13 the national milk production was estimated as 132.43 MT which accounted for 17 per cent of the world production. The national average annual growth rate of milk is 3.54 per cent against the world average of 2.2 per cent which shows the sustained growth in availability of milk and milk products for the growing population. India rank second in cow milk production next to USA and contributes around 45 per cent of the total milk production of the country. The overall average milk production of cattle (3.87 kg/day) is lower than buffaloes (4.80 kg/day) because of the larger population of low producing non-descript cattle (2.36 kg/day) and the lower number of high producing crossbred cattle (7.02 kg/day). The increasing human population demands to increase the milk productivity of the country at the rate of four per cent per year and is expected to produce 186.20 (Per capita availability 309gm/day) / 400 (Per capita 676.5gm/day) million tonnes of milk to meet the demand of an expected population of 1.62 billion in 2050. The cattle can contribute significantly to meet this demand as the scope for genetic improvement is more due to the availability of wide unexplored genetic variation among the cattle breeds, large population of non-descript cattle for up gradation and possibility of introduction of new superior germplasm.

National cattle breeding policy

The cattle breeding policy of the country can be summarized in nutshell as follows:

1. Genetic improvement of important indigenous breeds of cattle, for milk, draught and dual purposed through selective breeding in their home tract.
2. Upgrading of low producing non-descript cattle with acknowledged milch breeds of the country.
3. Crossing or upgrading of low producing non-descript cattle with exotic dairy breeds viz., Jersey and Holstein Friesian in areas having better feed and health facilities.
4. Jersey breed can be used in hilly region and Holstein Friesian breed should be used in plain region
5. The level of exotic inheritance should be restricted to 50 per cent
6. *Inter se* breeding among crossbred cattle using pedigreed or proven bulls.

Major issues and challenges in implementing the genetic improvement programmes

1. Genetic up-gradation of large population of non-descript cattle to recognized breeds

According to the 19th national livestock census, the indigenous/non-descript cattle constitute nearly 79.19 per cent of the total cattle population (190.904 million) of the country. Majority of the cattle are genetically inferior low producing non-descript animals with an average daily milk yield of 2.36 kg. The average annual milk yield of Indian cattle (including crossbreds) is 1172 kg which is only about 50 per cent of the global average.Nearly 97.17 per cent indigenous/non-descript cattle are maintained by the rural farmers. The genetic improvement of these non-descript cattle will be a difficult task as up gradation with tropical cattle breeds may be irrelevant under the small holding system of rural farmers having limited resources to maintain a high yielding crossbred cattle. Hence steps are needed to be taken to upgrade them with the indigenous cattle breeds relevant to the region and utility. The availability of Indigenous male germplasm is also another limiting factor which needs to be addressed seriously.

2. Establishment and strengthening of bull mother units for major breeds

The cattle genetic resource of the country is vast and divergent but majority of the breeds are under the threat of extinction. It is well-known that the distinct biodiversity of our indigenous cattle breeds has been diluted due to changing breeding policies, adoption of a fewer improved imported breeds and indiscriminate use of exotic semen even in violation of State breeding policies.Presently, the availability of genetically proven bulls of these indigenous breeds is limited which hinder the implementation of genetic improvement programmes for increasing the milk production. As per the 19th national livestock census, the indigenous/ non-descript female population is 89.224 million. The number of breedable males required to breed the female cattle population is calculated with the following assumptions: In Indigenous cattle during this decade 30 percent females will be covered under AI and the rest will be bred by natural breeding and the AI coverage will be increased by 10 per cent per decade; non-descript population will be reduced at the rate of 10 per cent per decade;the rest of the assumptions are similar to that of the crossbred cattle. The number of bulls required for AI and natural service are given in Table-. Based on this strategy by 2050, 820 and 50177 bulls may be required to carry out the required AI (70%) and natural service (30%), respectively (Table=3).

In order to cater the demand of superior indigenous male germplasm, it is necessary to establish the network of the farmers and organized herds maintaining the indigenous animals. To breed the larger population of the non-descript / indigenous or crossbred cattle, the male calves born to elite female and proven bulls of different breeds of indigenous or exotic origin need to be reared and progeny tested using the farmers herds along with the organized herds.The bull mother farms and bull rearing units or MOET Nucleus herds of elite cows of different breeds need to be established and strengthened to cater the future need of the country. The existing bull mother units are to be strengthened by procuring the male calves born to high yielding females.

Table-3 Number of bulls required to breed the indigenous/ non-descript female population

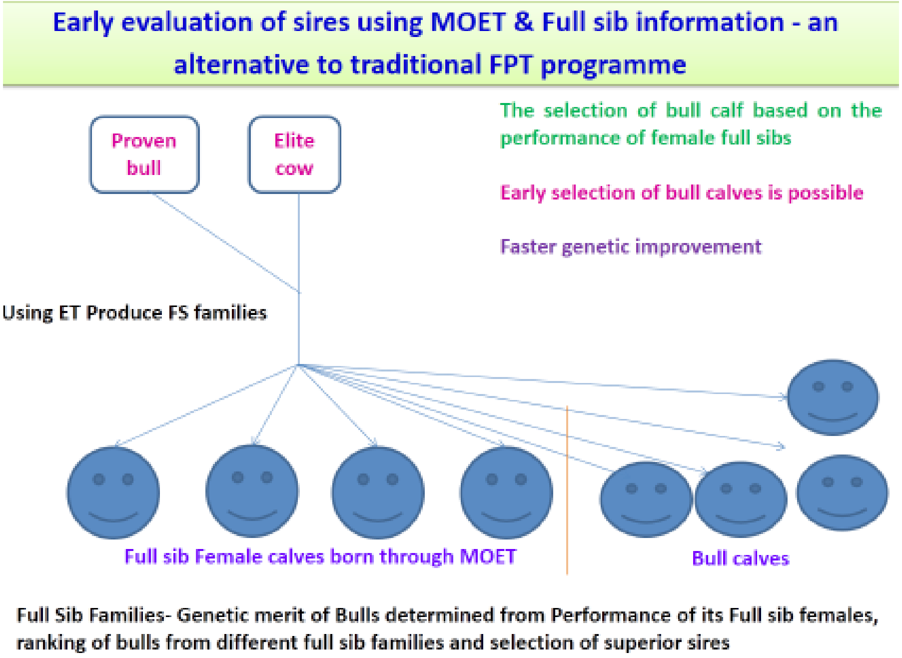
Year	Breedable female	% of breedable female covered with AI	Number of AI per	Frozen semen doses required (Million)	Bull requirement for semen production	Bull requirement for natural service	No. of sperm/ dose (Million)
Indigenous cattle							
Present	89.224	30	2.5	66.92	669	178500	20
2020	80.3016	40	2.0	64.24	642	137660	15
2030	72.27144	50	2.0	72.27	723	103245	10
2040	65.044296	60	2.0	78.05	781	74336	10
2050	58.539866	70	2.0	81.95	820	50177	10

3 Increasing the AI coverage

Even though, the country has the largest A.I. infrastructure facility, it covers only 25-27 per cent of the national bovine population and the rest are bred by natural mating which leads to indiscriminate breeding. The unavailability of proven male germplasm, lack of expertized technical man power, poor conception rate following AI, improper implementation of the recommended breeding policies, etc. are some of the reasons attributed for the poor coverage. Semen Production in the country has increased from 22 million straws (1999-2000) to 63 million straws (2010-2011) and the number of inseminations has increased from 20 million to 50.08 million. In order to increase the AI coverage from the present level of 25-27 per cent to 70 per cent the National Programme for Cattle and Buffalo Breeding (NPCBB) need to be strengthened and all the farmer herds are to be included under the genetic improvement programmes. The production of proven breeding bulls needs to be accelerated so as to provide the expected required number of nearly 51000 indigenous bulls by 2050.

4. Early evaluation of sires using MOET and full sib information as an alternative to field progeny testing programme

In traditional breed improvement programme the bulls are evaluated based on average performance of their daughters raised under field conditions. The small herd size, unavailability of required number of daughters, increased generation interval, poor performance recording, non-cooperation of farmers etc., are some of the major constraints in the field progeny testing (FPT) programme. The rate of genetic improvement obtained in FPT programme is also very low (0.5 to 1 per cent). To overcome these difficulties the MOET and full sib information model can be used as an alternative to the FPT programme. Here the MOET technique is used to produce full sib males and females and the males are selected based on the performance of full sib sisters as shown below:



5. Genetic improvement of indigenous breeds employing phenomics (precise performance recording), Genomics (Assessing genomic values for economic traits) and bioinformatics

The term phenomics is an area of biology which deals with the measurement of phenotypes namely the physical and functional traits of an individual or living organism. The term genomics refers to the study of gene and their functions with an aim to understand the structure of genome, and functions of genes and their role in the expression of a character and the genomic selection refers to selection decisions based on genomic breeding values

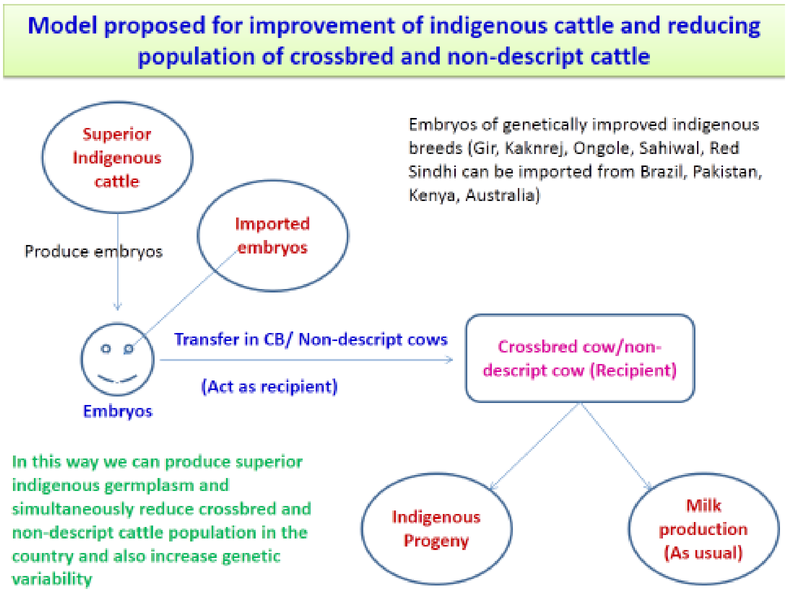
(GEBV) which are calculated as the sum of the effects of dense genetic markers, or haplotypes of these markers, across the entire genome, there by potentially capturing all the quantitative trait loci (QTL) that contribute to variation in a trait. The bioinformatics is the interdisciplinary field that develops methods and software tools for understanding the biological data. The advances in these genetic technologies will help to associate the genotype of an animal with the phenotype or trait of interest which will help in improving the cattle production to cope up with the current and future challenges. If we can able to integrate the phenomics with genomic approaches successfully and apply the appropriate bioinformatics tools to explore the significant association, we can able to improve the cattle milk production to a great extent.

6. Progressive increase of high producing indigenous cattle at the cost of crossbreds

The famous indigenous milch cattle breeds of our country viz., Gir, Sahiwal, Red Sindhi, Rathi are well adopted to the tropical climatic conditions and can thrive under the harsh climatic conditions, convert low quality feed and fodder into milk efficiently, resistant to various tropical diseases and are also known for their milk production and are to be propagated to a larger extent through selective breeding and up gradation of non-descript cattle using these defined indigenous breeds. The indigenous cattle available with the farmers, Government farms, NGOs and Gaushalas will be registered and the superior male and females will be selected based on their pedigree and bull calves will be produced to increase their population and milk production. As the indigenous cattle breeds may be economical than crossbreds under small holding systems, the indigenous cattle population may be increased by replacing the crossbred population at the rate of 25 per cent per decade as per the following model proposed. Embryos will be produced from the indigenous cattle and also imported from other countries and implanted in the crossbred cattle so as to produce indigenous calves and also to get higher milk yield from crossbred cattle.

7. Multiplication of high producing animals using emerging reproductive biotechnologies (MOET, IVM, IVF, cloning, commercial embryo production & transfer)

Genetic improvement of cattle requires the application of modern reproductive biotechnologies viz., multiple ovulation and embryo transfer MOET, IVF, IVM, cloning, commercial embryo production and transfer etc. These techniques will help for the faster multiplication of the superior female cattle germplasm. The cloning, a novel technique will also help to produce more number of genetically identical individuals. The practical application of these techniques on economically viable basis will definitely improve the reproductive efficiency of the cattle there by increase the milk production. These techniques can also be useful to conserve and propagate the endangered cattle breeds of our country.


Model proposed for improvement of indigenous cattle and reducing population of crossbred and non-descript cattle

Embryos of genetically improved indigenous breeds (Gir, Kaknrej, Ongole, Sahiwal, Red Sindhi can be imported from Brazil, Pakistan, Kenya, Australia)

In this way we can produce superior indigenous germplasm and simultaneously reduce crossbred and non-descript cattle population in the country and also increase genetic variability

8. Development of Sexed semen technology and its application for producing desired sex

In dairy farming female calves are more attractive than the male calves and this will help in production of replacement daughters from genetically superior bulls and also to get more daughters performance record for progeny testing. It will also increase the number of female cattle in milking which will in turn increase the milk production. Producing male calves is also required in bull mother farms to get the required number of proven bulls for breeding. Van Vleck (1981) estimated that the rate of genetic progress could increase by 15 per cent if sexed semen is widely available.

Morruzi in 1979 established that in most mammals, the Y chromosome contained slightly lower percentage of DNA than the X chromosome, thus, DNA might be a factor for separating X- and Y- sperm. During the same decade cell sorting equipment was developed and with limited success the sperm cells were separated. Later the technique was refined and the flow cytometry method helped to a larger extent and since then more than 20,000 calves have been born successfully with this technology. By this method the sperm cells can be separated in to male and female populations and according to the need of the stakeholders the sexed semen can be supplied. Internationally sexed semen is used more in cattle species than any other species. However, the technique is not common in our country due to the lack of expertise and cost involved. Hence research has to be undertaken to develop an accurate, effective, easy, non-invasive and cost effective method of sexing of cattle sperm for large scale production at lower price.

9. Genetic alteration of animals for obtaining tailor made milk of therapeutic use

The milk of indigenous animals has certain medicinal properties which can be exploited by genetic engineering so that more quantity can be produced from the cattle. It is reported that the milk containing beta casein A_2 genetic variant is associated with lower incidence of cardiovascular diseases and type-1 diabetes and also reduces the symptoms of autism and schizophrenia. As the frequency of A_2 is more in indigenous cattle, the production of more A_2 milk can also be explored. Alpha-lactalbumin, fibrinogen collagen I & II, lactoferrin and human serum albumin are some of the `drug/proteins which are under development for extraction from cattle. The genomic techniques can also be used to identify genetic markers associated with the production of functional milk which will help to develop non-transgenic herd for functional milk.

10. Management of fertility, reproduction and health of cattle for higher productivity

The reproductive efficiency of cattle in our country is suboptimal. The increased age at puberty, first calving, service period, calving interval, dry period etc. causes decrease in the efficiency which in turn decreases the milk production. It is estimated that if dry period is increased by one month the total milk production in the country will be declined by 11.25 Million Tonnes (As 75 million animals are in milk). It is also estimated that the problems in breeding and reproduction causes 21 per cent loss in milk production of the country. The higher incidence of reproductive problems viz., repeats breeding, anestrus, infertility etc., affects the efficiency and many intrinsic and extrinsic factors are associated with it. Hence efforts are needed to increase the reproductive efficiency of cattle through optimizing the health, nutritional and genetic selection.

11. Meeting the nutritional requirement of high producing indigenous cattle population

The large livestock population of our country demands higher quantity of feed and fodder for animal feeding and thisrequirement is ever increasing contrary to the decrease in their production. The major constraints are the reduced availability of crop residue as fodder, shrinkage of land area under fodder cultivation (only 4 per cent area), competition with the increasing human population forgrains, poor nutritive value of the feed and fodder etc. Presently the country is short of 35 per cent green fodder, 10 per cent dry fodder and 28 per cent concentrate. Understanding the nutritional requirement of high yielding dairy cows at various stages of lactation and feeding them with the various available feed ingredients at a cost effective manner will improve the production performance of the cattle. Increasing the feed efficiency, reducing the feed cost, formulation of balanced feed with locally available quality feed and fodder, development of total mixed ration, understanding the causes and variation of milk protein and fat in dairy cattle, role of rumen in increasing the feed efficiency, mineral and vitamin supplementation etc. are some of the points require immediate attention. Breed specific feeding standards are to be developed for increasing the feed efficiency of the cattle.

12. Genetic improvement of draught animal power

Cattle have been used in Indian agriculture for thousands of years supplying energy for crop production in terms of draught power and organic manure. Animal draught power was the first supplement to human energy inputs in agriculture. The use of animal power is unavoidable in slushy and water logged, hilly and narrow terraced fields where tractors and tillers are not suitable. Animal drawn vehicle are suitable for rural areas under certain circumstances viz, uneven terrain, small loads for small distances where travel time is not important. Inspite of high urge for mechanization among farmers, the energy for ploughing two-thirds of the cultivated area and two-thirds of rural transport are coming from animals in India (GOI, 2008). So the role of animal traction is still proved to be vital for food security and economy of small holder farming systems in India. Due to the changes in the agricultural and food pattern of the country, the utility of cattle has changed from non-food functions such as draught and dung to food functions especially milk production the draught cattle breeds lost their importance.

A sharp decline in the population of work animals happened between 1972 and 1980, even though there was an increasing tendency between 1982 and 1992. But the trend again reversed in the following years and during the last 10 years, the trend is only declining but at a lower rate (Table-4).

Table-4.Population trend of working cattle bullocks from 1972 to 2007

	1972	1982	1987	1992	1997	2003	2007
Cattle	73.2	61.1	63.6	70.3	55.8	54.3	53.3

Source: Livestock census 1972, 1982, 1987, 1992, 1997, 2003 and 2007

The contribution of animal power to the total power availability to the agriculture in 1971,1981 and 1991 were compared presented in Table=5. From the table, it is clear that per cent contribution by draught animals is significantly reduced from 61 to 23 between 1971 and 1991. But it is also to be noted that absolute contribution almost remained unchanged through these years, indicating the continued role of draught animals in Indian agriculture.

Table 5.Contribution of draught animal power to the Agriculture in comparison to human and machines

Source of power	**1971**		**1981**		**1991**	
	Power (mw)	**% in total**	**Power (mw)**	**% in total**	**Power (mw)**	**% in total**
Human	8385	18.7	10951	12.4	12906	10.1
Draught animals	30426	60.5	31556	35.8	29840	23.3
Machines	10487	20.8	45699	51.8	85226	66.6

Source: Adapted from the Report of the Steering Group on National Livestock Policy perspective, 1996, Department of Animal Husbandry, Ministry of Agriculture, Govt. of India

The draught performance of the cattle can be increased by undertaking research in areas such as studies on physiological, hematological and biochemical parameters, genetic improvement of draught performance, improvement in design of equipment, instrumentation for draught animal power research etc.

Conclusion

The dairy cattle production in India is rural based mixed farming system and majority of the cattle are genetically inferior non-descript cattle. The non-descript cattle can be upgraded by using the famous indigenous cattle breeds for their genetic improvement depending on the regional and economical interest and selective breeding is recommended for defined indigenous cattle. The availability of a larger population of non-descript cattle, unavailability of breeding bulls, poor coverage of A.I. to the cattle population of the country, erosion of the indigenous breeds due to indiscriminate crossbreeding, shrinkage of agricultural land, shortage of feed and fodder resources, unavailability of sexed semen technology, application of modern biotechnological techniques, effective utilization of draught animal power etc. are some of the issues and challenges need to be addressed for the genetic improvement of indigenous cattle. It is also recommended to use the MOET based full sib information for selection of bulls as an alternative to the FPT programme. It is also proposed to increase the indigenous cattle population at the cost of crossbred cattle.

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5. STATUS OF CAMEL GENETIC RESOURCES OF INDIA, CONSERVATION AND BREEDING POLICY FOR THEIR IMPROVEMENT

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The dwindling camel population in the country is a matter of major concern for the conservation biologist, policy makers and the state governments. The population of camel in India is 4 lakhs and it has gone down by 22.55% during the year 2007 to 2012 (Livestock Census 2012). India has four major breeds viz. Bikaneri, Jaisalmeri, Kachchhi and Mewari. The camels of Bikaneri breed are heavily built and are attractive with a noble look. It is a multipurpose breed. Jaisalmeri camels are gracious, lightly built and well known for riding and race potential.The Kachchhi breed is a multipurpose breed and the females are good milk producers.Mewari camels are stouter and well adapted to travel and carry loads across hills. They are exclusively used for milk production.The population of Bikaneri, Jaisalmeri, Kachchhi and Mewari camels in the respective breeding tract has been estimated to be 236367, 85512, 23338 and 6820 heads (Livestock Census 2012). The population of double humped camel has been reported to be 146 (Livestock Census 2007). The breed-wise population will settle at even smaller number if the camels breeds in the country are considered as eight viz. Bikaneri, Jaisalmeri, Kachchhi, Mewari, Jalori, Malvi, Marwadi and Mewatias per National Bureau of Animal Genetic Resources (NBAGR), Karnal or Bikaneri, Jaisalmeri, Kachchhi, Marwari / Sanchori, Mewadi/ Mewati, Sindhi, Shekhawati and Riverine as per the recommendations of National Commission of Agriculture (1976). Recently, Kharai (Sindhi) breed has been registered by NBAGR, Karnal as the ninth breed of camel in India.

Population Dynamics

Irrespective of the breeds of the camel, the population of the camel in the country is declining at a very fast rate(Table 1). The livestock census figures reveals that the camel population in the country was 0.61 m in the year 1951 and it continued growing till it reached it's ever time highest figure of 1.10 m in year 1972. However, the camel population in the country remained close to 1 million during for a period of about 25 years during 1966 to 1992. Since then the population has reduced by about 61% and the current population is 0.40 m (Livestock Census 20012).

Table 1. Camel population and growth trend in India

Year	Population ((in million)	**Growth (%)**
1951	0.60	29.6
1956	0.80	11.9
1961	0.90	10.65
1966	1.00	9.60
1972	1.10	0.00
1977	1.10	0.00
1982	1.08	-1.85
1987	1.00	-7.65
1992	1.03	2.95
1997	0.91	-11.65
2003	0.64	-29.65
2007	0.51	-18.25
2012	0.40	-22.55

The analysis of state-wise population of camels during the year 2007 and 2012 is very interesting and it reflects the current trend in camel husbandry that is prevailing in the country (Table 2). There are eleven states showing a decline in camel population during the year 2007 to 2012 but there are sixteen states showing an increase in the camel population during the same period i.e. 2007 to 2012 (Table 3). Similarly in the year 2007, there were 17 states in which the camel population was zero, the same has now reduced to 11. Reduced utility, mechanization and lifestyle are the chief reasons for the decline of camel population but increase in the population of camel and spread of camel population from 18 to 24 states and union territories of the country is intriguing. The increase in the number of camels in single digit such as in Goa, Jharkhand, Kerala and Meghalaya may be due to tourism or any other transient activity but the increase in two, three and four digits signifies alternate utility of the species. States viz. Nagaland, West Bengal, Chhattisgarh, Assam, Odisha, Delhi, Tamil Nadu, Arunachal Pradesh and Himachal Pradesh were having less than 128 camels in the state in the year 2007 but they now (2012) have camels in the range of 19-835. The increase in the number camels in the state of Bihar is highly significant. The number has increased from 215 to 8859 during this period.

Table 2: Livestock Census 2007 VS. 2012: States and Union Territories showing reduction in camel population

S. No.	States	2007	2012	Reduction (%)
1.	Rajasthan	421836	325713	-22.79
2.	Haryana	38608	18845	-51.19
3.	Gujarat	38454	30415	-20.91
4.	Punjab	2183	693	-68.25
5.	Madhya Pradesh	4456	3422	-23.2
6.	Uttar Pradesh	8959	7935	-11.43
7.	Jammu & Kashmir	1583	925	-41.57
8.	Karnataka	201	151	-24.88
9.	Chandigarh	5	0	-100
10.	Daman & Diu	1	0	-100
11.	Uttarakhand	1	0	-100
	India	516828	400274	-22.55

Table 3: Livestock Census 2007 VS. 2012: States and Union Territories showing increase in camel population

S. No.	States	2007	2012	Increase (%)
1.	Goa	0	1	100
2.	Jharkhand	0	3	100
3.	Kerala	0	6	100
4.	Meghalaya	0	7	100
9.	Nagaland	0	92	100
12.	West Bengal	0	267	100
13.	Chhattisgarh	0	645	100
14.	Assam	0	726	100
15.	Odisha	0	835	100
11.	NCT of Delhi	3	157	5133
5.	Tamil Nadu	7	19	171
7.	Arunachal Pradesh	11	45	309

10.	Himachal Pradesh	56	177	216
6.	Andhra Pradesh	121	154	27
8.	Maharashtra	128	182	42
16.	Bihar	215	8859	4020

The increase in the number of camels in the un-natural habitat indicates shift in the utility of the camels and transport / shift of camels from the breeding tract to the place of utilization. It is speculated that apart from tourism, the slaughter of camels for human consumption is picking up in this country either for domestic utilization or for export may be in its’ own name or in the name of other species. Being very huge in size (adult weight ~550-600 Kg) it is being used as a source of cheap protein in the African countries and it is expected that the same trend is coming up in this country.

Assessment and Impact

The male to female ratio in the year 2007 was 1:1.3 and in the year 2012 was 1:1.1. Surprisingly the sex ratio has not changed significantly despite of 22.55% reduction in the population and change in the spread of the species across the states in the country. However, it was observed that in majority of the states which are not the part of natural habitat as well some states which encompass natural habitat of camel, the males were proportionately very high. The same can be evidenced by the following figures (Table 4).

Table 4: States having distorted Sex Ratio

S. No.	States	Male	Female	Ratio (M:F)
	Bihar	8540	319	1:0.04
	Uttar Pradesh	6372	1563	1:0.25
	Odisha	820	15	1:0.02
	Jammu & Kashmir	803	122	1:0.15
	Chhattisgarh	625	20	1:0.03
	Assam	507	219	1:0.43
	West Bengal	248	19	1:0.08
	Himachal Pradesh	157	20	1:0.13
	Himachal Pradesh	157	20	1:0.13
	Karnataka	127	24	1:0.19
	Maharashtra	122	60	1:0.49
	NCT of Delhi	99	58	1:0.59

It is clear from above figures that despite of distorted sex ratio in several states, the overall sex ratio of camel in the country has not changed because of shifting of camel populations, predominantly comprising of males, to un-natural habitat for specified purpose. This trend indicates that the camel breeders are selling surplus males and defective females to the traders, which in turn are probably going for slaughter. Under such circumstances the structure and composition of the populations get distorted due to the disproportionate reduction in the animals of two the sexes, loss of elite animals, irrational breeding and associated factors. Such a situation results in increasein the rate of inbreeding, loss of genetic variation and fixation of mildly deleterious alleles, and thereby reduce adaptive potential and increase the probability of extension.

Camel :Declared as the State Animal of Rajasthan

The camel has so far been used as a pride animal. It has been used as an iconic animal to symbolise Rajasthan by Govt. of Rajasthan, Rajasthan Tourism, Rajasthan Bank, BSF- Camel corps and several other organisation. This pride animal still constitutes the glamorous part of republic day parade. Looking at the close association of camel in the art and culture of the society in the state and the current population status, the present Rajasthan Government under the leadership of Mrs. VasundharaRajeSindhia, honorable Chief Minister of Rajasthan, has declared camel as State Animal of Rajasthan on June 30, 2014 and for this declaration Bikaner city was choose probably because of the concentration of camel population around this place. Thus "The Camel" became the first domestic animal to be declared as "State Animal"in this country. In order to declare the camel as state animal of Rajasthan, appropriate preparation for drafting the document was done under the Chairmanship of Secretary, Animal Husbandry Department, Government of Rajasthan. The first draft was prepared under his chairmanship by Animal Husbandry Department and National Research Centre on Camel, Bikaner. Subsequently, the inputs were taken from other departments such as Rajasthan Cooperative Dairy Federation (RCDF), Forest, Rajasthan Livestock Development Board (RLDB), Insurance companies, NGOs, Rajasthan University of Veterinary and Animal Science (RAJUVAS), Health Department, Ayurved Department etc. and the draft "Camel Development Policy" was prepared. In brief, the actionable points of Camel Development Policy were: -

I. Policy Support

- Act (i) Ban on Camel Slaughter (Complete Ban or Females complete ban and Males after selection)(ii) Restriction on camel export /migration
- Breeding Policy : New breeding policy with emphasis on camel milk production
- Sale of Camel Milk : Collection, processing and marketing of camel milk by organized sector (RCDF)
- Inclusion of camel in famine code
- Pasture Development: (i) Forest Area –Rational entry of camels for grazing, (ii) Pasture Land: Re-seeding and Plantation.

II. Incentives for Camel Breeding

- Support to camel breeders on birth of a camel calf –cash incentive for calf born, feed and mineral mixture for dams, treatment and other services.
- Loans, Subsidy and Insurance Support : Loan for new purchase, subsidy on sale of camel milk and insurance cover to all camels.

III. Breed Registration and Camel Breeders Association

For their own welfare and to address the smaller and localized issues

IV. Camel Development Cell

To look after all camel development activities

Steps Forward

The state government took appropriate action for giving legal framework to the decision taken and "ABill" for the formulation of act on above lines was prepared by the Animal Husbandry Department of the Rajasthan Government and it was named "The Rajasthan Camel (Prohibition of Slaughter and Regulation of Temporary Migration or Export) Bill, 2014". Again the state government, under the leadership of honorable Chief Minister of Rajasthan Smt. VasundharaRajeSindhia, gave appreciable weightage to this species and the Bill was prepared on the lines of Rajasthan Bovine Animal (Prohibition of Slaughter and Regulation of Temporary Migration or Export) Act,1995.

The Rajasthan University Veterinary and Animal Science, Bikaner and Ayurved Department of Government of Rajasthan along with the National Research Centre on Camel have been asked to explore the therapeutic utility of camel milk for human health.

THE RAJASTHAN CAMEL (PROHIBITION OF SLAUGHTER AND REGULATION OF TEMPORARY MIGRATION OR EXPORT) BILL, 2014

"A Bill" to provide for prohibition of slaughter of camel and also to regulate temporary migration or export thereof from Rajasthan.Be it enacted by the Rajasthan State Legislature in the Sixty-fifth Year of the Republic of India. The Bill was given legal frame by the subject matter experts and covered under following 15 headings:-

1. Short title, extent and commencement.
2. Definitions
3. Prohibition of slaughter of camel
4. Prohibition of possession, sale or transport of camel meat and camel meat products
5. Prohibition of export of camel for the purpose of slaughter and regulation of temporary migration or export for other purposes
6. Transporter to be abettor
7. Custody and disposal of camel seized
8. Penalty
9. Punishment for causing hurt
10. Punishment for intentionally injuring any camel
11. Burden of proof
12. Power to enter and inspect places
13. Person exercising powers under this Act deemed to be public servant
14. Protection of persons acting in good faith
15. Power to make rules

The Bill was introduced and passed by the Rajasthan legislative assembly. It was sent to the President. The Bill was reserved and a template for examination by the line ministries was developed and sent for feedback. The points for feedback were:-

TEMPLATE FOR FEEDBACK

1. Whether the proposed legislation is Constitutionally valid : Yes/No

- Whether the subject matter of the Bill is ex-facie beyond the legislative competence of the State Legislature or not - Yes/NO
- If yes, how?
- Whether its provisions derogate from the scheme and framework of the Constitution so as to endanger the sovereignty, unity and integrity of the Nation or not: Yes/No
- If yes, how?
- Whether the provisions of the Bill clearly violate The Fundamental Rights or transgress into other Constitutional limitations and any other provision relating to its basic structure: Yes/No
- If yes, how?

2. Whether there is any conflict with an existing Central Law? Yes/No

- If yes, whether the conflict may be consciously permitted? Yes/No
- Which provision / provisions of the Bill is/are in conflict with an existing Central Law, and to what extent?
- Whether such Central Law has been enacted or is under consideration for enactment?
- Reasons due to which this conflict cannot be permitted consciously.

3. Whether the proposed State enactment involvesanydeviationfrom an existing National or Central policy to its detriment, or would be hindrance to enactment of uniform laws for the country: Yes/ No

- If Yes, Which provision(s) of the Bill involve(s) any deviation fromany existing National or Central policy, and to what extent?
- Whether this National or Central Policy has been notified or is still under consideration: Yes/No
- Reasons due to which this deviation cannot be-permitted consciously.

Progress So Far

The Bill was circulated and the feedback was received by the state government. A suggestion on custom clearance has been given. The same has been incorporated and the Bill will most likely be put up in the next session of Rajasthan assembly i.e. in February 2015 and after clearance from assembly it will be sent to the President for final approval.

The state government is all set to constitute a Committee under the chairmanship of Additional Chief Secretary of Rajasthan. The members of the committee would be Secretary, AnimalHusbandry Department; Director, Animal Husbandry Department andRepresentative of National Research Centre on Camel, RAJUVAS, Health Department, Ayurved Department, three camel farmers. Other probable members may be from Forest Department, Rajasthan Cooperative Dairy Federation, NGOs, Bank and Insurance Company representatives.

The Other Side

On one side the conservation biologist and a segment of society is very happy on this act of the government for the conservation of this pride animal of Rajasthan but on the other side few unorganized farmers/trader and the NGO LokhitPashupalkSanghtan, Pali, Rajasthan is opposing it. As per this NGO *The draft "Rajasthan Camel (Prohibition of Slaughter and Regulation of Temporary Migration or Export), Bill, 2014" will increase camel suffering and quicken the decline of the camel population in Rajasthan, as it removes all currently existing economic incentives for camel breeders.* They have prepared a Petition against the planned "Rajasthan Camel Bill, 2014" and have started a drive against it. They have launched a website http://www.change.org/p/vasundhra-raje-save-the-camels-of-rajasthan-stop-the-bill-that-will-undermine-pastoralist-livelihoods to see and sign the petition prepared against it.There are other small issues in the petition but some of the important points raised in this petitionare :-

- The proposed bill is in violation of Article 21 of the Constitution which provides for the right to life and liberty which includes within its ambit the right to livelihood.
- This right of livelihood when read with the fundamental right provided in Article 19 (1) (g) which provides from the freedom to practice any profession, or to carry on any occupation, trade or business.
- The provisions of the Rajasthan Camel Bill, 2014 are in violation of Article 19(1)(d) of the Constitution of India as it restricts free movement within the territory of India

It is felt that the darker areas of the Camel Development Policy have come in the public domain because of the movement of this Bill from Legislative Assembly to the President and its' circulation to line departments for feedback but the brighter areas regarding camel milk production, marketing, processing, subsidy, forest and pasture development, loan and insurance etc. have not came in the public domain to a desired extent. Hope, the complete knowledge of Camel Development Policy will minimize the resistance and with the kind of commitment of the present Rajasthan Government, it is all set to be protected by law.

The Dark Corner

In 1978 a case was registered regarding selling of camel milk and it was finally decided by the honorable Supreme Court of India in the year 2000 that:-

- For all the above reasons we are unable to agree with the finding of the High Court that camel milk is not fit for human consumption.
- This is an area where the attention of the Central Government must be focused for considering whether there should be re-fixation of the components as for the standard in respect of camels milk.

Unfortunately, even after the lapse of 15 years' time, appropriate notification for including camel milk in the list of edible items for human consumption has not been issued and standards in respect of camel milk have not be notified by the Food Safety and Standard's Authority of India (FSSAI).

National Livestock Policy:Camel Breeding Policy

It will aim at improving their desert specific draft power,milk production, disease resistance and sports traits. Breeding of Double hump camelin high altitude areas would be supported with import of semen to minimize otherwisehigh chances of inbreeding.

State Camel Breeding Policy

It has been dealt in detail in this document and the focus remains on milk production, processing, value addition, marketing and research on exploitation of the therapeutic utility of camel milk for human health.

6. ANIMAL GENETIC RESOURCES OF UTTARAKHAND, MANAGEMENT AND BREEDING POLICY FOR IMPROVRMENT OF AnGR IN HIMALAYAN REGION

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Introduction

Himalayan region of India have a mix of almost domesticated species of livestock, very large in number and very low in productivity across the board. In economic terms they are a wealth indeed, low productivity not withstanding as the sector supports livelihoods of nearly 80 percent of the rural households in the state, at least in part in the majority of cases and in full in some (tribal and nomads exclusively living off livestock).

Livestock production in Himalayan regions endeavor of the small holder (marginal, small and land less) and takes place in millions of small and tiny holdings scattered across the region. The predominant farming system is mixed crop livestock farming, both in the plains as well as in the hills, irrigated in the plains and rain fed in the hills.

Livestock provide gainful employment to a large section of population round the year. If we look at the various livestock species found in the region, cattle are most prominent (47.5 percent), followed by buffaloes (12.3 percent), goats (15.9 percent) and sheep (10.4 percent). Generally, cattle, goats and sheep constitute an important livestock wealth in Western and Central Himalaya, pig and poultry in Eastern Himalaya and ovine in alpine zones, yaks are also reared in alpine areas. Equines are essential for transportation as other means of transportation are meager and also beyond the reach of resource- poor farmers.

Individual livestock holdings are small (2 or 3 animals) after made up of a mix of different species, the combination made up invariably of cattle and or buffalo and goats. Cattle are the most popular species and are farmed for milk production in the plains (commercial) and in the hills for work animal production as well as for milk for home consumption. Sheep are held in larger flock of 10-15 animals along with a few goats in some cases except by tribal and nomads, where flocks are much larger (100-1000 of sheep, goats or both) migratory (summer grazing) in the alpine pastures in the upper reaches. The goats are kept as sources of additional in come and as an insurance against disaster. Goats are also used in ceremonial feasting and for the payment of social dues.

In spite of the substantial contribution of livestock towards the rural economy, these are still many populations of livestock at isolated locations which may be very important genetic resources and not enough seems to have been done to document his genetic diversity and production potential in their breeding tract.

Animal Husbandry have a very good prospect in this region due to availability of large proportion of indigenous animals and birds in pure form, though these are still non descript. Among livestock, meat producting animals and birds became integral part of an average family because meat is one of the important components of their food and small meaty animals/birds can be sold at any time to meat their emergency requirements.

Over the past four decades considerable efforts have gone into livestock research and development in the Himalayan regions of India. Policy approaches have cent red on the problems of animal breed, animal feed and animal health. Innovations, until now, have been designed to address technical/scientific problems and have neglected many interrelated socioeconomic and biophysical characteristics: more specially, they have failed to address the very particular characteristics of the mountains. Development effects have been geared towards improving animal breeds to increase incomes and improve the living standards of mountain farmers.

Livestock Population

Uttarakhand has a livestock population of 96.67 lacs as per 2012 animal census. The cow population stands at 20.61 lacs, which comprises of 5.78 lacs crossbred and 15.08 lacs of indigenous animals. Likewise the state has 9.88 lacs buffaloes. Sheep population stands at 3.69 lacs although its wool constitutes the most important raw material for the large carpet industry in the state and its population is showing a declining trend. Similarly, the goat population is 13.67lacs which is raised mainly for the production of chevon. The population of equine species is only 0.18 lacs used for transportation purpose in hilly areas. The population of equine in the recent past has been observed to show declining trend. Then, there are only 0.199 lacs pigs, the most proliferating species, low input and high output animal and its population is also decreasing over the years. The crossbred cattle population during 2007 -2012 showed 70.35% increase, while indigenous cattle in the same period showed -20.43 % decrease, the buffalo population also showed decline trend by 1.90 percent. The sheep population has been increased by 26.98 percent. There has been a increase (2.40%) in the population of goats during 2007-2012. The population of horses/ponies has reduced over the period. Within the indigenous stock, decline was drastic for horses/ponies. The main reasons for decline in horses/ponies are increasing substitution of these animals with mechanical power.

Individual livestock holdings are small (3 or 4 animals) after made up of a mix of different species, the combination made up invariably of cattle and or buffalo and goats. Cattle are the most popular species and are farmed for milk production in the plains (commercial) and in the hills for work animal production as well as for milk for home consumption. Milk at a large scale produced from buffalo and cow, which is sold at the service centers of the nearby villages and is the partial source of income of the people. Bullocks are mainly used for plowing the fields in hilly area..

Sheep are held in larger flock of 10-15 animals along with a few goats in some cases except by tribal and nomads, where flocks are much larger (100-1000 of sheep, goats or both) migratory (summer grazing) in the alpine pastures in the upper reaches. The goats are kept as sources of additional income and as an insurance against disaster. Goats are also used in ceremonial feasting and for the payment of social dues.

In spite of the substantial contribution of livestock towards the rural economy, these are still many populations of livestock at isolated locations which may be very important genetic resources and not enough seems to have been done to document his genetic diversity and production potential in their breeding tract.

Table 1. Species wise livestock population of Uttarakhand (Livestock census 2007)

S. No.	Species	Population (Lacs)	
		2007	2012
1	Cattle	22.35	20.061
2	Buffalo	12.19	9.88
3	Sheep	2.90	3.69
4	Goat	13.35	13.67
5	Horse/Pony/Mule/Donkey	0.39	0.18
6	Pig	0.20	0.199
7	Others (Yak/Dog/rabbit)	2.56	2.27
8	Poultry	26.01	46.72
	Total	79.95	96.70

Source: Deptt. of AH Uttarakhand

Table 2. Comparision Of Livestock Census 2012 With Livestock Census 2007 Of Uttarakhand

Species	2003	2007	2012	% Change
Crossbred	227614	339427	578210	70.35
Indigenous	1960568	1895689	1508461	-20.43
Total	2188182	2235116	2006053	-10.25
Buffalo	1228194	1219518	987775	-1.90
Sheep	295845	290411	368756	26.98
Goat	1158197	1335306	1367415	2.40
Pigs	32712	19822	19907	0.43
Poultry	1983983	2601852	4671937	79.56

Source: Deptt. of AH Uttarakhand

Livestock Production

Milk production is continuously increasing since the application of improved technological of animal raising and creation of market linkages between rural producers and urban consumers through the network of dairy co-operatives. Yet, the productivity in the state is low as compared to many other states of the country. Buffalo and cow are important milk species in the state. Goats in the hilly reason are mainly reared for meat purpose while in plain is used for meat and milk purpose. The milk production grew at a rate of 1.68% per annum during the period of 2001-2012, while growth in total milk production at national level was observed at a rate of 4.5% per annum. Livestock produced 14.78 million tones milk,3078.17lacs eggs and around 399937 kg of wool during 2012-13.

The growth in egg production has been faster as compared to milk production. The egg production grew at a rate of 112.53% per annum during the period of 2001-2012. Growth in total wool production, however, declined by 6.19% per annum form 2002 to 2012.

Animal Genetic Resources in The State

There is a large genetic diversity in livestock as reflected in important domesticated species and a large number of known breeds and non-descript populations. Species wise breeds, their breeding policies and priority attention for conservation, are as follows-

Cattle

Cattle breeds such as ***Sahiwal*, *RedSindhi*** *and* ***Haryana*** are available with a few institutional herds and private owners. These animals are mostly available in Haridwar, U.S. Nagar, Dehradun and Nainital districts. A new germplasm Jwalapuri also recognized. These animals are mostly available in Haridwar district. Crossbreeds of ***Jersey, Holstein Friesian and Red Dane*** also available in the whole state but maximum numbers of these animals were recorded mainly in U.S. Nagar, Dehradun, Haridwar and Nainital districts. The majority of cattle found in hilly areas of the state are non-descript and known as hill cattle. The breed is reared for milk, bullock power and manure. The hill cattle have three types of colour i.e black, redand white.The Red coloured animals are popularly recognized as ***Badri*** breed in Garhwal region. The milk yield of these animals is low and ranges between 1.0-3.0 kg per day.

Buffalo

Murrah, Murrah grade and Tarai are two most important breeds of buffalo found in the state. The Murrah buffaloes mainly found in plain areas i.e. U.S. Nagar, Haridwar and Dehradun districts and Tarai buffaloes (native to Uttarakhand) are found in Tarai and Bhabar areas of Nainital, U.S. Nagar and Champawat districts. In the hilly regions of the state, non-descript type of buffaloes are found and a large chunk belongs to Murrah and Tarai graded animals.

Sheep

The majority of sheep populations are non-descript type in the state sheep breeds such as Gaddi, Rampur Bushair etc which have their breeding tracts in Himachal Pradesh are available in high reaches of Dehradun, Nainital, Tehri Garhwal, Chamoli and UttarKashi districts of the state. The animals of Muzzafarnagari breed are also found in the Haridwar,U.S.Nagar and plains of Dehradun districts. The black coloured sheep are very popular in the Garhwal region. Fleece is of these sheep is medium quality and dense, and their legs, belly and face are devoid of wool.

Goat

The goats in villages of Uttarakhand are non-descript type. There is paucity of information on all the breeds regarding their description, native breeding tracts and demographical/geographical distribution patterns etc. Various morphological and production attributes of the native animal population still remain to be enumerated and quantified. Some of them are given below

Chaugarkha: -A breed in Almora district and adjoining area in Central Himalayas has been identified and characterized by Singh and Barwal (2007). This breed is small in size and reared for meat purpose. The animals of this breed are small with a lean body and black, fawn and white in colour. They kid once a in year with one or two kids. Meat of this breed is coarse and devoid of fat. The does do not yield any appreciable quantity of milk except for nourishing the kids.

Udaipuri:- This breed is found in Pauri district and adjoining areas in Western Himalayas has been identified and characterized by Singh and Barwal (2009). This breed is small in size and reared for meat purpose. The coat colour of this breed is tan. They kid once in a year with one or two kids.

Tarai:- The goat in villages of Tarai area of the state are non-descript. They constitute a mixture of different types of goats like Black Bengal, Barbari Jamunapari etc. Since there is no controlled breeding among these populations, the colour pattern of these goats is not specific and is black, tan, fawn, white and spotted. These goats are small to medium in size and reared for meat and milk purpose. These populations are existent since long in the area and are, therefore, well adapted to high rainfall and hot humid climatic conditions that prevail in the tarai region during raining season which is the most inhospitable season during the year. They kid once in a year with 2-3 kids. The udder of these goats is well set with small and large teats. The she goats yield 1-1.5 kg milk.

Gaddi (Also known as white Himalaya):- The animals of this breed found in Dehradun, Nainital, Tehri Garhwal and Chamoli districts of Uttarakhand. The animal of this breeds are medium sized, coat colour is mostly white, but black and brown and combination of these are also seen. Both sexes have large horns, directed upward and backward and occasionally twisted. Ears are medium long and dropping. The nose line is convex. The udder is small and rounded, with small teats. The hair are white lustrous and long. Flock size ranges from 20-500. They kid mostly single, twinning occurs in only 15-20% of births. She goats yield only 300-500 gm milk. Mostly farmers used pure breeding. There is little selection. Average fleece yield per clip 300 gm.

Chigu (Pashmina):- Animal of this breed found in high reaches of Uttarkashi, Chamoli and Pithoragarh district of Uttarakhand. The animal are of medium sized coat colour is usually white, mixed with grayish red. Both sexes have horn, directed upward, backward and outward. These goats are not different in conformation from Changthangi. Age at first kidding was observed as 615 days. They kid mostly single. Pashmina production observed 120 gm annually.

Horses/Ponies

Little is known about the genetic variation in horses/ponies in spite of their variation in phenotypic characteristics. The populations of horses/ponies mostly are non-descript type. These populations need to be surveyed for description and evaluation.

Pigs: There is a large variation in pigs as reflected in size, colour and performance in the state. The populations of pigs mostly found in U.S. Nagar and Haridwar districts of state are non-descript type, however, some belong to the improved breeds. There is a need to evaluate these populations for their unique traits and steps to be taken for their conservation and improvement.

Yak: Yak is a unique bovine species of economical and cultural importance to the tribal populations living in the difficult terrains in the hills of Himalayas. In Uttarakhand, there are only 351 yaks (17th livestock census, 2003) found in Pithoragarh (Kumaon) and Uttarkashi (Garhwal) districts. Yaks are used for milk, meat and draft purpose.

Poultry:A number of species of poultry viz. chicken, ducks, guinea fowl and quail make important contribution to human food chain and supplement family income. There is large genetic variation in these species which need to be identified for improvement and their conservation. The populations of these birds differ in their body size, conformation and colour patterns. These differences should be adequately described and evaluated using both phenotypic traits and their DNA profiles. Further, these populations must be studied for different unique traits associated with disease resistance and surviving ability under harsh climatic conditions.

Breeding strategies for hill livestock germplasm

Institutional programmes in livestock sector development have so far focused on improving animal breeds. The main purpose of improving animal breeds was to bring about the "white revolution" through livestock sector development for increased family incomes and employment for mountain farmers. Technical innovations were geared to meeting this objective and did succeed in some pockets of the foot hills and in the mid hill regions that were well connected with market towns through roads. In fact, the white revolution programmes mostly benefited comparatively well to do livestock farmers. Who happened to be located in dairy areas in the plains and had access to modern technology. The majority of mountain households- rural and inaccessible with a marginal and fragile resource base remained unaffected.

In the Uttarakhand hills, where the white revolution/programme has been going on for about three decades the number of crossbred cattle as per the 2012 livestock census was only 541921 out of a total breeding stock of 464319, furthermore, the number of crossbred cows was not evenly distributed. The reason for such poor performance was because improved breeds of cows were supplied to the weaker sections without providing poor farmers with the means of maintaining them. A large number of artificial insemination centres was opened, but these centre handily touched the rural areas. The state of Himachal Pradesh introduced programmes for up grading cattle in the 1950,s and again in the early 1970,s. The focus was on producing Jersey crossbreds. This succeeded to same extent in areas with access to milk markets through a well developed road net work. However, according to rough estimates crossbred animals constitute only six percent of total cattle population in Himachal Pradesh despite three decades of planned developments in improving cattle breeds. The number of crossbred cattle as per the 2012 livestock census was only 1129135 out of a total breeding stock of 971733.

On the other hand, the buffalo improvement programmes in Himachal Pradesh were a considerable success. Buffalo breeding, until the 1980s, was introduced in only a few areas. Now artificial insemination facilities for buffaloes are provided in 190 extension stations in the state. The technique has become so popular that demand for Murrah semen strains for exceeds the production. A study has revealed that in the total milk pool of the mountain villages, contribution of buffalo milk was as large as 98%. The number of buffaloes in the herds of H.P. increased significantly, while the number of cattle decreased or remained stagnant.

Management Practices

Livestock rearing in central Himalayan ecosystem is an unorganized, semi feral system of husbandry . They are taken out for grazing/browsing up to a distance of 1 to 2 kilometers for a period of seven to eight hours daily along road sides or on community land, on the denuded cliffs where other agricultural activities are barely, and harvested fields. The main sources of fodder are local weeds, shrubs, leaves from harvested crops and lopped tree leaves. During all the seasons the livestock remain dependent on grazing/browsing and farmers hardly offer concentrate to them. The calfsof cattle or buffalo are maintained at home up to completion of lactation and provided local weeds, grasses, tree leaves and harvested crops or milk of mother up to six months of age. Kids/ Lambs are maintained at home on local weeds, grasses, tree leaves and harvested crops or milk of mother up to three month of age, after which time they are allowed to browse. All livestock are housed during the night. The goats are housed before and after browsing of 7-8 hours. The small size herds of goats are mostly housed with cattle and buffaloes while herd size of more than 5 goats housed separately in closed type pens, which are not well ventilated. The kids are also housed with the goats. Leaf litter from the forest floors is collected during one or two months in fall and stored in heaps near each animal shed. A basketful or two of this leaf litter is scattered under the animals in the animal shed every day. This acts as bedding material sponge and absorbs the dung and urine of the animals. After 2 or 3 days, the soaked leaf litter is removed and put either in a pit or in a heap. This is done day after day for a long period and decomposed material is used for agriculture field as manure.

Improvement of non descript cattle by grading up

The non descript cattle constituting more than 75-80% of total cattle population under this production system can be genetically improved by grading up using high genetic merit pedigreed and preferably progeny tested proven bulls of well known indigenous cattle breeds. So far the impact of breed improvement through grading up of local non descript cattle has not been very encouraging. This may be non availability of adequate number of high genetic merit pedigreed or progeny tested bulls of indigenous breed, low production levels of indigenous breeds, irregular and short term basis breeding plan which could not wean away the farmers/breeders from using scrub bulls for breeding their herds. Therefore, for successful implementation of grading up programme, the adequate number of superior breeding bulls needs to be out sourced for production of quality frozen semen and AI infrastructure networking be strengthened.

Livestock production in the state presents two scenarios considering topographical and socio-economic conditions of the livestock keepers. In the tarai, Bhabar and other plain areas, the better basic support facilities exist and the farmers are resource rich, therefore, they feed the animals adequately and exploit the genetic potential to largest extent.

Animal raising in the hilly areas is, however, very challenging. The livestock keepers mostly belong to marginal farmers' category and their economic condition is also not very sound. The feeding of livestock which constitutes about 75-80 per cent of the total expenditure incurred on them is the limiting factor. The availability of green fodder remains only for three four months during the raining seasons and for rest of the period, it is the dry crop residue and low graded dried hay of pastures that forms bulk of the animal feeding. Concentrates are offered mostly to the productive animals. Thus, malnutrition and under-feeding lead to many problems most prominent among them the reproductive ones which reduce the productive life of the animals. Cattle which are rendered unproductive are disowned by their owners which are posing a threat to the field crops and the problem is unmanageable as there are no proper means of their disposal.

The state and central governments have been implementing many livestock improvement programmes in the state. There is a well defined livestock breeding policy in place implemented through ULDB and Animal Husbandry department. The GBPUA&T Pantnagar has been providing technical support by imparting training to the field functionaries and livestock keepers on various aspects of livestock production.

Breeding strategies for livestock improvement in Uttarakhand

1. Zone A: Upto 1000 m altitude Tropical Zone: Plains, Tarai, Bhabar, Shivalik & Vallies

Breeding policy	Remark
Cattle: 1. Crossbreeding of local cattle with pure HF 2. Inter se mating of half bred with F_1 Holstein x Sahiwal	Jersey and crossbred Jersey semen will be available to those who prefer Jersey
Buffalo: 1. Grading up with pure Murrah semen.	Policy universal for buffalo state wide.
Sheep: 1. Non-descript population may be improved by crossbreeding/ grading up with Muzaffarnagari. 2. *Inter-se* mating of half- bred with F_1 Muzaffarnagari x local.	
Goat: 1. Non-descript / local goat may be improved through crossing/ grading up with Beetal and Barbari goat. 2. *Inter-se* mating of half bred with F_1 Beetal/Barbari x Local.	For milk and meat production
Pigs: 1. Non-descript breed may be improved either by grading up or crossbreeding with exotic breed large white Yorkshire/ Hampshire	

2. Zone B: 1000-1500 m altitude Subtropical zone

Breeding policy	Remark
Cattle: 1. Crossbreeding of local cattle with pure Jersey. 2. *Inter-se* mating of half bred with F_1 Jersey x Sahiwal	Holstein and crossbred, Holstein semen will be available to those who prefer Holstein
Buffalo: 1. Grading up with pure Murrah semen.	Policy universal for buffalo state wide.
Sheep: 1. Non-descript population may be improved by crossbreeding/ grading up of Muzaffarnagari. *2.* *Inter-se* mating of half bred with F_1 Muzaffarnagari x local.	
Goat: **1.** Non-descript / local goat may be improved through crossing/ grading up by Beetal and Barbari goat. **2.** *Inter-se* mating of half bred with F_1 Beetal/Barbari x Local.	

Pigs: 1. Non-descript breed may be improved either by grading up or crossbreeding with exotic breed large white Yorkshire/ Hampshire	

3. Zone C: 1500-2400 m altitude Cool temperate zone

Breeding policy	Remark
Cattle: 1. Selective breeding among the local non-descript cattle.	Policy universal for draught animal production zone wide
Buffalo: 1. Grading up with pure Murrah semen.	Policy universal for buffalo state wide.
Sheep: 1. Breeds available in this zone for the wool production may be crossed with Rambouillet/ Russian Merino. 2. Selective breeding among the local breeds available.	Policy for temperate zone
Goat: 1. Selective breeding within the breed for Pashmina production (Chegu and Chanthangi). 2. Selective breeding in local non-descript goat.	
Pigs: 1. Non-descript breed may be improved by grading up or crossbreeding by Large White Yorkshire.	Policy universal for pig state wide

4. Zone D: Above 2400 m altitude Sub alpine zone

Breeding policy	Remark
Cattle: 1. Selective breeding among the local non-descript cattle.	Policy universal for draught animal production zone wide
Buffalo: 1. Grading up with pure Murrah semen.	Policy universal for buffalo state wide.
Sheep: 1. Breeds available in this zone for the wool production may be crossed with Rambouillet/ Russian Merino. 2. Selective breeding among the local breeds available.	Policy for temperate zone
Goat: 1. Selective breeding within the breed for Pashmina production (Chegu and Chanthangi). 2. Selective breeding in local non-descript goat.	
Yak: 1. Selective breeding is to be adopted to improve local yaks.	Policy universal for Yak zone wide
Horse/Ponies: 1. Horse true of the breed and unrelated may be mated by adopting selective breeding. 2. For Mule production quality Jacks should be mated to selected Mares.	Universal policy for state wide

Breeding policy for livestock of Himanchal Pradesh

The new breeding policy has been framed inconsonance with National Livestock Breeding Policy by making amendments to the previous policy keeping in view the resources and marketing facilities available with the livestock breeders, biodiversity preservation to prevent local germplasm from extinction, people's preference to rear the kind of breed of theirchoice, topography and agro-climatic conditions. A broad frame work of the policy includes the following:

1. According to livestock census report for the year 2012, 55% of total cattle in Himachal Pradesh are indigenous. Hill cattle plays crucial role in the economy of poor livestock breeders through supply of draught animal power, cow dung(organic manure) and milk to meet family requirement. Since resources deficient farmers with no marketing facilities prefers to rear these animals only for meeting family requirement of milk, manure and draught power, therefore, rearing of hilly cattle will be encouraged by providing option for breeding with semen selected from local hilly cattle having better milk yield and excellent draft abilities. Selective breeding in turn will help in conservation, proliferation and enhanced production of native hill cattle.
2. For small farmers of the State having limited resources and desirous of upgrading their hilly cattle for better milk production with higher fat content option of up gradation of nondescript hilly cattle with defined indigenous dairy breeds like Sahiwal and Red - Sindhi. These indigenous dairy breeds have potential for development as viable milch cattle if managed scientifically.
3. For farmers having feed, fodder, and marketing facilities to a certain extent, option of cross-breeding of hilly cattle with high yielding exotic breeds like Jersey and Holstein Friesian will be provided.
4. The farmers who want to adopt dairy activities on commercial basis and desirous of maintaining pure exotic breeds/indigenous breeds will be provided semen straws of pure exotic Jersey and Holstein Friesian or semen straws of ingenious dairy breeds like Sahiwal and Red -Sindhi.
5. To avoid the incidence of inbreeding, the Department will import/purchase the bulls or semen straws of Exotic/Indigenous breeds as per MSP fixed by Government of India from time to time. Guiding Principles for Livestock Breeders:-

Category of farmers Breeding Policy Marginal resource deficient Farmers

(i) Selective breeding with pure hilly bull/semen straws. Small Farmer having limited resources

(ii) Cross breeding of local hilly cows with recognized indigenous breeds like Sahiwal &Red Sindhi (bulls having dam yield 2000 litres or above) thus producing F1generation with50% indigenous and 50% Hilly traits.Subsequent A.I. of graded progeny will be done with pure indigenous semen.

Farmers with good resources

(i) Upgrading of local hilly cows with Jersey semen(bulls having dam yield 3750 litres or above) as per existing policy to be continued thus producingF1generation with 50% Jersey and 50% Hilly traits. Subsequent A.I. of graded progeny will be done with50% Hilly X 50% Jersey semen. As production of bulls with this type of inheritance shall take at least5 years, hence till then, present policy of use of 50% Jersey X 50% Hilly semen may be continued.

(ii) Cross breeding of local non-descript cows if available to be done with jersey or H.F. pure bred semen (bulls having dam yield 3750 litres or above in Jersey & 5600 lts or above for HF) (as per farmer's preference) up to 50% level and further grading up of Cross bred to be done with 50% RS /Sahiwal X 50% Jersey/ H.F. semen. Same pattern is to be continued in subsequent generations. For crossing F1 generation, crossbred bulls having dam yield (3000-3500 liters) are to be used and for subsequent generations, the bulls having 20% higher dam yield will be used.

Commercial Farmers having ample resources and marketing facilities. Apart from above mentioned options, facility of germplasm to rear pure Jersey/Holstein or pure Indigenous breeds like Sahiwal & Red Sindhi will be provided as per choice of the farmer.

Existing Policy for Buffalo which envisages upgradation of non descript buffaloes with Murrah Buffalo semen will be continued as such.

Guiding Principles for Livestock Breeders

Category of farmers Breeding Policy Marginal resource deficient Farmers

(i) Selective breeding with pure hilly bull/semen straws. Small Farmer having limited resources

(i) Cross breeding of local hilly cows with recognized indigenous breeds like Sahiwal &Red Sindhi (bulls having dam yield 2000 litres or above) thus producing F1generation with 50% indigenous and 50% Hilly traits. Subsequent A.I. of graded progeny will be done with pure indigenous semen. Farmers with good resources

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(ii) Cross breeding of local non-descript cows if available to be done with jersey or H.F. pure bred semen (bulls having dam yield 3750 litres or above in Jersey & 5600 lts or above for HF) (as per farmer's preference) up to 50% level and further grading up of Cross bred to be done with 50% RS /Sahiwal X 50% Jersey/ H.F. semen. Same pattern is to be continued in subsequent generations. For crossing F1 generation, crossbred bulls having dam yield (3000-3500 liters) are to be used and for subsequent generations, the bulls having 20% higher dam yield will be used. Commercial Farmers having ample resources and marketing facilities. A part from above mentioned options, facility of germplasm to rear pure Jersey/Holstein or pure Indigenous breeds like Sahiwal & Red Sindhi will be provided as per choice of the farmer. **Threat to Bio diversity:** - The indiscriminate use of crossbreeding programme prescribed in existing policy has posed a threat to biodiversity preservation specially for the native hill cattle .The native hill cattle are well suited to the climate and environment of our state, performs better on low inputs and are robust, resilient, disease resistant and have ability to thrive under extreme climatic stress and less than optimal nutrition. If the existing breeding policy is continued then the pure germplasm of native hilly cattle will become extinct in near future.

Impact of Genetic Improvement

Positive environmental impact

Reduction of animal pressure (since the animals are more productive, the production system can be intensified and thus one can have fewer animals to maintain for the same level of production).

Negative environmental impact

- Reduction of animal biodiversity.
- Introduction of new pathology.
- Increase in grain field areas.

Impact on livestock productivity (milk, reproduction, meat, health, etc.)

- Meat: increase by 1 to 2 % per annum.
- Milk: increase of 0,5 to 1 % per annum (these increases are cumulative).

- Meat quality: this may improve, but the quality of meat from older varieties of livestock is often considered to be better (and may therefore obtain higher prices, e.g. rare breeds).
- Reproduction: increase obtained by cross-breeding, (but not cumulative).
- Health: animal more productive but often more fragile (requiring more expensive veterinary and other external inputs).
- Feed: animals may require higher quality fodder and external feed inputs.

Recommendations

- Indigenous cattle and buffalo breed conservation programmes should be integrated with breed improvement and development programmes.
- Superior breeding bulls should be identified and evaluated through large scale collaborative progeny testing programmes.
- Herd registration and Animal performance recording system at farmer herds should be developed and linked with P T Programmes.
- Nucleus herds/Bull mother stations & germplasm centre for different cattle & buffalo breeds should be established for production and dissemination of superior germplasm.
- To make available the superior germplasm and breeding facilities at the door steps of small holders, infrastructure facilities such as AI centers, animal health centers, Milk procurement and Extension centers fully equipped with trained man power should be developed.

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7. THE VECHUR MODEL FOR CONSERVATION

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Introduction

Animal husbandry is one of the major occupations of villages in the country. Kerala was no exception to this, The cattle of the state were predominantly, used as work animals with a very low milk production capacity. As the demand for milk increased keeping cows with better milk production also became a practice. The high humidity of the state due to nearness to sea and backwaters , increased stress on the animal. As a natural size of the cows reduced. This can be the reason for the smaller size of indigenous cows in the state.

Evolution of Vechur breed must have been through these sequences. Vechur is a village in Kerala, situated in the Kottayam district. Vechur and nearby places are having natural barriers like rivers, rivulets and backwaters which made free movement of animals restricted, This geographic isolation must have contributed for development of a group of homogenous animals in the area. These animals were with comparatively better milk production capacity. They were small in size and came to be known as Vechur cattle

As for other indigenous groups of cattle of the country, Vechur was also threatened with the prospect of extinction. This paper is an effort to document the chronological events and efforts for conservation of the valuable germplasm., Effort is also made to consolidate and present the research done on Vechur germplasm of the state.

HISTORY

Travancore was a princely state before independence of India and had a long history. The rulers of the state were mostly progressive and wealthy. They had immense wealth through merchanting of spices and other valuable goods with overseas customers even in ancient days. The mention of the breed is available in Travancore state manual (1940). The relatively higher production of Vechur cows is mentioned in the manual.

Kerala was the first state to accept crossbreeding as the breeding policy for cattle of the state. Semen of exotic breeds Brownswiss and Jersey were used on indigenous cows to produce the better milk producing crossbreds. To undertake this mission, a law was made named as Kerala Livestock Improvement Act 1961. This law bans the keeping of endogenous bulls for breeding purpose, The veterinary doctors of the state were entrusted to castrate all the indigenous bulls , which was done through well planned and state supported campaigns. This resulted in endangering the population of indigenous cattle of the state. Only very few of these animals were allowed to survive in nook and corner of the state because of unacessablilty of the region or through adamant stand of some of the keepers. By 1990s most of these indigenous animals were converted as crossbreds. The crossbred population of the state was steadily increasing and at that stage reached a proportion of 80%.

The efforts to identify and conserve the breed was tried in 1980s by Kerala Agriculture University. But it was not successful. Students of College of Veterinary and Animal Sciences were instrumental in reviving the efforts. Through one of the projects for student's magazine they were able to locate some of the cows of the Vechur breed, which was till then thought to be extinct.

The next significant event was the work of Dr Sosamma Iype , Professor, Animal Breeding and Genetics, College of Veterinary and Animal Sciences Mannuthy. Through her concerted efforts she was able to get sanction from Kerala Agricultural University to start the Vechur conservation project. With meager funds provided by the University she purchased seven cows and one bull. Subsequently the herd strength was increased to more than 20 through purchases. Indian Council of Agricultural Research then sanctioned a research project on conservation of Vechur cows with a total outlay of around 47 lakhs (1993-98).

Since then University is funding the project with its own resources. Currently a nucleus herd of more than 120cows with 10-15 bulls is maintained at Centre for Advanced Studies in Animal Genetics and Breeding, Mannuthy. Farmers were supplied with the surplus animals and currently there are more than 160 herds linked with the nucleus herd. The breeding of these farmers animals are mostly through the semen supplied from the nucleus herd.

Some farmer organisatins, NGOs, and other groups are also maintaining Vechur animals . All these efforts had contributed their part to save his valuable germplasm from the clutches of extinction.

Extensive research work were undertaken to study the special traits of the breed. Studies on its thermal tolerance, adaptive attributes, milk composition, unique genetic makeup and also he growth and reproductive traits were undertaken and results were published. Currently three post graduate research projects are under way.

ABSTRACTS

TS-I-01

PRODUCTION AND REPRODUCTION PERFORMANCE AND MILK PRODUCTION EFFICIENCY OF RED SINDHI COWS

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Red Sindhi, also known as Sindhi and Red Karachi is one of the most popular zebu dairy breeds. The breed originated in the Sindh province of Pakistan and is widely kept for milk production across India, Pakistan, Bangladesh, Sri Lanka and other countries. They have been used for crossbreeding with temperate (European) dairy breeds in many countries to combine their tropical adaptations (heat tolerance, tick resistance, disease resistance, fertility at higher temperatures, etc.) with the higher milk production found in temperate regions. To assess the production and reproduction performance at Dairy Farm, College of Agriculture, Dhule, the data spread over a period of 20 years (1991 - 2010) were used. The overall least-squares means for lactation length (LL), dry period (DP), calving interval (CI), lactation milk yield (LMY) and 300-day milk yield (300 DMY) in Red Sindhi cows were 310.876 ± 6.07 days, 81.99 ± 4.78 days, 392.86 ± 7.92 days, 1816.66 ± 38.95 kg and 1820.56 ± 34.18 kg respectively. The lactation length had a significant effect over lactation milk yield, whereas, period of calving had significant effect over lactation milk yield and 300-day milk yield. The effect of age at first calving, season of calving, period of calving and lactation order over all the other traits under study was non-significant. The overall least-squares means obtained for daily milk yield per day of lactation length (DMY/LL), daily milk yield per day of 300-day lactation (DMY/300 D), daily milk yield per day of calving interval (DMY/CI), milk production efficiency per kg body weight at first calving (MPEK) and milk production efficiency per kg body weight and per day of first lactation length (MPEKD) were 5.96 ± 0.11, 6.06 ± 0.11, 4.72 ± 0.10, 6.75 ± 0.23 kg and 20.82 ± 0.92 gm respectively. Period of calving had highly significant effect over DMY/LL, DMY/300D and DMY/CI. Age at first calving, season of calving and lactation order exerted non-significant effect over all the traits.

TS-I-02

GENETIC AND PHENOTYPIC PARAMETERS OF FIRST LACTATION AND LIFE TIME TRAITS IN SAHIWAL CATTLE

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The present study was conducted on first lactation and life time performance traits of Sahiwal cattle from Government Livestock Farm, Chakgangaria, Lucknow. First lactation and life time performance records of 1367 Sahiwal cows born to 75 sires spread over a period of 71 years from 1944 – 2014 were utilized for the present study. The overall least-squares mean of first lactation traits viz. AFC, FLMY, FLL, FDP, FSP, FCI, LTMY, LTLL and ADMY were estimated to be 1287.12±6.81 days, 1941.16±27.66 kg, 321.60±2.80, 195.57±4.07 days, 231.34±4.88 days and 514.86±4.82 days, 9262.50 ± 272.92 kg, 1534.28±36.84 days and 5.94 ± 0.10, 0.14 ± 0.07 kg respectively. The overall least-squares means for the pooled data over the 7th lactation *viz.* LMY, LL, DP, SP and CI were 1815.192 kg, 300.77 days, 163.74 days, 192.60 days and 475.64 days respectively. Season effect was significant on most of the first lactation and life time production traits except first lactation milk yield. In contrast different periods of calving were found to have not significant influence on all the traits except life time milk yield. Similarly, sire effect was found significant on all the traits except first service period and first calving period. The heritability for AFC, FLMY, FLL, FDP, FSP, FCI, LTMY, LTLL and ADMY were estimated to be 0.39±0.16, 0.25±0.08, 0.27±0.08, 0.06±0.10, 0.15±0.10, 0.10±0.10, 0.17 ± 0.07 and 0.49 ± 0.09 respectively. The genetic and phenotypic correlations among all the traits were observed to be very low to high. The results of present study pointed out that most of variations in the traits were due to non-additive genetic variance. Therefore, improvement in these traits can be brought by the better management practices at the farm.

TS-I-03

LACTATIONAL PERFORMANCE EVALUATION OF FRIESWAL COWS IN NORTHERN ZONE OF INDIA

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Frieswal is a national milch crossbred evolved through a collaborative research project with ICAR and Military Dairy Farms in India with 5/8 Holstein Friesian and 3/8 Sahiwal blood. The present study was conducted to evaluate the non-genetic factors affecting the lactational traits in Frieswal cows in Northern zone of India. Data pertaining to 9148 lactational records of Frieswal cows sired by 97 bulls from 1991 to 2012 maintained at Military Farms at Meerut and Ambala were used in the study. The overall total lactation milk yield, peak yield and lactation length were 3409.04±16.62kg, 15.69±0.08 kg and 322.84±0.87 days respectively. The factors such as farm, parity, season and period of calving had significant effect on the lactation traits like total lactation milk yield, peak yield and lactation length ($p<0.001$), except farm for peak yield. Military farm Meerut had higher total lactation milk yield and lactation length (3461.11±17.08kg and 327.24±0.89 days) than Military Farm, Ambala (3356.97± 23.91 kg and 318.44±1.25 days). Animals calved in winter had significantly higher total lactation milk yield (3495.00±21.23 kg) and peak yield (16.91±0.83 kg) in comparison to other two seasons, whereas summer calved animals had an extended lactation (333.00±1.33 days). Animals calved during the period 1997-2001 had significantly higher milk yield and peak yield (3634.15±26.56 and 16.57±0.10 kg) followed by period 2002-07 (3353.64±18.78 and 15.87±0.07 kg). The total lactation milk yield is less in first lactation (2885.71±19.99 kg), and it showed an increasing trend in subsequent parities up to 4th parity. A similar trend was observed in the case of peak yield and lactation length. Results of the study clearly indicated that all the effects taken in the study were highly significant sources of variation on the lactation traits and adjustments has to be done for accurate estimation of genetic parameters and breeding values.

TS-I-04

STUDIES ON SOME PERFORMANCE TRAITS IN SAHIWAL AND JERSEY X SAHIWAL CATTLE

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An investigation was carried out utilizing the records on 719 Sahiwal cattle and 147 Jersey X Sahiwal cattle maintained at Government Livestock Farm, Chak Ganjaria, for studying the replacement rate and its components. The study comprised a total of 3583 calving records spread over a period of 35 years. The data were classified according to date of birth into four seasons and six periods. The data were analyzed using least-squares analysis and mixed model. The average values for abnormal births, sex ratio (per cent male birth), mortality and culling of

female calf up to AFC and replacement rate (female calf basis and total calf basis) were estimated as 4.86, 49.52, 15.92 and 19.52, 64.56 and 31.01 per cent, respectively. This indicated that about 3-4 (3.23) pregnancies are required for one heifer entering the milking herd. One third of the total pregnancies resulted in the successful heifers to reach the milking herd and two third were failed either due to abnormal birth, male birth and death or culling of the female calves. The effect of period on abnormal birth, mortality, culling and replacement rate was found to be significant, while for sex ratio it was non-significant. The sex ratio, mortality, culling and replacement rate did not vary according to genetic groups, however, abnormal birth was affected by genetic group. The season of birth did not influence any of the above traits.

TS-I-05

GENETIC ANALYSIS OF PRODUCTIVE AND REPRODUCTIVE PERFORMANCE OF FRIESWAL CATTLE AT MILITARY FARM, AMBALA

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A total number of 3005 lactation records of 1147 Frieswal cows born and reared at Military Dairy Farm, Ambala, sired by 64 sires over a period of 15 years extending from 1993 to 2007 were analysed to assess the production and reproduction performance, to study the effect of genetic and non-genetic factors on production and reproduction traits and to estimate genetic and phenotypic parameters of production and reproduction traits. The least- squares means of age at first calving, total lactation milk yield, 300-day milk yield, peak yield, lactation length, dry period, calving interval and service period were 980.41±8.22 days, 3299.35±136.21kg, 3285.23±92.50kg, 15.83±0.55kg, 309.91±5.82 days,115.29±8.83 days, 423.05±12.24 days, and 148.24±12.66 days, respectively. The age at first calving differed significantly across the periods of calving. The effect of season and period of calving, lactation order and regression of age at first calving on TLMY, 300-day milk yield, peak yield, lactation length, dry period, calving interval and service period was highly significant. The sires were found to have no significant effect on any trait under study. TLMY was highest in cows calved during summer season (3340.75±139.59kg), second period (3622.52±145.41kg) and in fourth lactation (3442.80±143.42kg). The average 300-day milk yield was highest in the cows calved in winter season (3359.16±96.76kg), second period (3589.14±110.04kg) and in sixth lactation (3579.26±214.40). The heritability estimates for age at first calving, TLMY, 300-day milk yield, peak yield, lactation length, dry period, calving interval and service period were 0.15±0.06, 0.14±0.03, 0.13±0.04, 0.13±0.03, 0.07±0.02, 0.009±0.028, 0.04±0.03 and 0.03±0.03 respectively. TLMY had high genetic correlation with peak yield (0.93±0.045) and low (0.359±0.199) with lactation length. The phenotypic correlation of TLMY was high (0.726) with peak yield and low (0.425) with lactation length

TS-I-06

DIFFERENCE BETWEEN VARIOUS PRODUCTION AND REPRODUCTION TRAITS OF SAHIWAL AND CROSSBRED CATTLE

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The present study was undertaken on 752 lactation records of 190 Sahiwal cows maintained at Government Sahiwal Cattle Breeding Farm, Chakganjaria, Lucknow, over 17 years (1983-1999) to evaluate the performance of lifetime traits. The traits considered for the study were herd life (longevity), productive herd life, life time calf production, life time milk yield, total lactation length, age at first service and age at first calving. The season and period of birth had no effect on TLL and LTMY. However significant effects were reported on AFS and AFC. The effect of genetic group was significant on AFC, FLMY, MY/PL and MY/TL while the effect of parity was significant for all the traits. For data set II, the effect of year of first calving was significant only for AFC, FLMY and PL while the first calving was significant for FLMY and PL; but the effect of genetic group was significant only for MY/HL. Results indicated that milk yield, length of dry period, service per conception and post-partum heat period were significantly affected ($P<0.01$) by different crossbreds. However, lactation length and service per conception were significantly affected ($P<0.01$) by parity and interaction of breed x parity. The average number of lactation as life time productivity of crossbreds are nearly three lactations whereas in native (*Bos indicus*) it was 6 to 7 lactations. The crossbred perform better at 5 to 25ºC whereas production decline of indigenous cows is not alarming even at 38ºC. When crossbred / exotic cows pant, indigenous cows are quite comfortable and the basic reason is that indigenous cattle population has emerged out by natural relation through generations that are adopted to stressful environment.

TS-I-07

BODY MEASUREMENTS AND MORPHOLOGICAL CHARACTERISTICS OF KANGAYAM BULLOCKS IN HOMETRACT AND ADJOINING PALAKKAD, KERALA

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A study was conducted to analyse the farming systems involving Kangayam breed of cattle in two different locations, in their home tract in Tamilnadu and adjoining Palakkad region of Kerala, where the Kangayam cattle forms inseparable component of the integrated crop-livestock production system. As a part of the study, body measurements and morphological characteristics of Kangayam bullocks were documented. Horn length, horn circumference, face length, ear length, height at withers, body length, chest girth, fore limb, tail length and switch length were measured in cm in different age groups of Kangayam bullocks in both the regions. Some differences in the size and morphological characteristics were found. Differences were also noted in the relative speed of growth of certain appendages like horns. Horn length in the Palakkad region was higher in the early stages. However as the bullocks matured, the trend was reversed with the bullocks in the Kangayam region possessing longer horns. The horn circumference at the base was more in the Palakkad region in the early life. But as the age advanced, the difference between the two groups became less and less with respect to this character and in the above 5 years group it became similar in both the groups. In the 1-2 year group there was no significant difference in the face length between the two regions. However, as the animals grew, a significant difference became apparent with the Palakkad strain having a longer face. The height at withers of the bullocks from the Palakkad region showed a trend of higher values compared to that of Kangayam tract. The body length showed a trend of higher values in Palakkad region from young age up to 4 to 5 years of age. However, as the age advanced, Kangayam tract bollocks measured longer than that from Palakkad region. In above 5 years of age, chest girth had practically little difference between the two groups.

TS-I-08

PRODUCTIVE AND REPRODUCTIVE PERFORMANCE OF PROGENIES OF FRIESWAL BULLS IN HOT, HUMID TROPICAL CLIMATE

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A study was conducted to evaluate the performance of progenies of Frieswalbulls based on 1st lactation performance for production and reproduction traits in field condition.Data on 143 first lactation yields of daughters of different sets (3rd to 11th) of Frieswalbulls of ICAR Field progeny testing scheme for the period 1997 to 2011 were analysed by F-test and univariate analysis of variance using SPSS (Statistical Packages for Social Sciences) for this study. The average values from 3rd to 11th set for age at first calving(days), peak yield(kg), 305-day milk yield (kg) were 1021.8±91.52to 747±113.16, 10.34±0.96 to 12.43±1.46 and 1969.8±193.86 to 2675.6±129.11 respectively. The morning and evening per cents of milk fat ranged from 3.62±0.21 to 3.09±0.18 and 4.14±0.27 to 3.56±0.24 for early lactation, 4.18±0.22 to 3.73±0.39 and 4.56±0.21 to 4.00±0.25 mid lactation and 4.34±0.27 to 3.87±0.50 and 4.82±0.56 to 4.52±0.53 for late lactation respectively.The result showed that the effect to sets of bulls for age at first calving ($P<0.01$), peak yield ($P<0.05$) and milk fat ($P<0.01$) were significant.

TS-I-09

PERFORMANCE OF MINIATURE PUNGANUR CATTLE UNDER CONSERVATION

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Punganur is one of the shortest humped cattle (*Bos indicus*) with a long tail and black switch touching the ground and originated in the surrounding areas of Punganur, Madanapalli, Palamaner places of Chittoor district in Andhra Pradesh. Punganur breed of cattle is under the threat of extinction as the population is dwindling. A small herd of Punganur animals being maintained at Livestock Research Station, Palamaner under Sri Venkateswara Veterinary University as a part of *in situ* conservation of the miniature *Bos indicus* Punganur breed is needed for future use for a low input system, environmental considerations etc. All breedable female animals were bred to Punganur bulls available by natural service. A total of 26 Punganur calves were born during 2013-14. The data were collected on birth weight, biometrical measurements and production performances. The average birth weights of male and female calves were 12.56 ± 0.39 kg and 11.58 ± 0.53 kg, respectively. The mean height at withers, body length, chest girth, paunch girth, poll length, pin bone width, tail length and ear length in male calves in the present study were 49.60 ± 1.25, 44.40 ± 1.51, 50.9 ± 1.14, 50.50 ± 1.06, 18.4 ± 0.27, 9.30 ± 0.45, 28.80 ± 1.86 and 9.90 ± 0.43 cm, respectively while in females the corresponding values were 50.00 ± 1.84, 42.4 ± 1.24, 50.9 ± 1.15, 50.3 ± 1.38, 18.8 ± 0.52, 10.40 ± .35, 29.90 ± 0.90 and 10.0 ± 0.30 cm respectively. The average body weights of punganur male calves at 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10 months age were 20.35, 26.72, 33.25, 41.40, 48.10, 55.20, 60.30, 63.83, 73.50 and 75.75 kg respectively, while in females the corresponding age body weights were 19.37, 26.25, 32.86, 39.60, 44.78, 50.43, 57.50, 61.50, 65.67 and 63.25 kg respectively Majority of the calves were born with a mixture of white and brown coat colour, but 93.10 % of calves were born with black colour muzzle, 3.44% pink colour muzzle and 3.44% white color muzzle. In punganur calves 96.55% of black color tail switch and 3.44% was mixed colour. While majority of animals were (96.55%) having black colour hoof. The average lactation milk yield was 281.30 ± 61.91 liters with a lactation length of 106.77 ± 22.75 days. The daily average milk yield and peak yield were 2.53 ± 0.34 and 3.01 ± 0.38 liters, respectively. The average age at first calving, service period, gestation period, dry period and calving intervals were 1385.1 (10) days, 166.6 (14) days, 284.9 (24) , 311.1 (13) and 522.9(18) days respectively.

TS-I-10

MORPHOLOGICAL CHARACTERIZATION OF NON-DESCRIPT CATTLE BREED IN RAIGAD DISTRICT OF MAHARASHTRA

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India has large amount of biodiversity of cattle and various domesticated animals. As per the NSSO observation, the stock of working cattle in rural area declined by 25 per cent between 1991-92 and 2002-03. The stock of milk cattle in rural area also showed a fall about 2 million in 2002-03 from 1991-92 level of 30 million. It necessitates to improve upon local non-descript cattle population for dual purpose. The data of 200 cattle on various characters of the non-descript cattle of five tahsil in Raigad district in Maharashtra were collected. The characteristics features of the non-descript cattle are small in size having body length, chest girth, height at wither and body weight as 95.69 ± 0.41 cm, 139.55 ± 0.69 cm, 85.01 ± 0.12 cm and 228.3 ± 1.94 kg, respectively. The coat colours observed were brown, black, white, grey and mixed colour in proportions of 32.72, 25.83, 17.22, 3.89 and 13.33 per cent, respectively. The average length of hair on body coat was 9.06 mm, ear length of 18.16 ± 0.22 cm, head length of 39.96 ± 0.24 and horn length of 18.35 ± 0.50 cm. The horns were medium in size, curved with backward orientation. The animal possesses black colour hooves and horizontal ear with lack of prominent poll and poorly developed udder with small teats. The average lactation milk yield, daily milk yield, lactation length and dry period were 256.84 ± 1.88 kg, 1.47 ± 0.21 kg, 202.108 ± 1.88 days and 165.75 ± 2.49 days respectively. The average age at first calving was 47.85 ± 0.40 months.

TS-I-11

PHENOTYPIC CHARACTERIZATION OF NON-DESCRIPTCATTLE BREED IN RATNAGIRI DISTRICT OF MAHARASHTRA

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Indigenous breeds of livestock possess special allelic combinations which enable them to survive the vagaries of climate, biotic and abiotic stresses and also produce and reproduce efficiently in their own environment. In order to meet the current and future challenges of food security with reference to climate change and rapidly expanding human population with sustainable management of animal genetic resources for livelihood security in developing countries, the present investigation was undertaken to study the phenotypic characteristics of non-descript cattle of Konkan region of Maharashtra. The data pertained to 360 non-descript cattle. The physical characteristics included were colour pattern of body coat, muzzle, tail switch, hoof and horn, body length, height at wither, heart girth and length of head. The main body coat colour of non-descript cattle was brown (44.44 per cent) followed by black (21.67 per cent), grey (23.89 per cent) and mixed (10 per cent). Most of the animals had black muzzle (90 per cent) and black hooves. The data on phenotypic characteristics were classified according to location, age group and sex of the animals. The means for body length, height at wither, heart girth, head length, ear length, horn length and circumference of horn at base were 97.28±0.51, 84.63±0.37, 126.97±0.49, 40.48±0.18, 18.06±0.21, 18.06±0.63 and 11.43±0.11 cm, respectively. The characteristics features of the non-descript cows are small in size having variation in colour pattern. The data generated for non-descript cattle of Ratnagiri district would be useful to characterize them.

TS-I-12

PRODUCTIVE AND REPRODUCTIVE PERFORMANCE CHARACTERISTICS OF DIFFERENT TYPES OF BUFFALOES: A REVIEW

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The birth weight in various buffalo breeds varies between 26-41 kg. As per the reports available in literature on body weights across the breeds revealed that Nili-Ravi had higher body weights at different ages followed by Murrah; while, Surti had the lowest weight at all the ages . The weight at first calving is found to range between 335-542 kg, being highest in Nili-Ravi and lowest in medium-sized buffaloes. Growth in general was linear from birth to 36 months. The average daily gain ranges from 548g (3-6 months) to 404g (birth to 36 months). Buffaloes continue to come to heat regularly in all months, highest being in October and lowest in April. However, around 75 per cent of total calving took place during July to January (the most calving season) and 25 per cent during February to June (the least calving season) suggesting that buffaloes are seasonal breeder. Buffaloes come to oestrus in cold month and are sub-fertile during hot month. A large variation in age at first calving among different breeds of buffaloes was observed with the highest value of 54.6 months in village buffaloes. The averages based on large numbers in Murrah and Nili-Ravi were between 40 and 45 months. In Surti and Bhadawari buffaloes, the age at first calving was slightly higher (46-54 months) while Pandharpuri buffaloes had an average age at first calving between 38.4 and 39.8 months. The first calving interval in Murrah and Nili-Ravi buffaloes varies between 480-573 days. In Bhadawari buffaloes it was 525 days. Average calving interval in Surti buffaloes was 462 days. The overall dry period ranged from 90-126 days in different buffalo breeds.A large variation in service period across the breeds has been observed. The overall service period in different buffalo breeds ranged from 115 days to 202 days. Lactation length is an important trait influencing the lactation milk yield in buffaloes. The overall lactation length in Murrah buffaloes ranged from 245 days to 355.39 days. However, in Nili-Ravi and Surti buffaloes, average lactation length ranged from 300 days to 356 days. In Bhadawari, Marathwada and Nagpuri buffaloes, the overall lactation length was 376, 310 and 200 days respectively. The use of part lactation records is made to reduce testing period to rank the bulls for their merit at an early age. Several workers reported that selection for milk yield could more effectively be done on part lactation because of its high heritability than the complete lactation yield. Around 10.75% of total milk yield was produced in first month of lactation while around 12.5% and 11.25% of total milk were produced in second and third months of lactation respectively. About 34.40% of total milk was produced in first three months of lactation.

The average first lactation milk yield in Murrah buffaloes varied between 1540 to 1867 kg. The first lactation averages for Bhadawari, Nagpuri and Marathwada were between 693 and 926 kg. Pandarpuri buffaloes gave a first lactation milk yield of 1375 and 1226 kg respectively in urban and rural areas. Comparison of performance details of Nili-Ravi breed of Pakistan, Murrah of India and Egyptian buffaloes revealed that 38% of all lactations in Nili-Ravi had more than 2700 kg of milk as against 14% of all lactations in Murrah and 6 % in Egyptian buffaloes. Milk yield increased over the lactations with peak yield in fourth lactation. More than 50% of the buffaloes left the herd by the end of fourth lactation and between 1 and 3% completed 10 lactations. Percentage of lactation terminated due to health and reproductive problems and death were around 30% each in lactation 1 and 2. Nili-Ravi and Murrah breeds on an average completed three lactations; some studies reported the average number of lactations completed in Murrah to vary from 4.4 to 5.8 with life time yield 8914-9994 kg and 4.5 to 5.6 lactations in Nili-Ravi buffaloes. The average number of lactations completed and life time milk yield in Surti were 3.72 and 4960 kg respectively. The average productive life in Murrah and Nili Ravi buffaloes ranged between 72.0 and 83.29 months.

Buffalo has not been exploited fully as a meat animal in India though there is little religious taboo to their slaughter. About 86% of the world buffalo meat production is in Asia and mostly from old and culled animals.

This meat is dark and less tender, has a strong odour and thus is generally unacceptable. However, when young buffaloes are raised under intensive feeding, their meat is lean, tender and highly palatable and comparable with beef from cattle of similar age and weight. The dressing percentage in buffaloes is slightly lower than in cattle. In India, 60% of the total farm power is derived from draught animals of which about 10% is from buffaloes. A buffalo can pull loads more than six times of its own body weight, but its usual load carrying capacity is 1-5 to 2.0 tonnes i.e. 3 to 4 times of its body weight. It can pull the loads for 2-3 hours continuously and for 6-8 hours in a day during winter and 5-6 hours in a day during summer with rest in between.

TS-I-13

GENETIC EVALUATION FOR FERTILITY TRAITS OF MURRAH BUFFALOES UNDER THREE DIFFERENT ZONES

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The aim of the present study was to assess the influence of temperature and humidity prevalent under subtropical climate on breeding values for fertility traits viz. service period (SP), pregnancy rate (PR) and conception rate (CR) of Murrah buffaloes in NDRI herd. Fertility data on 1379 records of 581 Murrah buffaloes spread over four lactations and climatic parameters viz. dry bulb temperature and relative humidity spanned over twenty years (1993-2012) were collected from NDRI and CSSRI, Karnal. A fixed least-squares model was applied to identify threshold temperature humidity index (THI) value for fertility traits. Three zones like non-heat stress, heat stress and critical heat stress zones were developed in a year. Genetic evaluation of Murrah buffaloes was performed in each zone with respect to their expected breeding values for fertility traits. Effect of THI was found significant ($p < 0.001$) on all fertility traits with threshold THI identified as 75. Based on THI values, a year was classified into three zones: non- heat stress zone (THI 56.71 - 73.21), heat stress zone (THI 75.39 - 81.60) and critical heat stress zone (THI 80.27 - 81.60). The expected breeding value (EBV) for SP, PR and CR were estimated as 138.57 days, 0.362 and 69.02 % in non-heat stress zone while in heat stress zone EBV were found as 139.62 days, 0.358 and 68.81 %, respectively. EBV for SP was increased to 140.92 days and for PR and CR, it declined to 0.357 and 68.71 % under critical heat stress zone. The study concluded that THI had negative influence on EBV for fertility traits under critical heat stress zone.

TS-I-14

EX SITU CONSERVATION OF BHADAWARI BUFFALOES

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Bhadawari is one of the recognized buffalo breeds of India and is famous for high fat content in their milk. These buffaloes are found in the ravines of Yamuna and Chambal rivers spread over in Uttar Pradesh and Madhya Pradesh. The buffaloes have adapted to the harsh conditions of the ravines with undulating topography, thorny and scanty bushes, climatic stress and draught conditions. The buffaloes are of medium size with moderate milk yield but the fat content in their milk. There has been a steep decline in the population of Bhadawari buffaloes from 0.1139 million to 30-40 thousand over 30 years, mainly due to the growing popularity of Murrah buffaloes in the breeding tract and non-availability of the purebred Bhadawari bulls. Indiscriminate breeding with Murrah

bulls is further diluting the purity of the breed. Looking into the reducing population of the breed, Indian Council of Agricultural Research has initiated efforts on conservation and improvement of Bhadawari buffaloes at Indian Grassland and Fodder Research Institute, Jhansi (IGFRI) under Network program since year 2001. A small herd of 50 breedable females is maintained under the project. Efforts are being made to increase the Bhadawari population in the field. Superior breeding bulls/frozen semen are being made available to different government/non government organization/farmers for AI in the Bhadawari breeding tract. More than 3 lakh doses of semen have been frozen by different agencies. Artificial insemination in the field is continuing and more than 5000 calvings have been recorded so far. A farmer has established a new herd of Bhadawari buffaloes and presently there are 30 purebred Bhadawari animals in his herd.

TS-I-15

JOWARI BUFFALO OF NORTH WEST KARNATAKA

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Jowari buffaloes are phenotypically unique and spread across the areas of Bagalkot, Belagavi and parts of Bijapur districts, the core tract being the terrains of Badami and Ramadurga blocks in Maharashtra. The tract further progresses into irrigated tracts in the periphery of Jamkhandi, Athani and Gokak areas. The area is largely rain dependent, generally dry and drought prone. The animals are reared in groups of 2-6, typically in integrated farming systems consisting of crop-livestock combinations. This population has earlier been referred as "Jowari" by Robert Wallace in a book published way back in 1888. He described the breed as local breed of the Southern Maratha country. The horns are moderately long, which go backwards, curving up, so as to form almost half circle. Though black is the prevailing colour of skin, in some cases it is brown or chestnut, and the hair is usually of a dun or dirty-whitish colour. The shanks, tip of tail, eyes, and patches on the head are generally white. The breeders, primarily the communities like Kurubas and Lingayats, attach lots of economic and nutritional value for the milk and milk products made from this breed. They prefer "Jowari" buffalo for the household milk consumption. They have expressed that the milk from Jowari buffalo is excellent for the children for their growth as it is good in taste and has many therapeutically acknowledged properties. The quality and taste of products like curd and buttermilk of Jowari buffalos also typical and preferred by the people. They also acknowledge that these buffalo are cheaper to maintain as they go for open grazing on their own and there is no dependency on stall feeding. The communities own the breed and see it a significant part of their livelihoods and culture. Majority of Jowari buffalo have medium and compact body. The animals yield an average of 4 litre per day with a fat content of 6.8% and the lactation is of around 210 days. The buffalo keepers and the local veterinarians say the animals exhibit fairly good breeding habits, first oestrus within 40-50 days, and the intercalving period of 14-16 months. The breed is locally well adapted and there is a need to conduct a detailed survey and characterisation of Jowari buffaloes.

TS-I-16

CHARACTERIZATION OF INDIGENOUS BUFFALOES OF BIRBHUM DISTRICT OF WEST BENGAL

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In the present era of extreme energy crisis, draught buffaloes act as blessings for rural poor farmers. The present study was conducted for characterization of indigenous buffaloes in Birbhum district of West Bengal (dry arid region with water scarcity and average temperature between 40°C and 15°C and average rainfall about 1430 mm) and to find out its genetic uniqueness or identity from other Buffalo breeds. Buffaloes were reared for draught purpose for pulling cart and ploughing the paddy field. They are popularly named as '***Kara***' in this region. The breed is known for more than 80 years. Mostly the Muslim farmers rear these buffaloes. The buffalo is utilized for pulling cart with coal, which can travel longer distance for the whole night around 10-12 hrs with rest period of 1-2 hrs. It forms the basis of livelihood for the rural people. The average weight carrying capacity for a pair of bullock is 1820 ± 0.65 kg, distance travelled per day 72.0 ± 0.57 km, speed of travelling 9.00 ± 0.04 km/hr, working period during agriculture (approx 4 months in a year) was 8.0 ± 0.05 hr, at other time 9.5 ± 0.06 hr, working 12 months during the year, working area ploughed 1805.976 ±15.483sq m), speed of ploughing 5.2 ± 0.02 km/hr. The basic temperament for these buffalo is docile. Coat colour is black with copper coloured, black muzzle, white or black tail switch, and hooves are black. Horn is grey coloured, curved, in upward direction. Horn length is 33.34±2.45 cm. Buffaloes were measured for body weight, chest girth, body length and height at withers, paunch girth, head length, ear length and ear width. The body is characterized by small hump, small naval flap, small dew lap. Forehead is straight. Fatigue score has been calculated based on increased rectal temperature respiration rate, pulse rate, frothing, leg incordination, excitement, inhibition of progressive movement and tongue protrusion. Drought tolerance is excellent but heat tolerance is average. These buffaloes are observed to be most resistant to diseases; specifically systemic infectious diseases (only 13.39%) compared to other livestock species in this region. Molecular characterization with mitochondrial DNA marker for these buffalo is under progress. Molecular characterization of Kara buffalo of Birbhum with functional genes as growth hormone gene and CD14 gene has been characterized, revealing distinct identity of the breed.

TS-I-17

PRODUCTION AND REPRODUCTION PERFORMANCE OF ASSAMESE BUFFALO UNDER KHUTI MANAGEMENT IN ITS BREEDING TRACT

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The Assamese buffaloes are being reared by the farmers for milk, meat as well as for draught purposes. These buffaloes are known for higher fat content in their milk (8.5 per cent on an average) and isin great demand in the market and it is also known as "Khuti milk". About 17-18 per cent of milk produced by this breed is converted to curd and ghee, being a good source of livelihood for breeders. The present study was organized by considering the data on total 324 Assamese buffaloes distributed over three districts namely Kamrup, Nagaon and Darrang in Assam covering 35 *khutis* in a period of one year and six months. The lactation milk yield of Assamese buffalo was observed as 448.38±1.67 kg with a lactation length of 237.06±0.74 days and the peak yield and days to attain the peak yield were measured as 3.41±0.02 kg and 54.16±0.19 days respectively. The reproduction traits like age at first calving, gestation period, service period and inter-calving period were estimated based on pre-structuredinterview schedule. The age at first calving was recorded as 52.28±0.81 months, the gestation period was observed as 323.10±0.68 days with an inter-calving period of 465.70±1.67 days. The service period and dry period for Assamese buffalo were estimated as 171.34±0.82 and 252.84±1.47 days respectively. The production and reproduction performance of Assamese buffaloes are poor and need special attention for further improvement to help the livestock keepers, whose livelihood is depending on these valuable AnGR (buffaloes) of Assam.

TS-I-18

BIOMETRICAL MULTIVARIATE STUDY OF MUNJAL SHEEP

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The Munjal, a mutton-type sheep, is popular among the farmers of Haryana for their heavy body weight. Munjal animals have massive body with a dark brown face. The present study was undertaken to have an assessment of type characteristics of Munjal sheep and their association with body weight. Measurements were recorded on nine morphological characteristics and adult body weight on 91 ewes and 36 rams of Munjal breed maintained at sheep farm of LUVAS, Hisar. The adult body weight in females and males were estimated as 35.28±0.61 and 45.00±0.82 kg, respectively. The height, length, heart girth and paunch girth in females were estimated as 71.07±0.34, 70.43±0.41, 80.29±0.43 and 81.93±0.55 cm, respectively. The corresponding estimates in males were obtained as 73.97±0.62, 74.08±0.73, 86.92±0.70 and 89.22±0.72 cm, respectively. The face length and head circumference in ewes were 20.81±0.12 and 44.67±0.20 cm while the corresponding estimates in rams were 23.36±0.23 and 48.50±0.41 cm, respectively. Ear length and width in Munjal ewes were estimated as 18.97±0.32 and 9.77±0.12 cm while in males these estimates were 17.81±0.43 and 8.69±0.15 cm, respectively. The tail length in females and males were estimated as 36.60±0.42 and 40.72±0.73 cm, respectively. It was observed that Munjal males had higher body linear measurements than females except for ear length and width. The association of linear body measurements with body weight indicated the highest phenotypic correlation with heart girth (r_P=0.90) followed by paunch girth and head circumference (r_P=0.83). The body index in ewes and rams were 87.80 and 85.27 per cent, respectively pointing towards the rectangular shape of Munjal sheep. Multivariate regression analysis indicated that body weight can be predicted with higher accuracy (R^2=0.85) by incorporating body length and heart girth of the animal.

TS-I-19

EVALUATION OF PRODUCTION TRAITS OF MUZAFFARNAGARI SHEEP

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Muzaffarnagari, the heaviest sheep breed of India, is distributed in and around Muzaffarnagar district of western Uttar Pradesh and also in some parts of Rajasthan, Haryana and Delhi states. The wool production of this breed is low with course quality, not suitable for carpet manufacture; hence it is mainly reared for mutton production. For evaluating production traits i.e. body weights at birth, 3, 6, 9 and 12 month age, average daily weight gains (ADG) during 0-3, 3-6, 6-9, 9-12 and 3-12 months and greasy fleece yields in lambs at first and second clip and adults (annual), the data on 690 Muzaffarnagari lambs born under ICAR-Network Project on Sheep Improvement during years 2011-13 at Central Institute for Research on Goats, Makhdoom, Farah, Mathura (UP) were recorded for various production traits. The overall least-squares means for body weights at birth, 3, 6, 9 and 12 months age were 3.75±0.02, 16.77±0.15, 24.57±0.21, 28.98±0.20 and 33.32±0.22 kg, respectively and average daily gains (ADGs) during 0–3, 3-6, 6-9, 9-12 and 3-12 months age groups were 144.50±1.61, 84.25±1.28, 53.71±1.27, 51.90±1.23 and 60.08±0.75g, respectively. The overall least-squares means for lambs 1st and 2nd six monthly and adult annual clips were 531.51±6.35, 540.01±6.52 and 1248.04±17.89g, respectively. The effect of sex and year of lambing had highly significant (P<0.01) influence on all production traits except non-significant effect of sex and year of lambing on birth weight, year of lambing on 9-12 month ADG and sex on first lamb clip. On comparison, male lambs were found superior than female lambs for all body weights, ADGs and greasy fleece yields. During the year 2013, all the body weights, ADGs and greasy fleece yields were recorded to be the highest. The maximum

growth recorded during 0-3 month (pre-weaning period) age was followed by 3-6, 6-9 and 9-12 age groups. This study indicated pre-weaning (0-3 month) growth period as most crucial with regard to lambs growth, hence it is essential to ensure proper management, feeding and health care of lambs during 0-3 month age for higher mutton production in Muzaffarnagari sheep.

TS-I-20

EVALUATION OF REPRODUCTION TRAITS OF MUZAFFARNAGARI SHEEP

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Muzaffarnagari, known for its heaviest body weight among 42 defined sheep breeds of India, is mainly distributed in Muzaffarnagar and its adjoining districts of Western Uttar Pradesh. In addition to its true breeding tract, some animals of true to breed are also found in Rajasthan, Haryana and Delhi states. Being large-sized, this breed has comparatively low reproductive efficiency as compared to small sized sheep breeds. But in this project tremendous improvement in the twinning rate has been achieved through proper screening of breeding stock using selective breeding. For this study, the data were recorded on weight at first service, date of birth of ewe, date of successful conception, date of lambing, dam's weight at lambing, number of ewes available for breeding, number of ewes bred, number of ewes lambed and number of ewes gave birth to twins/triplets from years 2011 to 2013 (3 years) maintained under Network Project on Sheep Improvement at Central Institute for Research on Goats, Makhdoom, Farah, Mathura (UP). The data were generated for age at first service, age at first lambing and gestation period from recorded data. Muzaffarnagari sheep is a mutton type breed, hence reproduction is one of the important aspect in this breed for better profitability of sheep keepers. Lower age at first service, higher conception and lambing rate with multiple births gives the number of more lambs per ewe for sale which improves return of the sheep breeders. The overall means of age at first service, weight at first service, age at first lambing, dam's weight at lambing and first gestation period were 442 days, 31.5 kg, 605 days, 36.6 kg and 153.5 days, respectively. Lambing on available and bred basis and twinning rate recorded to be 99.0, 88.2 and 11.8%; 74.3, 86.7 and 20.3%; and 76.9, 83.2 and 14.9%, respectively for the years 2011, 2012 and 2013. Results revealed significant improvement in the twinning rate over the years indicating suitability of selective breeding for improving multiple births in this breed. Findings of this study also indicated that age at first service and age at first lambing were on higher side which needs to be reduced through proper breeding management of ewes and culling of ewes with poor reproduction efficiency.

TS-I-21

SURVIVAL RATE OF MUZAFFARNAGARI SHEEP UNDER ORGANIZED FARM

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Muzaffarnagari, a heaviest mutton type sheep breed of the country, is distributed in Muzaffarnagar and its adjoining districts of Western Uttar Pradesh viz. Meerut, Bulandshahar, Saharanpur and Bijnor. However, the animals are also found in good number in some of the parts of Delhi and Haryana and Rajasthan states. For this study, the data were recorded from the research project entitled "Genetic evaluation and improvement of Muzaffarnagari sheep for body weights" for a period of four years (2010-11 to 2013-14) maintained under Network Project on Sheep Improvement at Central Institute for Research on Goats, Makhdoom, Farah, Mathura (UP). For a mutton breed, survival rate is the single most important factor which directly determines the profitability of sheep breeders. In this project, the lambs were weaned at 2 months of age due to poor milk production and short lactation period of their dams. After weaning, the lambs were maintained under semi intensive feeding system, in which they were provided 100- 400g growth ration (concentrate) during various growth stages with some dry and green fodder and 5-6 hours grazing daily. Breeding rams were selected based on their 6 month body weights. To study survival rate, the data were recorded on number of animals survived in various age groups viz. suckling males, suckling females, weaner males, weaner females, hogget males, hogget females, rams and ewes. The survival per cent were 95.9, 97.2, 93.4, 98.8, 100.0, 100.0, 96.7 and 97.2 (2010-11); 98.4, 99.5, 98.1, 99.3, 99.2, 99.1, 97.6 and 98.4 (2011-12), 96.3, 96.1, 93.5, 97.1, 100.0, 99.29, 98.7 and 97.7 (2012-13) and 98.7, 98.0, 99.4, 98.0, 96.3, 95.6, 100.0 and 96.7 (2013-14), respectively. The overall survivability in Muzaffarnagari sheep was recorded to be 97.5, 97.3, 98.5, 97.8 and 96.01%, respectively in 0-3, 3-6, 6-12, adults and in total. The results of this study indicated the hardiness of the breed which may further be improved by providing effective health and other environmental conditions to the animals.

TS-I-22

A STUDY ON PHYSICAL CHARACTERISTICS OF MANDYA SHEEP UNDER FIELD CONDITIONS

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A study was conducted to characterize the physical/ conformation characters of Mandya sheep under field conditions. The location of the study included villages of Malavalli taluk, Mandya district, Karnataka (home tract). A typical Mandya sheep is relatively small, having white to cream coat colour, long and droopy ears, possessing squarely placed short legs and typical reversed U shape conformation from rear indicative of high fleshiness. The birth weight of lambs is around 2 kg and an adult female and male animal weigh about 25 and 35 kg, respectively. The flock strength was found to be in the range of 04 to 81 animals with average flock strength of 19 animals per family. In the present study physical characteristics of 939 Mandya sheep belonging to different age groups were recorded. The least-squares means for body weight, face length, tail length, chest girth, body length, wither height, shoulder width, fore leg length, chest depth, distance between hip bones and distance between withers to pin bone were 27.64±1.08 kg, 15.12±0.31, 13.35±0.33, 67.96±0.59, 63.96±1.03, 49.73±0.83, 50.39±1.26, 23.92±0.48, 39.54±0.70, 15.73±0.55 and 57.46±0.70cm, respectively in adult rams (n=26); 23.84±0.15 kg, 13.64±0.07, 12.70±0.07, 66.25±0.20, 61.47±0.21, 46.24±0.16, 48.20±0.19, 23.15±0.10, 37.63±0.16, 16.69±0.17 and 54.18±0.20 cm, respectively in adult ewes (n=608); 13.45±0.78 kg, 12.45±0.42, 11.75±0.38, 58.95±1.26,55.45±1.13, 45.30±1.07, 44.90±2.12, 22.00±0.64, 37.15±1.44, 14.80±1.69 and 49.50±2.21 cm, respectively in 6 months old ram lambs (n=20); 12.68±0.20 kg, 11.98±0.11, 11.62±0.14, 56.90±0.59, 55.19±0.59, 42.31±0.30, 43.61±0.51, 21.44±0.23, 33.96±0.34, 13.41±0.16 and 48.56±0.38 cm, respectively in 6 months old ewe lambs (n=124); 7.23±0.34 kg, 10.54±0.10, 10.61±0.28, 48.95±0.72, 48.39±0.70, 37.05±0.72, 39.61±0.73, 20.39±0.93, 31.54±0.81, 11.58±0.23 and 43.49±0.68cm, respectively in 3 months old ram lambs (n=41); and 7.38±0.23 kg, 10.94±0.13, 10.67±0.14, 49.43±0.57, 47.85±0.57, 38.11±0.36, 38.19±0.53, 19.56±0.18, 30.03±0.35, 13.36±0.94 and 43.57±0.40 cm, respectively in three months old ewe lambs (n=120). These body measurements are helpful in describing breed characteristics, evaluation of meat production potential and prediction of body weight under field condition.

TS-I-23

STUDY ON PRE-WEANING MORTALITY PATTERN OF NELLORE LAMBS IN AN ORGANIZED FARM

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A study was conducted to ascertain the information on different causes of lamb mortality before weaning at 3 months of age and also to guide the farmers to undertake suitable measures for controlling mortality. Data on pre-weaning mortality of lambs of both sexes were collected from the records of the farm dispensary from April, 2007 to March, 2014. The present investigation had revealed that the winter and rainy seasons have crucial role in lamb survivability. During the study period, a total of 1753 lambs were born and 110 lambs died and constituted an overall mortality of 6.27 per cent. Out of the total deaths, high mortality was noticed in the month of February (23.64%) followed by December (16.36%) and January (13.64%). There was a high mortality (59.1%) during winter season and less mortality was recorded in rainy season. Among the total mortality majority (37.27%) of lambs died with respiratory diseases especially pneumonia followed by digestive system disorders (31.82%).

TS-I-24

GROWTH PERFORMANCE OF MADGYAL: AN UNEXPLORED SHEEP BREED

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The records on body weight of Madgyal Sheep available at Madgyal Sheep Farm of Punyashlok Ahiladevi Sheep and Goat Development Corporation, A/p. Ranjhani, Sangali, Maharashtra were used for present investigation.The overall least-squares means were 2.94 ± 0.031, 19.39 ± 0.098, 32.94 ± 0.159, 37.42 ± 0.423 and 41.65 ± 0.465 kg for body weight at birth, three, six, nine and twelve months of age respectively. While the means for daily gain in weights at corresponding ages were 0.182 ± 0.001, 0.151 ± 0.001, 0.054 ± 0.003 and 0.046 ± 0.003 kg respectively.The effects of year and season of birth were significant ($P < 0.01$) on body weights at all the ages, except effect of year of birth on birth weight where it was non-significant. The effect of sex on body weights at all ages was non-significant. The year of birth showed significant effect on daily gain in weight at all the growth stages. Similarly, season of birth also exerted significant influence on daily gain in weight from birth to three months, three to six months, six to nine months.However, it was non-significant during daily gain from nine to twelve months age group. Sex had significant influence ($P< 0.01$) on daily gain in weight from birth to three months and nine to twelve months, while it was non-significant in daily gain weight from three months to six months and six months to nine months of age groups.The type of birth had significant influence ($P < 0.01$) on birth, three, six and nine months weight and daily gain in weight at birth to three months and nine to twelve months. Whereas, it was non-significant on twelve months weight, daily gain in weight at three to six months and six to nine month weight.The significant influence of year and season of birth indicated that the environment and management plays the vital role in growth performance of Madgyal Sheep.

TS-I-25

DUMA SHEEP OF GUJARAT: A POTENTIAL NEW RESOURCE

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Duma (Dumma) is a breed of sheep native to Gujarat not yet recognized as distinct breed. Its home tract is Saylataluka of Surendranagar district. The breed is very popular among the breeders and has spread to Bhavnagar, Kutch, Anand, Kheda and Ahmedabad districts. The breed is also known as Dumba or Baraiya. Mainly Rabari&Bharwad communities rear this breed. Government of Gujarat recently initiated the project on "Characterization and Registration of Lesser Known Livestock Breeds of Gujarat". Sahjeevan Trust has been entrusted with the survey and characterization of such local breeds in the State. Sahjeevan trust conducted preliminary survey in the breeding tract. Its population is estimated to be 1,62,996 as per the recent census. The animals have blackish to light brown face; colour extending upto ventral part of neck, body, covering both fore & hind quarters. Animals are majestic in appearance, large in size having long legs and long tail. The sheep have excellent migratory ability. Animals migrate for around 8-10 months soon after the lambing season, September/October. They gain 18-20 kg weight at the age of four months showing its excellent suitability to be developed as a mutton breed. It is interesting to note that Duma sheep also have well developed udder and teats and the animals show good milk yield. Ears are long and pendulous. Annual wool production of the sheep is nearly one kg. In some cases, tactile hairs have been found on wattles. Duma sheep breeders live nomadic lifestyle, and follow extensive grazing system. Duma sheep owners usually keep only one breedable ram in the flock. They follow selective breeding, and prefer rams with high milk yield of dam. They also follow controlled breeding. Ram is always kept with the flock, but the owners allow breeding only during April/May so that lambing occurs during September/October (around Navratri/Diwali) and hence there is only one lambing per year.The animals have good walking ability and meat characters, have wool quality better than Marwadi and good milk capacity hence very popular among the breeders. The breed has potential to be developed as meat and milk breed. There is need to conserve this valuable genetic resource.

TS-I-26

CHARACTERIZATION OF INDIGENOUS SHEEP OF BIRBHUM DISTRICT OF WEST BENGAL

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West Bengal has varied agroclimatic regions, like hilly mountain, dry arid, alluvial and coastal regions. The present study was conducted for characterization of indigenous sheep in Birbhum district of West Bengal (dry aid region, with water scarcity, average temperature between 40°C and 15°C and average rainfall about 1430 mm) to find out its genetic uniqueness or identity from other sheep breeds of West Bengal. The sheep maintained by farmers at village were interrogated, samples collected and measurements taken. The sheep were characterized based on phenotypic characters such as body colour, shape, growth (body weight and body measurement), reproductive traits (litter size, age at first kidding/ lambing, age at first service, weight at first service, gestation period and post-partum estrus), wool characteristics (greasy fleece weight, clean fleece weight, staple length, fibre diameter, medullation percentage), disease resistance(incidences of infectious diseases and nematode count through faecal egg count) and blood biochemical characteristics (haemoglobin percentage, total erythrocytic count, total leucocytic count, differential leucocytic count and packed cell volume). Multivariate cluster analysis revealed that Birbhum sheep were clustered separately in the phylogenetic tree, indicating a new breed distinct from other previously reported breeds of West Bengal, namely Garole, Bonpala and Chotanagpuri. These Birbhum sheep were originated in the Birbhum district of West Bengal and they are known for more than 80 years, reared mostly for meat purpose. Body colour ranges from white, grey to deep brown, either intact or patchy. They have slightly convex head, with horizontal ears, two horns (black or grey-coloured) present only in rams not in ewes. Wattles were absent. The head, face and legs were devoid of wool, whereas rest of the body is covered by wool of medium staple length, non-lustrous, straight or low crimp. Beard is absent and tail is drooping downwards. The peculiarity of these Birbhum sheep is that 30.6% of sheep had rudimentary ear, high disease resistance and better litter size. Hence, rudimentary ear may be one of the breed characteristics of these Birbhum sheep. The wool obtained as by-product may be utilized for carpet wool production.

TS-I-27

STUDIES ON REPRODUCTIVE TRAITS OF LOCAL GOATS OF KARNATAKA

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A study was conducted to assess the reproductive status of local goats of southern Karnataka. Two hundred and fifteen flocks were randomly identified and were followed for a period of three years to assess the different reproductive traits under field conditions. The approximate mating ratio of 20 females: 1 male was maintained and the males were replaced from local shandy or neighbouring villages after two to three years. None of the rearers were maintaining breeding records except that some of the older males and females were retained without culling in few of the flocks. The age at maturity in males was 10 months onwards but was allowed to mate only at one and a half years of age. The males which were not used for breeding were castrated and allowed to fatten and sold off. The age at maturity ranged from 7.5 to 8.25 months (approximately 225 to 250 days). The average gestation period was 151.53 ± 0.27 days. The average litter size was 1.67 ± 5.08 with more frequent occurrence of twins. The percentage of multiple births was 46.97 per cent. The average age at weaning was 4.44 ± 0.09 months and that of age at first kidding was 16.94 ± 0.24 months. The mean lactation period was 5.08 ± 0.08 and the average kidding interval was 9.53 ± 1.04 months.

TS-I-28

CHARACTERIZATION AND PERFORMANCE OF SIKKIM GOATS IN ITS NATIVE TRACT

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Nestled in the lap of the Himalayas, bounded by some of the highest mountain peaks, amidst spectacular terrains, pristine lakes, luxuriant forests, Sikkim is one of the 26 biodiversity hot spots. Coming to the type of species, mammals found are 150, birds 552 and fishes 48. Among the livestock species cattle, sheep, goat and yak are the important resources supporting the livelihood of poor and marginal farmers. The goat population of Sikkim state of NEH region of India has increased from 110120 (18th Livestock Census, 2007) to 113364 (19th Livestock Census, 2012) spread in all the four districts i.e. East Sikkim (18046), West Sikkim (45232), North Sikkim (15018) and South Sikkim (31824). The males and females are almost in equal proportion (53103 and 60261 respectively. The study was planned to know the phenotype and biometry of Sikkim goats. The visits were made to all the four (East, West, North and South) districts of Sikkim to record information on phenotypic and biometric traits of its native goats. The flocks seen consisted of Jet black, white, and brown coats. Animals with mixture of these colours were also seen. The goats having stripes on face extending from base of horn to the muzzle mainly constituted the flocks. These goats are called as Singharey by the local people. These goats have been surviving in the Himalayan terrain of Sikkim since ancient times. The goats are maintained on semi-extensive management by small and marginal farmers mainly for meat purpose. They are small to medium-sized. In Singharey breeding males, black ring is present around the neck but not in castrated males. The horns are strong orienting upward and backward. The under belly is generally light brown or white. Ears are medium and semi- pendulous. Legs are short and stout. Black top line was seen in Singharey goats. The flock size with a farmer varied from 2 to 15. Body measurements were recorded for height at withers, body length, chest girth, paunch girth, face length, horn length, ear length and tail length of 239 male and female adult goats belonging to different districts. Body weights were also taken with the help of spring balance. Analysis of data revealed the mean body measurements for height at withers, body length, chest girth, paunch girth, face length, horn length, ear length and tail length of adult females (131) as 51.39±0.56, 59.47±0.47, 69.41±0.48, 77.76±0.83, 16.71±0.14, 9.56±0.30, 12.92±0.16 and 10.55±0.16 cm, respectively. The corresponding estimates in adult males (108) were 55.86±0.69, 61.94±0.69, 72.96±0.70, 78.29±0.91, 17.48±0.16, 14.55±0.44, 13.12±0.18, and 11.83±0.19 cm, respectively. The adult body weights in female and male goats were 28.07±0.45 and 32.31±0.76 kg respectively. District-wise body weights (kg) of adult females were 26.31±1.11 (East), 29.38±0.87 (North), 27.84± 0.65 (South) and 27.51±0.80 (West) and of males were 28.80±0.79 (East), 36.06±2.4 (North), 30.43±1.40 (South) and 33.86±1.28 (West) respectively. Natural service is preferred for breeding. Goat shelters are made temporarily of bamboos and wooden logs. Most of the houses were made 3 to 4 feet above the ground level with wooden floor. This type of raised housing keeps the houses free from accumulation of urine and feaces and thus prevents the animals from infections. Stall-fed goats are kept on local grass, crushed maize and tree leaves.

TS-I-29

A REPORT ON THE MILK PRODUCTION PERFORMANCE OF INDIGENOUS GOAT BREEDS UNDER INTENSIVE FARMING SYSTEM IN KARNATAKA

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Four indigenous goat breeds maintained in a private dairy goat farm (Yashodavana goat farm, Yadehalli, Nanjagud Taluk, Mysore dist.) were considered for this study. The goat breeds viz., Beetal, Zalawadi, Sirohi and Parbhatsari procured by the farmer from different parts of Rajasthan are manitained in the farm since 2011. Intensive system of management is practised in the farm wherein the goats are maintained in the sheds constructed on a raised platform with a pen and run. *Ad libitum* chaffed green and dry fodder is fed to the goats that are culitvated in the farm along with pelleted concentrates and azolla grown in the farm. The birth weight of the kids was in the range of 3.28 to 4.28 kg. The goats at maturity were weighing from 20 to 22 kg and the fully grown adult males were in the range of 40 to 60 kg. The milk production per day from lactating goats ranged from 0.7 to 1.225 litres. The fat content in the milk samples of Beetal, Zalawadi, Sirohi and Parbhatsari were observed to be 4.9, 6.1, 5.2 and 5.1 percentages respectively, while SNF was 8.2, 7.85, 8.39 and 8.49 percentages respectively. The total protein and casein content were highest in Parbhatsari breed (3.4% and 2.8%), followed by Sirohi (3.23% and 2.66%), Zalawadi (3.2% and 2.63) and Beetal (2.66% and 2.38%) breeds of goats. Based on these observations and other information pertaining to breeding and kidding performance, it is found that the four indigenous goat breeds can adapt well to the intensive system of rearing for milk production in Karnataka.

TS-I-30

REPRODUCTIVE PERFORMANCE OF SIROHI GOAT IN AN ORGANIZED FARM IN RAJASTHAN

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Sirohi is a very popular medium-sized dual purpose goat breed widely distributed in Sirohi, Ajmer, Tonk, Nagaur, Bhilwara, Udaipur, Jaipur and other districts of Rajasthan, and adjoining areas of its neighbouring states. Reproductive traits are important indicators of the doe's production and productivity. The data pertaining to the period of kidding from 2009 to 2014 related to different parameters of reproductive traits of Sirohi does maintained in semi-arid condition under All India Coordinated Research Project on Goat Improvement (AICRP) at ICAR - Central Sheep & Wool Research Institute (CSWRI)), Avikanagar, Rajasthan, were analyzed. The does were maintained separately from the bucks under controlled breeding condition and only bred during the specific breeding season. The overall least-squares (LS) means of age at 1st service, age at 1st successful service, age at 1st kidding and 1st gestation period were 593.93±5.86, 600.58±5.93, 749.13±5.85 and 147.76±0.15 days, respectively. The overall LS means of weight at 1st service, weight at 1st successful service, weight at 1st kidding and no. of services per conception were 30.92±0.23, 32.18±0.29 and 32.81±0.22 kg, and 1.21±0.04, respectively. The overall tupping percentage was 88.39. The breeding efficiency on does available and tupped basis were 69.0 and 78.28 per cent, respectively. The kidding percentage on does available and tupped basis were 76.29 and 86.55, respectively. The overall litter size was 1:1.13.

TS-I-31

KATHEWADI GOAT: A BOON TO HILLY AREAS OF KHANDESH REGION OF MAHARASTRA

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The migratory nomadic shepherds / cattle grazers from Kathewad region of Gujarat used to migrate to Dhulia district for grazing their animals being it an assured rain fall area with some goats as a leader. They donate some males while returning to their native place which were used as a buck for breeding of local does. This practice was followed for a long time, resulted into development of a new phenotypically stabilized breed, locally called Kathewadi goat breed. The survey was carried out to characterise the breed by using the proforma developed by the NBAGR, Karnal. The breed is having predominant black colour, white spot on body and some brownish black colour with long hair, strong compact body, long ear, short tail, well developed udder, long twisted horns, black hooves. Wattle and beard is present in males. It produces an average of 2.5 to 3 L milk per day. It thrives well by grazing on agricultural residues after harvest. In first kidding, single kid is common; however, twining and triplet percentage (about 45 %) increases in subsequent kiddings. In Kathewadi goats coat colours were black, black with white patches, brownish black and brown in the proportion of 88.37, 4.75, 3.42 and 3.46 per cent respectively. All goats had black coloured muzzle, eyelid and hooves. The skin colour observed in surveyed population of all Kathewadi goats was gray. About 94.55% of Kathewadi goats had horns while lesser proportion of animals were polled (5.45%). The horn pattern revealed spiral and curved (100%) shapes. Horns were oriented upward and backward (86.38%) and downward (13.62%). In most of horned goats average length of horn was 19.42 ± 0.18 cm. All goats had pendulous ear with average ear length of 23.18 + 0.34 cm. Fore head of Kathewadi goat was overall convex type (93.33%) followed by straight and flat head type (6.67%). The overall percentage of wattles in goats was 98.70 per cent and only 1.30 per cent goats did not have wattles. The overall percentage of the goats not having beard was 90.29 per cent and only 9.30 per cent (male and female) goats had beard. The shape of tail was medium in all goats with average length of 19.18 ± 0.17 cm. The tail types were slender type (86.33%) and bunchy type (13.67%). The tail shapes were recorded as straight tail (98.33%) and curved (1.67%). All does had bowl shape udder with cylindrical teats having pointed tip. The average weight at birth, 3 month, 6 month, 9 month, and 12 month was 2.91± 0.17, 11.45±0.36, 17.12±0.93, 21.51±0.42 and 26.21± 0.97 kg, respectively. Average body length of 73-75 cm, chest girth of 75-80 cm, height of 80-85 cm, horn length of 15-17 cm, ear length of 24-26 cm, tail length of 16-19 cm and teat length of 12-14 cm were observed in Kathewadi goat.

TS-I-32

EVALUATION OF PRODUCTION TRAITS OF JAMUNAPARI GOATS

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Jamunapari, known for highest milk yield and body growth, is native of Chakarnagar area of Etawah district in western Uttar Pradesh. The breed is highly adapted to the ravines of Yamuna, Chambal and Kwari rivers, which have dense vegetation for browsing. For evaluating production traits i.e. body weights at birth, 3, 6, 9 and 12 month age and milk yields in 90 and 140 days, the body weight data on 1583 Jamunapari kids and 1025 lactation records of does maintained under All India Coordinated Research Project (AICRP) on Jamunapari goats during years 2010-14 at Central Institute for Research on Goats, Makhdoom, Farah, Mathura (UP) were recorded. The overall least-squares means for body weights at birth, 3, 6, 9 and 12 months age were 3.20±0.03, 11.29±0.10, 16.00±0.22, 19.61±0.23 and 25.04±0.29 kg, respectively and 90 and 140 days milk yield were 77.670±1.998 and 109.783±3.066 L, respectively. The effect of sex, year of kidding, season of kidding, type of birth and parity had highly significant ($P<0.01$) influence on all the body weights and milk yields except non-significant effect of season of kidding on birth weight, season of kidding and type of birth on 90 and 140 days milk yield. Comparison of body weight in two sexes indicated that male lambs gained significantly higher weights than female lambs at all stages which might be due to quantitative differences in the secretion of growth and sex hormones in two sexes. The body weights were also found significantly higher in the kids born in season two as compared to season first born kids due to availability of better environmental conditions to kids born during season second. As compared to twins and triplets, the kids born as singles, gained heavier body weight might be due to availability of better nutrition during pregnancy and availability of more milk after birth through suckling. The body weights of kids in different years did not show any definite trend. However, the kids born in year 2014 were found to be superior in growth as compared to previous years. The difference in the weights in different years may be attributed to variation in availability of foraging material in pasture during different years and variation in the genetic composition of the flock over different years. Results indicated that around 59% body weight gain was only during pre-weaning (0-3 month) growth period and hence it is essential to ensure proper management, feeding and health care to kids during 0-3 month of age for achieving higher body weight gain in Jamunapari goats.

TS-I-33

ROLE OF BARBARI GOAT NUCLEUS FARM FOR ITS FIELD IMPROVEMENT AND CONSERVATION

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Barbari is one of the dual purpose goat breed with greater recognition as a meat breed due to higher body weight gain per unit of time, prolificacy, reproductive efficiency and sufficient milk to nourish high litter size. The Barbari goats are maintained under All India Coordinated Research project from 1993 with the objectives of enhancing genetic potential of these goats through selection, supply of superior germplasm to the goat keepers for field improvement, conservation and livelihood improvement of stakeholders. Data on production and reproduction performance of these goats were analysed for the period from 2009 to 2013. Population growth of Barbari goats varies from 1.43 (2009) to 1.60 (2013). The overall means of body weight of kids at birth, 3, 6, 9 and 12 month of ages were 1.77±0.01, 7.63±0.06, 11.21±0.10, 15.71±0.17 and 19.16±0.20 kg, respectively. Year, season, sex of kid, type of birth and parity had significant effects on body weight at different stages of growth. Kids born during autumn season attained significantly higher body weight at 6, 9 and 12 months of ages. Single born kids were significantly heavier than those born as multiple. Similarly males were heavier than their counterpart right from birth to 12 months of ages. The estimates of heritability (h^2) for body weight of kids at birth, 3, 6, 9, and 12 months of age were 0.189±0.043, 0.231±0.048, 0.260±0.051, 0.494±0.074 and 0.655±0.088. The overall means for 90-day milk yield, 140-day milk yield, total lactation yield and lactation length for the does kidded in 2013-14 were 58.10, 81.78 and 69.67 liters, and 132 days, respectively. Does kidded during spring season produced significantly higher milk production for 90-day, 140-day milk yield, lactation yield, and lactation length than those kidded in autumn season. Ninety days milk yield increases up to 3rdlactation then remained highest in 4th and 5th parity thereafter declined with the advancement of parity order. The estimates of h^2 for MY90, MY140, LMY and LL were 0.465±0.131, 0.483±0.133, 0.445±0.129 and 0.309±0.115 respectively. Overall means for age and weight first mating, age and weight after first kidding, kidding interval and gestation period were 354.7±6.4 days, 15.01±2.3 kg, 422.3±5.2 days, 16.01±2.3 kg, 221.04±7.2 days and 145.4±1.4 days, respectively. During the period from 2009 to 2013, about 1255 superior Barbari were distributed to the farmers and goat development agencies. More than 5000 doses of semen of superior bucks preserved for field improvement through artificial Insemination.

TS-I-34

EVALUATION OF SECOND GENERATION (S_1) OF INDIGENOUS CHICKEN PERTAINING TO TWO DIVISIONS OF KARNATAKA

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A study was undertaken to evaluate the S_1 generation of indigenous chicken pertaining to Bengaluru and Mysore divisions of Karnataka, being maintained at AICRP on Poultry Breeding for Meat, Bengaluru centre and to compare with S_o generation for morphological and production traits. The chicks were wing-banded and reared under deep litter system between zero and fifty two weeks. The feather distribution, plumage colour, primary and secondary plumage patterns, comb types, ear lobe colour, shank colour, eye colour, presence or absence of wattles, egg shell colour and skin colour were visually examined. The shank length, keel length, albumen index, shape index were measured by vernier callipers. The body weights, albumen weight, yolk weight and egg weight were measured by weigh balance. Breast angle and shell thickness were measured by Anglo meter and Screw gauge. Percentage hatchability on TES and FES were also measured. The morphological features recorded revealed 100%

normal feather morphology indicating no structural variations in feather such as frizzle, silky and crested. The most prevalent plumage colour observed was brown followed by mixed. Other coloured plumages recorded were black, red, blue and white in small percentages. The most prevalent primary plumage pattern observed was solid and dull colour. Other primary plumage patterns recorded were patchy, mottled, striped, spotted and barred. The major secondary plumage pattern observed was self-red and self-black colour. Other secondary plumage patterns recorded were self-white, self-blue, mottled, barred and lacing. All the birds evaluated had red ear lobes. Major eye colour observed was brown and grey. Majority of birds had yellow shank. The predominant egg shell colour recorded was brown followed by light brown and creamy. The average egg weight and shape index of indigenous chicken ranged from 45.22 to 46.53g. The shape index was between 74 and 75. The average values for albumen weight, albumen index, yolk weight, yolk index, Haugh unit score and shell thickness of the eggs ranged from 23 to 24g, 0.061 to 0.068, 14 to 16g, 0.42 to 0.44, 65 to 70 and 0.35mm. The present study indicated no significant difference between the two generations with respect to morphological and performance parameters.

TS-I-35

STUDY ON PRODUCTIVE PERFORMANCE OF UTTARA FOWL

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Present study was conducted to evaluate the productive performance of Uttara fowl under farm conditions which was carried out at Instructional Poultry Farm of University. The experimental Uttara fowl were divided into two groups, *viz*. comb and crown type ecotypes consisting of fifty five birds under each ecotypes. The mean values of egg and body weight at day old. 4, 8 and 12 weeks of age were 48.16±0.83, 33.61±0.47, 181.24±5.55, 476.32±6.06 and 832.72±9.17g in comb type and 49.66±0.58, 32.42±0.54, 173.92±7.79, 435.10±12.30 and 812.48±5.85g in crown type of Uttara fowl. Results revealed that the egg and body weights observed in these two ecotypes had significant difference and these two ecotypes have great potential to develop as dual purpose bird for hill backyard poultry which can be achieved through intensive selection and breeding programme.

TS-I-36

PERFORMANCE OF NANDANAM B_3 CHICKEN UNDER FIELD CONDITIONS

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A total of 2333 Nandanam B_3 (synthetic multi-coloured broiler strain developed for meat purpose by Poultry Research Station, TANUVAS) chicks were distributed to rural poultry farmers during 2014. The performance data were collected from six progressive farmers in and around Chennai and Kanchipuram district of Tamilnadu who have adopted scientific management practices and the birds were fed with commercial broiler diets as prescribed by BIS 2007 i.e. pre-starter diet up to 7 days, starter up to 3 weeks and finisher up to marketing age (8 weeks). The analysis of data revealed that the Nandanam B_3 attained a body weight of 1.368 kg with a feed efficiency of 2.80 and livability of 91 per cent at 8 weeks of age. The average dressing yield was 71 per cent. The sensory attributes such as taste and flavour of the meat were well relished by the consumers when compared to commercial broiler meat. This variety has got very good demand among rural poultry farmers because of its multi-coloured plumage, higher body weight and meat with desirable flavour.

TS-I-37

INHERITANCE OF GROWTH AND CONFORMATIONAL TRAITS IN PB-2 LINE

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PB-2 is a synthetic coloured broiler female parent line with multi-coloured plumage and developed by independent culling level method of selection with 5 week body weight and 40 week part period egg production as the traits for selection. This line has been used as a female parent line for the production of KrishiBro, a coloured commercial broiler developed by the Directorate for the niche market. In the present study, the juvenile growth and conformational traits were evaluated from the data collected from 4791 chicks during the S-24 generation. These chicks were obtained from 60 sires and 300 dams in four hatches. The pedigreed data were analyzed using the least-squares technique and the hatch corrected data were used for estimation of heritability by variance component analysis. The genetic and phenotypic correlations were estimated from the variance-covariance component analysis. The per cent fertility was 88.14 while the hatchability on TES and FES were 78.84 and 89.45%, respectively. The least-squares means for day-old, two and four week's body weight were 40.15±0.06, 229.47±0.52 and 681.43±1.81 g, respectively. The body weight, shank length and breast angle at five weeks was 987.41±2.17g, 82.03±0.08mm and 86.44±0.08°, respectively. The heritability estimates (sire+dam) for the body weight, shank length and breast angle at five weeks were 0.16±0.02, 0.13±0.02 and 0.004±0.001, respectively. The sire and dam component of heritability for the primary selection trait i.e., 5 week body weight was 0.12±0.04 and 0.21±0.04, respectively. The genetic and phenotypic correlation for the five week body weight and shank length was 0.77±0.07 and 0.39±0.06, respectively. The body weight and breast angle and the breast angle and shank length also were positively correlated. The study indicated that the heritability estimates were low to moderate for the growth and conformational traits. The lower heritability of the sire component for the 5 week body weight in the present study shows reduced additive genetic variance indicating the decreased variability in the population which might have been due to continuous selection for body weight for past twenty three generations.

TS-I-38

GROWTH STUDIES ON BLACK, BROWN AND CARI STRAINS OF JAPANESE QUAILS

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The Black (203), Brown (204) and CARI (427) strains of Japanese quails obtained in eleven hatches and maintained at the College of Veterinary Science, Rajendranagar, Hyderabad were utilized for the present investigation. The data on body weights at day-old, 2, 4, 6, 8, 10 and 14 weeks were recorded. The ADG from day-old to 14 weeks of age at bi-weekly intervals and cumulative body weight gains from day-old to 6 weeks age were obtained. The effects of strain, hatch and sex of the birds on body weights, average daily gain and cumulative growth rates were obtained by least-squares analysis. The effect of strain was significant on body weights at all the ages studied except at 2nd week, while it has significantly affected the ADGs during 2-4, 6-8, 8-10 and 10-14 weeks of age. The black birds were significantly heavier than the brown and CARI strain throughout the period of study. The ADG also followed a similar trend. The body weights at hatch, 2, 4, 6, 8 and 14 weeks of age were significantly influenced by hatch and it was also having significant influence on average daily gain at all the age's studied except at 10-14 weeks of age without showing any predictable trend. The females weighed significantly heavier than the males. The cumulative growth rates at 6th week was significantly influenced by strain, hatch and sex of the bird and black quails recorded highest cumulative growth rate of 4.93 g, while lowest of 4.57 g was recorded by brown strain. The overall least-squares means for body weight at hatch, 2, 4, 6, 8, 10 and 14 weeks of age were 8.26, 66.04, 156.99, 208.78, 243.58, 267.02 and 294.76 g, respectively while the overall average daily gains from day-old to 2, 2-4, 4-6,

6-8, 8-10 and 10-14 weeks of age was 4.13, 6.50, 3.78, 2.83, 1.73, 1.05 and 1.13 g respectively. The average daily gain increased from birth to 4th week and decreased gradually thereafter. The overall performance of Black strain of Japanese quails was the best followed by the brown and CARI strains.

TS-I-39

A STUDY ON THE GROWTH PERFORMANCE OF NEW ZEALAND WHITE RABBITS

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Data on growth traits of 610 New Zealand White bunnies born out of 89 litters sired by 25 bucks mated to 46 does maintained at Rabbit Research Centre, College of Veterinary Science, Hyderabad were utilized for the present study. Mean litter size was 5.91 ± 1.73 at birth and 3.64 ± 1.72 at weaning. Litter size at birth had a significant influence on all the body weights studied with bunnies from smaller litters recording higher weights than those from larger litters. The overall mean body weights at birth, 1, 2, 3, 4, 6, 8, 10, 12, 14 and 16 weeks of age were 49.39 ± 0.50, 108.60 ± 1.77, 149.18 ± 1.81, 189.57 ± 4.96, 397.27 ± 14.15, 546.00 ± 16.65, 733.91 ± 21.05, 951.37 ± 21.84, 1,168.79 ± 22.96, 1,361.20 ± 26.55 and 1,636.48 ± 40.39 g, respectively. Heritabilities for body weight at birth, 1, 8, 10, 12, 14 and 16 weeks were estimated to be 0.52 ± 0.22, 0.75 ± 0.24, 0.67 ± 0.23, 0.49 ± 0.22, 0.59 ± 0.23, 0.51 ± 0.22 and 0.61 ± 0.23, respectively while the heritabilites for body weights at 3, 4, 5 and 6 weeks were outside the normal range. The phenotypic correlations among pre-weaning body weights ranged from 0.29 to 0.67 while that among post-weaning body weights ranged from 0.21 to 0.85. Substantial phenotypic association among body weights and medium heritability recorded by body weights hint at the possibility of improving the performance of New Zealand White rabbits.

TS-I-40

KACHCHHI HORSE OF GUJARAT: A VALUABLE RESOURCE

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Kachchhi is a lesser known breed of horse native to Kachchh district of Gujarat and is distinctly different from other two native recognized horse breeds of Gujarat, Kathiawadi and Marwadi. Rearing of this breed is known since more than a century. Rulers of Kachchh province are known to have kept Kachchhi horses in their stables. The breed is preferred locally for multiple purposes, including mainly the load carriage and transportation. However, they are also in demand outside the Kachchh district mainly for its 'Rewalchal' - a special type of gait with speed and stamina. Kachchhi horses can perform 'Rewal' gait with great speed covering much longer distance than Kathiawari or Marwari horses. According to Kachchhi horse breeders, "rider can carry buttermilk (liquid) on the back of Kachchhi horse in open vessel to a long distance without any drop spilling out". Earlier, these horses were used especially in police, irrigation and revenue departments for various services notably during the pre-partition time. This breed has also been promoted for local horse races and regularly used in traditional *mela*. This trend has declined in the last few decades. As a result, the Kachchhi horse lovers have moved to other professions leaving

this breed to its own fate. Hence, the population and purity of this breed has declined and the breed is under threat. Considering its status, Gujarat Government has initiated a project on "characterization and registration of lesser known livestock breeds of Gujarat" including this breed. Preliminary survey conducted in the tract by Sahjeevan Trust with the help of *Ram Rahim Kachchhi Sindhi Aswhapalak Sahkari Mandali*, Anjar has revealed that its population has declined considerably. In the 10 taluks of Kachchh district, the population of Kachchhi horse was recorded to be 3,136 only. Kachchhi horses have distinct physical features. Coat color is bay (*Kumedh*), dun, grey and chestnut. Height at wither ranges from 56 to 60 inches, forehead and nasal bone are convex. Ears are curved at tips, but not touching each other. The keepers maintain breed purity by following selective breeding and avoiding crossbreeding with other breeds. Majority of breeders maintain horses under intensive system of rearing in most taluks of Kachchh. Some follow semi intensive pattern specifically in Khavda and Banni areas of Bhujtaluk, which according to the breeders is native tract of origin of Kachchhi horse. However, the survey revealed that the originality and uniqueness of Kachchhi horse is under dilution. As such, there is an urgent need to characterize and conserve Kachchhi breed of horse.

TS-I-41

CHARACTERIZATION OF DONKEYS OF ANDHRA PRADESH

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Majority of the donkeys in Andhra Pradesh are predominantly of light brown to brown coat colour. The bellies of these animals are lighter than the dorsal aspect of the body. Some animals have white markings around muzzle and eyes. The animals of light brown or brown coat colour were found admixed with some percentage of animals with grey coat colour. The donkeys in Andhra Pradesh are mainly reared by washermen, Chenchu and SC communities. The housing is mainly thatched type with some households having either pucca or open housing. They are raised both on grazing and stall feeding. They are also provided with some green fodder and concentrate which is mainly sorghum and rice polish. Water is provided twice a day. Open mating is practiced. No vaccination or deworming is practiced. The means for height at wither of brown type donkeys in males and females are 94.12 ± 4.8 and 89.82 ± 3.36 cm, respectively. The mean body length of the male and female animals is 91.21 ± 5.27 and 88.36 ± 3.36 cm. The heart girths in the male and female animals are 101.21 ± 5.92 and 99.46 ± 5.24 cm. The estimated mean body weight of the male and female animals is 79.02 ± 13.05 and 73.69 ± 9.87 kg. The tail extends slightly beyond hocks with a mean length of 57.12 ± 4.94 and 56.11 ± 3.52 cm in male and female animals, respectively. The animals with grey coat colour, which are significantly larger and heavier, have a mean height at wither of 103.67 ± 1.86 cm and 97.0 ± 6.83 cm, in male and female animals, respectively. The estimated mean body weight of male and female animals is 105.51 ± 11.88 and 94.77 ± 16.02 kg, respectively. They are mainly used as pack animals for carrying clothes for washing and transportation of bamboos from the forest area. They are also used for carrying construction material like soil and sand etc. Some income is also generated by selling milk of these animals which is supposed to have medicinal value and is used for treatment of asthma. They are able to carry up to 100 kg load for 20-25 km. Young animals are sold for about Rs. 3000/- per animal whereas adults are priced around Rs.10000/-.

TS-I-42

PHENOTYPIC CHARACTERIZATION OF LOCAL DONKEYS IN AKOLA DISTRICT OF MAHARASHTRA

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The present study was conducted to assess the phenotypic characters i.e. both morphological and morphometrical indices of local donkeys in Akola with special reference to drastically declining donkey population in Western Vidarbha region. The donkeys in this region are well known as medium-sized pack animals with magical tolerance ability to work under harsh climatic conditions. In view of this, a pilot survey using preformed questionnaire was conducted in and around Akola city during 2012-2014. A data of various phenotypic characters observed in 101 donkeys (Female-54 and Male-47) belonging to 20 donkey owner families was collected by personal interviews at their doorstep. The prominent coat colour of donkeys was grey (68%) followed by dark brown or black (13%), roan i.e. mixture of black and brown (11%) and white or light grey (8%). Typical white band around muzzle, a strip of dark shade across the shoulder and back are observed in almost all donkeys. The ears were long (19.38 cm), erect and alert with slightly lateral and backward orientation (79%). Peripheral area of ear was marked with dark hairs. Eyes were black. Neck and back were straight. Thin hair coat all over the body except mane and around ears and face in some cases was observed. Forehead was concave (93%) with length 44.06 cm and width 40.73cm. Eyes were black and spaced about 9.52 cm from each other. Back was straight (81%) or curved (19%). Mean values for various morphometric traits viz. Body length (scapula to pin bone), whole body length (forehead to base of tail), chest girth, forearm length, hind arm length, height at wither, height at croup, height at knee, height at hock and tail length were 67.38 cm, 137.97 cm, 93.22 cm, 81.56 cm, 86.42 cm, 88.11 cm, 94.78 cm, 30.83 cm, 36.97 cm and 51.64 cm, respectively were noticed, which did not differed in male and female, significantly. Phenotypic characterization of local donkeys provides baseline information for strategic planning of its conservation against declining population.

TS-I-43

CHARACTERIZATION OF CHIPPIPARAI DOG BREED- AN UNEXPLORED CANINE GENETIC RESOURCE OF INDIA

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Dog (Canis lupus familiaris) is the first animal domesticated by human being and has been most widely kept as guarding, hunting and pet animal. It belongs to sub-species of gray wolf (Canis lupus), a member of the Canidae family of the mammalian order Carnivora. Dog, particularly the exotic breeds are companion animals in recent days but the Indian breeds are mainly utilized for guarding the farm and farm house and for shepherding the livestock during grazing, migration and hunting. So far, adequate attention has not been given to characterization of Indian dog breeds and registering them at national level. Keeping this in view, the present investigation was carried out for phenotypic characterization of Chippiparai dog population of Tamilnadu state. A survey on Chippiparai dogs was conducted in Madurai, Virudhunagar, Tirunelveli and Thoothukudi districts of Tamilnadu. Chippiparai dogs are medium in size with coat colors varying from fawn to dark brown, brownish black and black. The animals with dorsal black coat have white markings on both sides above inner canthus of the eyes whereas the animals with

other coat color had black circle around the eyes particularly lower eyelids, sometimes extending up to head. The phenotypic data on twenty six morphometric traits were collected on 90 animals belonging to different age and sex groups (dogs and bitches). The mean height at withers, height at base of the tail, body length, chest girth, punch girth, head width, snout length, face length, neck length, tail length (in cm) and body weight (kg) were 64.61±0.46, 57.70±0.45, 57.38±0.43, 63.21±0.56, 42.24±0.51, 5.16±0.07, 11.82±0.15, 20.88±0.15, 19.79±0.18, 43.08±0.44 and 20.27±0.42 respectively. The bitches attain sexual maturity at an age of about 12-14 months and usually mating is not preferred at first heat. The age at first whelping is about 20 months. The age at sexual maturity in dogs ranges from 12-16 months. Most of the breeders are not selling puppies instead it is being given as gift to friends and other close relatives who can rear the puppies properly. Most of the breeders maintain their dogs with non-vegetarian food. Few breeders used to sell their puppies at a rate ranging from Rs. 4000 to 10,000/- according to the demand. The utility of animals is mostly guarding and hunting, kept as hobby and pride of their owners. Chromosome analysis of Chippiparai dog revealed common fundamental number (2n=78), with 38 pairs of acrocentric autosomes, one large sub-metacentric X-chromosome and a small sub-metacentric Y-chromosome. This unique canine germplasm needs to be documented and registered at national level, which will also be beneficial for the dog owners, dog breeders and Kennel clubs for breeding and sale of native pups.

TS-I-44

COAT COLOUR VARIATION IN KANNI DOG THE INDIGENOUS HOUND DOG OF TAMILNADU

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'Kanni' a hound dog variety found in the southern district of Tamilnadu state particularly Tirunelveli, Tuticorin and Virudhunagar districts. In the past, this breed of dogs were maintained for hunting and now this breed gets popularized among the pet owners for its elegant appearance, speed and watchfulness. The coat colour variation in Kanni dog makes confusion among pet lovers while selecting this breed. Keeping this fact in mind, a study was carried out on coat colour variation in Kanni dog breed. A total number of 485 Kanni dogs with distinguished breed characteristics from 225 Kanni dog owners were included for this study. The common coat colour of the Kanni dogs were black, brown, fawn, tan and light grey colours. The fawn and light grey coat colours are major coat colours (75.26 %) and the dog owners called this colour as "*Pillai*" colour. The brown and tan colour are known as "*Sevalai*" (Sevalai denotes red colour) and this coat colour contribute about 16.91 per cent. The dog with black coloured coat has brown or white patch above the eyes and the extremities of four legs and the owners use the word "Kanni" for this coloured dogs and the percentage contribution of black coloured coat is about 7.84. From the discussion with the knowledgeable dog owners, they do not prefer the black coat coloured dog due to the incapability to tolerate severe heat while hunting. So, they select the light coloured dog for breeding. This sort of preference and selective breeding may be the reason for the availability of low percentage of this black coat coloured dogs.

TECHNICAL SESSION – II

Molecular characterization and biotechnological interventions for sustainable management of AnGR

INVITED PAPERS

1. GENOMIC SELECTIONTO IMPROVE LIVESTOCK PRODUCTION IN DEVELOPING COUNTRIES WITH A FOCUSON INDIA

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Abstract

Global livestock production has increased substantially during the last decades, in both number of animals and productivity. Meanwhile, the human population is projected to reach 9.6 billions by 2050 and most of the increase in the projection takes place in developing countries. Rapid population growth will increase the demand for food as well as animal products,particularly in emerging economic giants like India. Moreover, the urbanizationhas considerable impact on patterns of food consumption in general and on demand for livestock products, in particular and the increased income growth led to more expenditure on livestock products. Since livestock production in developed countries haswell adopted livestock genomic selectiontools to improve both productivity and quality of animal products, opportunities to increase productivity in developing countriesvia genomic tools/selection have not been fullyexplored. The future of livestock breeding focuses on both product quality and productivity, animal welfare, disease resistance and reducing environmental pollution. Among the breeding tools, molecular genetics and genomics and modern reproductive techniques such ovum-pick up and in vitro production (OPU-IVP) of embryos will have a considerable impact in the future. This paper attempts to provide basic concepts of using genomic tools for livestock production with the focus on genomic prediction and selection methods and discuss about the potential application of genomic selection to increase livestock productivity, to enhance the disease resistance, fertility, resource use and the ability to adapt to climate changes.The paper also highlights the potential of genomic selection to overcome these challenges in Indiaand other developing countries.

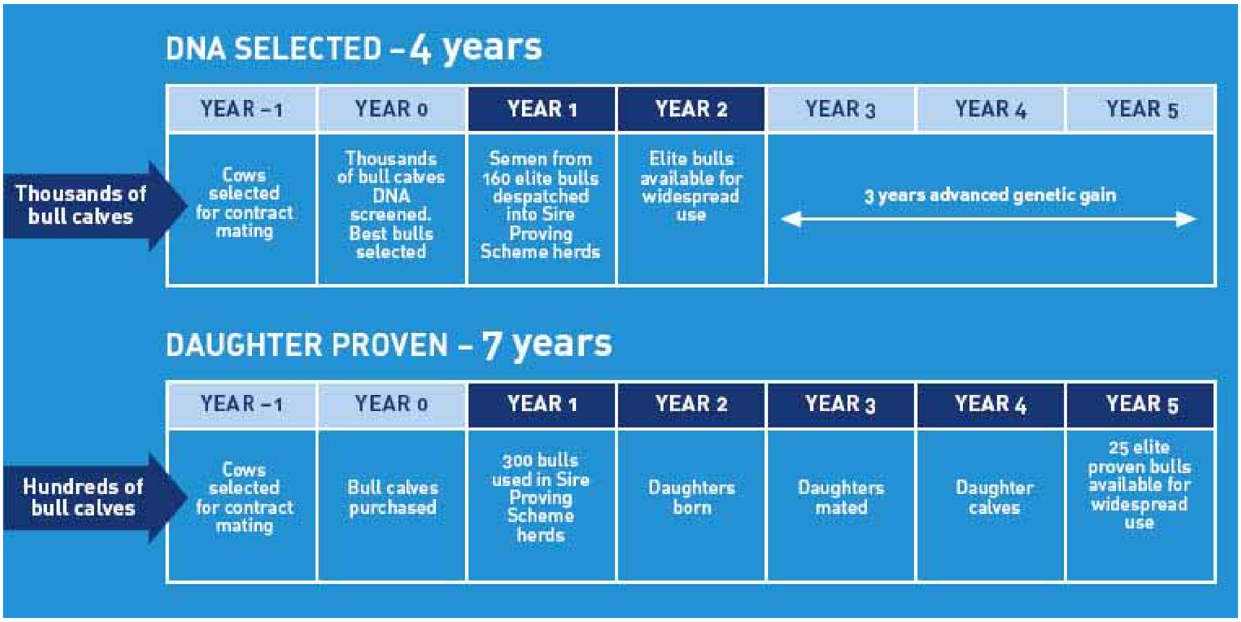
Introduction to genomic tool and genomic selection

Application of molecular genetics in livestock before genomic prediction

The application of molecular genetics to animal breeding started in the 1970's, scientists used the DNA markers to detect genes or genomic regions that control traits of interest. Then, these identified genes or markers allowed breeders to make improvements using marker-assisted selection as part of their overall improvement programme(Kadarmideen et al. 2006). Many genes have been identified for different production traits in livestock species, for instance *Halothane (HAL)*, *estrogen receptor (ESR)*and Melanocortin 4 receptor *(MC4R)* in the pig; DGAT1 diacylglycerol O-acyltransferase 1 (*DGAT1)*, Growth hormone receptor (*GHR)*, Melanocortin 1 receptor *(MC1R)*, and calpastatin *(CAST)* in cattle(Rothschild and Plastow 2014). To identify causal genes/markers for traits of interest, many quantitative trait loci(QTL) have been detected. To date (January, 2015), more than 12,000 QTL have been identified in cattle and pigs and around 4,000 QTL for chicken (http://www.animalgenome.org/cgi-bin/QTLdb/index). However, the implementation of QTL information in breeding programshas beenrarely successful because of several reasons. Many QTL have not been functionally validated, so it is difficult to use them in practice. Moreover, these QTL have explained very small proportion of the variation in the traits, often the highest phenotypic variation explained by a single QTL is only a few percentage of total variance. Since many complex traits (especially the production traits) are controlled by a large number of QTL, it has not only madeit difficult to identify the causative variants for a given trait, but also limited use of these causal variants or QTL in the breeding program. The use of significant markers of a marker assisted selection method is unlikely to improve genetic gain (Goddard and Hayes 2009).

Principle of Genomic prediction

High-throughput genomic technologies, especially high-throughput SNP genotyping methods were commercially available for several years (commercial SNP chips exist for cattle (750,000SNPs), pigs (60,000SNPs), dogs (250,000SNPs), sheep (56,000SNPs), horses (55,000SNPs) and chickens (600,000SNPs). This has led to increased adaptation of genomic/ sequencing technologies in the livestock sector, particularly in the area of animal genetics and breeding. In the context of animal breeding, perhaps a genomic prediction / selection was the biggest change that resulted as a consequence of adaptation of high-throughput genotyping technologies in the livestock sector. Genomic selection refers to making breeding decisions based on genomic estimated breeding values (**GEBVs**) that are computed by estimating SNP effects from prediction equations (Meuwissen et al. 2001). These SNP effects are normally estimated from a reference population consisting of a subset of animals with both SNP genotypes and phenotypes for traits of interest. Estimated SNP effects are then used to determine the merit of other genotyped animals that are not yet phenotyped. Two major advantages of genomic selection compared with traditional selection based on pedigree and phenotype alone are (i) it can select animals accurately early in life using their GEBVsfrom genomic predictions, (ii) it can also predict phenotypes that are very difficult or expensive to measure, including but not limited to fertility, meat quality, disease resistance, methane emissions, and feed conversion (Hayes et al. 2013). In dairy cattle, for example, dairy bulls are traditionally selected following progeny testing, because genetic merit for milk production of a bull can only be accurately evaluated through the milk production of his daughters. From the time dairy bulls' daughters are born, reach puberty, get inseminated, get pregnant, give birth to a calf and complete a full lactation (first lactation heifers), it can take anywhere between 5-7 years depending on the country (in tropics it takes more time) (Figure 1).It comes with enormous costs as well as time for each bull to be progeny tested. Although progeny testing results in accurate selection, genomic selection can reduce the generation interval by atleast two years as we can pre-select the young bulls to be either progeny tested for the milk production or used directly in the breeding programmes without ever progeny testing.



DNA SELECTED – 4 years

	YEAR -1	YEAR 0	YEAR 1	YEAR 2	YEAR 3	YEAR 4	YEAR 5
Thousands of bull calves	Cows selected for contract mating	Thousands of bull calves DNA screened. Best bulls selected	Semen from 160 elite bulls despatched into Sire Proving Scheme herds	Elite bulls available for widespread use	3 years advanced genetic gain		

DAUGHTER PROVEN – 7 years

	YEAR -1	YEAR 0	YEAR 1	YEAR 2	YEAR 3	YEAR 4	YEAR 5
Hundreds of bull calves	Cows selected for contract mating	Bull calves purchased	300 bulls used in Sire Proving Scheme herds	Daughters born	Daughters mated	Daughter calves	25 elite proven bulls available for widespread use

Figur 1: Generation inverval using genomic prediction compared to traditional methods (daughter proven)) (Adapted fom http://www.licnz.com/genomic_selection_dna_.cfm).

The first option can save costs and increase accuracy and the second option dramtically increases costs, time and increase accuracy of selection. It is stated increase in genetic gain or income is 60%-120% compared to traditional methods of progeny testing (Schaeffer 2006; Pryce and Daetwyler 2012).

Methods of Genomic prediction

Genomic prediction models vary based on several assumptions regarding the variance of traits of interest. Genomics best linear unbiased prediction (GBLUP) is a prediction method that assumes that all markers contribute to the additive genomic variance. This method is similar to the traditional BLUP method applied for in animal breeding for over 20 years, except that a genomic relationship matrix replaces the numerator relationship matrix computed from the pedigree information. Another method called Random regression BLUP (Meuwissen et al. 2001) assumes SNP effects are randomly distributed, and is considered equivalent to GBLUP (Goddard et al. 2011). Single-step BLUP (ssBLUP) jointly analyzes phenotypes and genotypes of all animals in one step(Aguilar et al. 2010). Inclusion of all animals (with and without genotypes) results in the better correction of genomic preselection effects; and consequently provides more accurate estimation of GEBVs. Several Bayesian approaches have been used for genomic prediction, and these methods assume a prior knowledge about distribution of SNP effects influencing a trait. BayesA assumes that all SNPs have an effect, but each SNP has a different variance that is assumed to be equivalent to a scaled inverse-χ^2 prior (Meuwissen et al. 2001). The BayesB and BayesCπ assume that each SNP has either an effect of zero or non-zero with probabilities π and 1-π, respectively (Habier et al. 2011). Gianola et al. (Gianola et al. 2006) introduced semi-parametric methods (reproducing kernel Hilbert spaces (RKHS) regression) for whole-genome analysis of quantitative traits. Genomic prediction accuracy gets better as the trait heritability and the reference population used for calculating GEBVs increases. Overall, genomic prediction methods are improving, especially with advent of whole genome sequence data from next generation sequencing. At present, the difference between performances of different methods is marginal for most traits because they are controlled by many QTLs with small effect sizes. Genomic BLUP and its single step extension that includes non-genotyped animals (ssBLUP), remain the most commonly used methods.

Genomic selection to improve livestock in developing countries with a focus on India

Genomic toolsin general and genomic prediction or genomic selection, in particular significally improve livestock productionand the theorical background in animal science (Kadarmideen 2014), however, its application to developing countries have been limited. The constraining factorsare lack of nation-wide or state-wide phenotype and pedigree recording/ keeping schemes across all dairy farms (or sheep or pig farms), the type of livestock production systems (often small holder systems in India with a few exceptions), co-ordinated use of breeding animals, formal genetic evaluation centers for entire state or nation in addition to many other factors such as the funding for livestock keepers,infrastruture, human resources and so on. The livestock production system in developing countries varies by the geographic and climate conditions. Genomic prediction can focus small holder farmers to reduce hunger and poverty or to medium size farm to quickly improve the productions. Livestock is an important subsector of agricultural production system in India. It plays major role in the national economy as well as in socioeconomic development of millions of rural households spread across more than 600,000 villages(Pattnaik et al. 2012). The overall contribution of livestock sector to the agricultural growth domestic product (GDP) is 24–32% and to national GDP is 4–6%(Pattnaik et al. 2012).

Potential of Genomic selectionto improve production/reproduction traits

Perhaps, improving production/reproduction and health traits are among the most important task for livestock production in developing countries since the productivity of livestock is far below potential. With genomic prediction in cattle, the sire with higher genomic breeding values can be selectedfor use in Artificial insemination (AI) or to produce the embryos for transfer (via either conventional embryo transfer (ET) or via OPU-IVP ET programs.However, it is necessary to consider the physical infrastruture such as devices to store sperm, embryos, AI tools andtransportation services. In pigs, Akanno et al. (Akanno et al. 2014) showed accuracies of GEBVs in the range of 0.30 for number born alive to 0.86 for backfat in the validation population which is better than pedigree-based approach in a simulation to mimic pig populations in develiping countries. In another study, the authors also suggest that the high density SNP chip can help improve the indigenous pig populations with low linkage disequilibrium and combination of genomic selection with repeated backcrossing of crossbreds to exotic pigs in developing countries promises to rapidly improve the genetic merit of the commercial population (Akanno et al. 2013). The authors showed that clear opportunities to improve production traits in pig breeds. The potential of improving genetic merit by genomic selection for beef cattle in Latin America is also highlighted by (Montaldo et al. 2012). We developed the GIFT project (Genomic Improvement of Fertilization traits in Danish and Brazilian Cattle) to help improve fertilization traits in Brazil cattle (http://gift.ku.dk) as an example to implement the genomic prediction in developing countries. The GIFT project conducts quantitative genetics and animal breeding research on important attributes or traits related to OPU and in vitro production (IVP) of embryos. These embryos undergo “genomic selection” thus an animal is already pre-selected using an embryo stage based on their genotypes! Thus contributing dramatically to reducing generation interval and to profitability of

OPU-IVP operations in the Brazilian and Danish cattle industry. The GIFT project operates in the state of São Paulo to identify high genetic merit donor cows and recipient heifers with higher pregnancy rates via Genome-Wide Association Studies and genomic selection for OPU-IVP and pregnancy traits in several thousands of Brazilian cattle.In Denmark, transcriptomics experiments using RNAsequence profiles of OPU-IVP recipient cows are conducted to identify differentially expressed genes and gene regulatory networks in maternal-conceptus tissues in recipient cows that do and do not maintain pregnancy.

Regarding to the situation in India, the milk production (both in cattle and buffaloes) have significant impact on the economy, the genomic improvement for these traits needs to be highly prioritized. India has the highest number of live cattle in the world with around 214,350,000 stocks in 2012 (http://faostat.fao.org).Genomic prediction can be used to identify best bulls and cows for milk production (milk, fat, protein yield) and milk quality (milk self-life extending lactoperoxidase thiocyanate systems, healthy Solids Not Fat etc.), reproduction (insemination success, calving rates etc.) in each community. This bull or cow can be used for mating and/or to produce semen for AI. The distribution of semen to small holders across many many villages is encouraging therefore there is a high posibility that genomic selection can be achieved successfully even within villages.

Potential of Genomic selectionto improve disease resistance/tolerance

Livestock disease is one of the major concerns for livestock breeders because of its impact on economics, its transmition to other species, potential to affect human and its cause to animal welware concern. Genomics of disease resistance has been reviewed in many studies across different species (Yáñez et al. 2014; Lunney 2007; Bishop and Morris 2007). Bishop and Woolliams (Bishop and Woolliams 2014) indicated focus on major endemic diseases included bovine tuberculosis and paratuberculosis in pigs and nematode infections in sheep. Kadarmideen et al.(Kadarmideen et al. 2011)andAli et al. (Ali et al. 2013) have shown that bovine tuberculosis in African Zebu cattle have genetic basis and that certain SNPs, microsatellite markers and candidate genes such as NRAMP1 gene polymorphisms can be used in marker assisted selection schemes to reduce the incidence or increase resistance to bovine tuberculosis, particularly in Zebu cattle. This in combination with existing genetic diversity in disease resistance in developing countries in Africa that we have reported earlier (e.g. (Flury et al. 2009) it can certainly help genetic improvement of disease reistance. Many studies have shown that the animal species in developing countries are less susceptible to common disease than exotic animals. For instance, Zanga et al.(Zanga et al. 2003) showed that indigenous pigs are better adapted to local production conditions and environments and less susceptible to common disease exotic pigs in Zimbabwe. Selection for disease resistance based on DNA technologies is possible and can be done by either marker assisted selectionor genomic prediction. Genomic prediction have been showed ist potential application for Tuberculosis resistance in dairy cattle (Tsairidou et al. 2014), for porcine reproductive and respiratory syndrome virus infection in pigs (Boddicker et al. 2014) or for newcatles disease in chicken (Liu et al. 2014). In India, Sekar et al.(Sekar et al. 2011) interviewed that experts and showed that controlling Tuberculosis dieasesamong the highest prioties among other zoonotic disease. In India, higher incidence of tuberculosis in buffaloes as compared tocattle has been estimated on the basis of tuberculin (Shukla and Singh 1972). A report have shown that 60 per cent of the total 520,000 cattle in the Kerala State were partially or fully affected by the tuberculosis disease and almost all crossbred cattle were suffering with tuberculosis (http://en.engormix.com/MA-dairy-cattle/news/india-bovine-alarms-health-t539/p0.htm). Scince estimated a heritability for TB resistance of 0.18 ± 0.04 (Brotherstone et al. 2010), it can be removed by a breeding program. Genomic selection for TB resistance therefore is important task to substainable development of livestock production in India.Tick infestation is another common ecto-parasitic infection in Indian cattle. In tropical part of Northern Australia,we (O'Neill et al., (2010) demonstrated greater genetic variation (high heritability) exists in tick resistance in Indian derived tropical composite breeds such as Brahman cattle. There are also many other cattle diseases such as infectious bovine keratoconjunctivitis for which we reported substantial genetic variation(Ali et al. 2012)and hence a potential for genomic selectionAnother disease can be important is Foot-and-mouth disease, which remains a serious threat to the livestock populations. Especially in India, with 528 million foot-and-mouth disease (FMD) susceptible animals, primarily cattle and buffaloes of India, where the disease is endemic.However, there have been no report how genetically determined FMD is and hence it may be worthwhile to make a population genetic study on FMD.

Potential of Genomic prediction to improve heat stress, climate resilence and methan emission

Around 55% of India population directly or indirectly depends on the climate sensitive agriculturesector(Ahmad et al. 2011). Livestock production is the driving force to climate change (green house gas) but also very sensitive to climate change. Climate change is not only affectingfeed supply, increased drought, changes in disease prevalence and increased incidence of heat stress (Rothschild and Plastow 2014)but also brings many new diease germs for livestock (Singh et al. 2011). Rothschild and Plastow (Rothschild and Plastow 2014) indicated that long-term genetic solutions are needed to identify genomic signatures of selection related to heat stress.In tropical part of Northern Australia, we (O'Neill et al., (2010) demonstrated greater genetic variation (high heritability) exists in heat stress or tolerance in Indian derived tropical composite breeds such as Brahman cattle. Therefore, it offers an opportunity to study the level of genetic variation in heat tolerance and drought tolerance among Indian breeds and use the better animals in genomic selection. In practice, several studies have found individual genes or genomic regions associated with mechanisms to combat climate issues(Liao et al. 2013). The reviewe by (Hayes et al. 2013) indicate the possibility of genomic selection for resistance to heat stress. Hayes et al. (Hayes et al. 2009) report the accuracy of genomic prediction fortolerance to heat stress was moderate at 0.37, which much higher than accuracy based on pedigree information (0.16). Breeding for methane emission migh be difficult because it is more expensive to measure (compared to other production traits) although the traits is moderately heritable. However, selection for for improved feed efficiency can lead to reductions in methane emissions (Hegarty et al. 2007). Selection for improved feed efficiency can also help to reduce the nitrogen/phosphorous emission in pigs (Saintilan et al. 2013) and enhance sow performance to tropical climate condition(Renaudeau et al. 2014). In our study on pigs, we reported substantial genetic variation in feed efficiency in pigs(Do et al. 2013). However, the problem will be to design an effective breeding programs for climate change or resource use efficiency. As mentioned by (Naskar et al. 2012) breeding for climate change adaptation or mitigation will not be necessarily different from existing breeding programs but success depends on measuring the phenotypes at individual animal level and traits relevant for adaptation or efficiency. Care must be taken to ensure that right balance between breeding objectives for all the traits (heat resilience, fertility, feed conversion efficiency, disease tolerance and longevity in addition to higher productivity etc.) are implemented. It is important to consider genotype by environment interactions to identify animals most adapted to specific conditions and natural stratification of breeds and species by climatic zones.Since India has seven climatic zones, the selection of genomic merit can be tailored to each climatic zone and that could benefit the farmers in different regions of India.

Concluding remarks

The demand for livestock products is increasing and application of genomic selection in livestock species has been significantly contributing to meet that deamnd in several developed countries, already for over 7 years. Employing genomic selection to increase livestock production and its efficiency to meet these modern demands for food of animal origin in the developing world will be critical and required. Faster genetic gains for these traits can be achieved with new technologies, including genomic selection and advanced reproductive technologies such as OPU-IVP (www.gift.ku.dk).Adoption of genomic tools, especially genomic prediction will be very necessary to accelerate enough genetic gain for production traits as well as to improve the genetic merit of disease resistance and adaptation ability, in developing world. Certainly, many other facilities and concerted efforts are required to overcome the challenges, includingimproved policies, and development of human and institutional capacities. Forcertain, livestock production to contribute significantly to Indian economy, adoption of genomic solutions to livestock production is very critical and important. India and other developing countries will have to focus on the production, but efforts must be made to balance the productivity with conservation of genetic resources or genetic diversity, reduceing environmental impact and improve animal welfare. This will facilitate sustainable animal agriculture.

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2. APPLICATION OF MOLECULAR TOOLS IN LIVESTOCK PRODUCTION SYSTEMS IN DEVELOPING COUNTRIES

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Exponential increase in the global human population (estimated 9.6 billion by 2050; UN 2013) would increase the demand for food which is expected to be doubled in the next 40 years. While the agricultural productivity is declining, largely due to shrinking of resources particularly cultivable land, the role of livestock sector has increased to fulfill the growing food demand. Livestock production is growing faster than any other sector and by 2020, in terms of added value the livestock sector is predicted to become the most important agricultural sector. However the production environments, and the intensities and purposes of production, vary greatly within and across countries. The livestock production systems are generally shaped by prevailing biophysical and socio-cultural environments. The livestock element in these systems is more often interwoven with crop production, as in the rice/buffalo or cereal/cattle systems of Asia. Animal manure is often essential for maintaining soil fertility, and the role of animals in nutrient cycling is often an important motivation for keeping animals. Many of these systems that are the result of a long evolution are currently under pressure to adjust to rapidly evolving socio-economic conditions and intensive livestock production systems.

The livestock sector has emerged as one of the key drivers of agriculture growth, especially in the developing countries. In a predominant agrarian economy like India, livestock owners and farmers own the animals as their natural capital, and an insurance against income shocks of crop failure and natural calamities. Small and marginal farmers, landless labourers and women are more dependent on livestock for supplementing incomes and generating gainful employment in rural areas. It is projected that by the year 2025 over 60% of meat and 50% of milk will be produced in the developing countries. The livestock sector in India in recent times has been growing faster than crop sector. The contribution of livestock output to the total output of the agriculture sector has significantly increased from 15 per cent in 1981-82 to 26% in 2010-11.

Animal diseases are a major and increasingly important factor reducing livestock productivity in developing countries in particular. The most promising applications of biotechnology to livestock systems is the improvement of animal health and production, in areas such as assisted reproduction, increased disease resistance, nano-based point of acre and refined diagnostic techniques, and increasingly improved vaccines with effective delivery systems. Use of biotechnology tools in animal health may contribute significantly to improved animal disease control, thereby stimulating both food production and livestock trade. The modern biotechnology tools are likely to have significant impact to answer most if not all the questions related to better utilization of livestock genetic resources in developing countries.

Molecular tools/approaches applied to livestock systems

Reproductive technologies : Some tools that are applied to livestock to develop genetically valuable stock are:

*Artificial insemination (*AI) is the first method developed and underpins the application of other reproductive technologies applied to livestock. This procedure involves the collection of semen from males which is then used to impregnate females and has been applied in dairy cattle for over 65 years.

Multiple Ovulation and embryo transfer (MOET) is the hormonal manipulation of females is undertaken to induce multiple ovulation prior to insemination which is then combined with the transfer of embryos into hormonally primed surrogates. This also allows offspring and milk to be produced outside usual seasons and has been shown to increase the rate of genetic improvement.

Cloning is the production of offspring by embryo splitting (naturally or artificially induced to form 2 or more genetically identical animals) or nuclear transfer (creation of an animal from a reconstructed embryo made by transferring the nucleus of a donor cell into an oocyte from which the genetic material has been removed.

National Dairy Research Institute, Karnal, India has earned a worldwide repute for cloning and in vitro fertilization (IVF). The major achievements/chronology of events at NDRI are (source ICAR/NDRI):

Pratham, was the first IVF (in vitro fertilization) buffalo in the world was produced at NDRI in 1990.

First cloned Calf was born on Feb 6, 2009. However, it survived for only six days and died on February 11. The Scientists of NDRI had developed a landmark "Hand guided Cloning Technique".

Garima, the world's second cloned buffalo calf through the Advanced Hand-guided Cloning Technique was born at NDRI, Karnal on June 6, 2009. It survived for more than two years but she died of heart failure on August 18, 2011.

Gamini a cloned calf of female buffalo from embryonic stem cell was born on Aug 22, 2010. Later, she gave birth to a calf named 'Mahima' on 25th January 2013.

Shrestha: a cloned calf of a male buffalo from somatic cell of an ear from an elite bull was born on Aug 26, 2010.

Purnima: a clone of female buffalo from high milk-yielding animal was born on On Sept 6, 2013. However, it survived only for 21 days.

Lalima born on May 2, 2014 was the 7th buffalo calf cloned

Rajat a clone of a Progeny Tested Bull with superiority of >22% was born on July 23, 2014

Deepasha clone of an endangered Wild-Buffalo of Chhattisgarh was born on 4th January, 2015,

Apart from cloning buffalo, Noori, the world's first pashmina goat was cloned at the Centre of Animal Biotechnology at Sher-i-Kashmir Agriculture University for Science and Technology (SKAUST), in Kashmir, India as a joint venture of SKAUST and National Dairy Research Institute (NDRI), Karnal.

Interventions through Animal Breeding

Marker Assisted Selection

Selective breeding has produced enormous improvement in farm livestock in the latter part of the twentieth century. Such progress has largely been achieved through selection on phenotype: the identification of genetically elite animals through their own performance and physical characteristics and those of their relatives. However, the explosion in our understanding of the genome and accompanying technological innovations are opening up possibilities for direct identification and selection of animals carrying the best genes: selection on genotype. A majority of the traits of economic importance in farm animals are polygenic in nature and are influenced by a variety of environmental and developmental factors, which makes them difficult to isolate and identify at the genome level. Although, screening and identification of some of the quantitative trait loci (QTL) using molecular markers has been successfully carried out in cattle, pigs and other livestock species, most of the genes affecting polygenic traits are still unknown and identification of major genes/alleles underlying these QTL effects remains a challenging task.

The past decade has witnessed an increasing interest in gene mapping efforts in several farm animal species. These efforts for the development of dense genetic maps to facilitate the identification of genes of economic importance became the major objective of livestock genomic research. Physical and the genetic linkage maps developed in recent years have started to play significant role in developing broader understanding of complex livestock genomes. Attention has now shifted towards further improving the resolution of these maps and their utilization in finding QTLs through whole genome scans and performing fine mapping, marker-assisted selection (MAS) and marker-assisted introgression (MAI).

Once associations between genetic markers and performance have been detected, they can be harnessed in a breeding programme. Selection for a marker allele known to be associated with a beneficial Quantitative Trait Loci (QTL) allele will increase the frequency of that allele and hence enhance performance. One of the potential major benefits of selection based upon marker information is that marker genotypes can be determined based on easily collected samples (e.g. hair, blood etc.) that can be taken from an animal as soon as it is born. Thus, marker information can be used to predict an animal's genotype before the animal has records for the trait or even for animals which will never express the trait. For example, we might be able to predict whether males carry genes for good female reproductive performance, or predict meat quality in an animal without its slaughter. Such marker assisted selection (MAS), may not only make current breeding more efficient, but may also open up possibilities for selecting for new traits.

Most reproduction traits are complex traits with low heritability, which means that they are regulated by many genes and, to a great extent, by environmental factors. The underlying genes or chromosome segments affecting such complex traits are called quantitative trait loci (QTL). By using traditional methods of selection it has been difficult to improve reproduction traits due to their low heritability. If one can identify QTL responsible for a significant proportion of the genetic variation in these low heritability traits, or detect closely linked genetic markers that are co-inherited with the QTL, the genetic progress could be enhanced by using marker-assisted selection.

Identification of gene(s) of economic importance/unique gene(s)

Another thrust area is identification of genes of economic importance to further categories functional differences amongst indigenous animal genetic resources. Much of the cutting-edge research in animal sciences will be based on functional genomics. Emphasis must be placed on identifying the technologies, resources and information needed to support the gene discovery, gene expression and gene function research in farm animals.

Gene expression profiling and functional annotation of gene

To drive QTL research in farm animals and isolate tissue specific and regulated genes, a greater effort should be made to construct tissue specific high quality libraries of cDNA. This would help to generate numerous expressed sequence tags (ESTs) for various tissues and these libraries will represent the repertoire of expressed genes. Such an effort would be expected to bring a speedy change in the strategies used to identify and clone novel genes of biological interest.

Gene Introgression

Gene introgression can be used as a tool for genetic improvement by the introduction of new alleles into a population to address challenges facing current breeding goals. In animal science the striking example of introgression is the introgression of fecundity Booroola (FecB) gene in sheep. The Booroola (FecB) phenotype is associated with a mutation in the bone morphogenetic protein (BMP) receptor 1B. and is shown to be associated with increased ovulation rate in ewes. In India, the Nimbkar Agricultural Research Institute (NARI) introduced the FecB mutation, which increases prolificacy, into the Deccani breed from the Garole breed of West Bengal to increase lamb production and incomes of smallholder shepherds. Two fecund strains were developed - the NARI Suwarna, with contributions from only Garole and Deccani breeds, and the NARI Composite, with additional contributions from Awassi and/or Bannur breeds. One copy of FecB led to an increase in ovulation rate from 1.0 to 2.0 eggs, and an increase in live litter size (LS) at birth from 1.0 to 1.6 in the NARI flock and from 1.0 to 1.4 in smallholder flocks. This introduction of the FecB mutation in Deccani sheep proved to be successful in increasing both lamb production and incomes(ACIAR, 2013 Proc.)

Genomic selection

To overcome difficulties associated with QTL-MAS, a variant of MAS called Genomic selection(GS) was proposed by Meuwissen et al. (2001). The advantage of this approach is that DNA markers covering the whole genome are used so that potentially all the genetic variance is explained by the markers. Traditional marker-assisted selection (MAS) focuses only on those regions which are relatively certain to influence the trait of interest and leaves most of the genome and much of the genetic variation unaccounted. Conversely genomic selection puts the greatest emphasis on those regions with the largest effects, while still accounting appropriately for the more ambiguous genetic variation in the remainder of the genome. This approach holds importance as in livestock genes affecting most economically important traits are distributed throughout the genome and there are relatively few that have large effects with many more genes with progressively smaller effects (Shrimpton and Robertson, 1988; Hayes and Goddard, 2001; Sanna et al. 2008, VanRaden et al. 2009).

Next-generation sequencing (NGS) technologies are widely used for detection of millions of Single Nucleotide Polymorphisms (SNPs) and also provide a means of assessing their variation. This information is useful for composing subsets of highly informative SNPs for region-specific or genome-wide analysis and to identify mutations regulating phenotypic differences within or between populations. SNP identification through NGS led to the development of Genome-wide panels of SNPs. The genetic merit of animals can be estimated by genomic selection, which uses genome-wide SNP panels as markers and statistical methods that capture the effects of large numbers of SNPs simultaneously. This approach is expected to double the rate of genetic improvement per year in many livestock systems. The availability of large panels of SNP markers created an interest in genomic selection (Meuwissen et al., 2001) as a tool to increase the accuracy of prediction for young animals. These tools were first used in selection of dairy cattle (Hayes et al., 2009; VanRaden et al 2009)

Potential of genomic selection

One of the most economically important aspects of GS is the possibility to use it for improving selective breeding. The DNA marker data as well as phenotypes and pedigrees on potential selection candidates could be combined to estimate improved EBV. EBV obtained from this 'genome-wide' selection is of comparable robustness to a conventional EBV based on analysis of pedigree and phenotype data. Once the associations between chromosome segments and phenotypes are established, it should be possible to make selection without phenotypic information. Genomic selection approach is particularly attractive for expensive-to-measure traits. It also can be more easily applied to traits where the heritability is low and genetic change is slow, and traits that are difficult to measure. The most likely application of this approach will be in dairy cattle where, in principle, bulls could be selected on the basis of genomic information alone and used for mating long before their progeny test results would be known – considerably reducing generation interval and accelerating progress.

Genomic selection and accelerated genetic progress

There are three practical ways of increasing genetic progress: (1) increase the accuracy of selection; (2) increase selection intensity; and (3) decrease the generation interval, which also results in more selection steps per unit time. Whole-genome selection is one of the few tools that can affect all three of these components affecting genetic progress. Accuracy is clearly increased with genomic selection using SNPs. Generation interval can be lowered easily because SNP evaluations of embryos are equally valid as evaluations for young or old animals. Because the technology can be applied broadly at relatively low cost (screening hundreds of samples), practical opportunities are provided for increasing selection intensity as well. The combination of these advantages, when added to pedigree and phenotypic information on each respective individual, becomes the most powerful, practical approach available for making genetic changes.

Molecular tools for exploring the genome

The transcriptome is the complete set of transcripts in a cell, both in terms of type and quantity. Transcriptome analysis is a powerful strategy in dissecting the relationship between genotype and phenotype of a cell. The complete transcriptome profiling of cells is crucial for the characterization of gene expression signatures that contribute in defining biological and physiological processes in the cells. Various technologies have been developed to characterize the transcriptome of a population of cells, including Real time PCR, hybridization-based microarrays and Sanger sequencing based methods (Yamada et al., 2003; Bertone et al., 2004; David et al., 2006). The advent of high-throughput sequencing based methods has changed the way in which transcriptomes are studied.

Microarray analysis can be used to screen the entire genome for differences in gene expression with a single experiment, producing thousands of data points. It is ideal for screening the expression levels of thousands of genes in a limited number of samples. RT-PCR is a faster and less expensive method for gene expression (mRNA) profiling than array analysis. However, these two methods are complementary techniques—array analysis is often used to identify candidate genes for further detailed study by real-time RT-PCR.

Deep RNA Sequencing (RNA-Seq)is a recently developed technique that uses massively parallel sequencing to allow transcriptome analyses of genomes at a far higher resolution than is available with Sanger sequencing- and/or microarray-based methods.RNA sequencing (RNA-Seq) involves direct sequencing of complementary DNAs (cDNAs) using high-throughput DNA sequencing technologies followed by the mapping of the sequencing reads to the genome. It provides a more comprehensive understanding than has hitherto been possible of the complexity of eukaryotic transcriptomes. The intrinsic experimental limitations of microarrays seem to make RNA-seq the method of choice. Recently, Canovas et al.(2010) confirmed that analyzing the transcriptome using RNA-Seq technology is an efficient and cost-effective method to identify SNPs in transcribed regions on analysing milk transcriptome using RNA-Seq.

The cost of the technologies mentioned above is significant and its time in India for the institutes to collaborate to develop tools for properly exploiting farm animal genomics. World over all the sequencing projects for farm animals are funded through collaborations. Key targets now include the development of more sequence data, SNP panels and, with care, phenotype databases (the "phenome"). The phenotype databases necessarily need to be based on large populations and this, together with massive phenotypic diversity, means that they are expensive and will need careful planning to maximise their utility.

Animal health

Successful control of a disease requires accurate diagnosis. This has been greatly improved in recent years through developments in biotechnology. Possibility to immortalise individual antibody-producing cells by hybridisation to produce antibodies of a given class, specificity and affinity (i.e. monoclonal antibodies) has provided a tool that permits the analysis of virtually any antigenic molecule. The use of monoclonal antibodies has revealed that the failure of vaccines (e.g. of rabies) to provide protection in all parts of the world was due to the diversity in the antigenic composition of the causative virus. The (monoclonal antibody) technology is relatively simple and can readily be applied in developing countries.

The ability to generate highly specific antigens by recombinant DNA techniques has made it possible for an increasing number of enzyme-linked immunosorbent assays (ELISA) to have the capacity to differentiate between immune responses generated by vaccination from those due to infection. This has made it possible to overcome one of the major drawbacks of antibody detection tests: the fact that, because antibodies can persist in animals for long periods, their presence may not indicate current infection. ILRAD has developed a technique to overcome this problem in diagnosis of trypanosomiasis. The parasite antigen detection test uses monoclonal antibodies raised in laboratory mice to capture the parasite antigens which are then revealed by their reaction with a second layer antibody to which is conjugated an easily detectable enzyme. This test reveals current infections and facilitates differentiation between the major trypanosome species. This has important implications for disease control, especially because of the association of different parasite species with different epidemiological and disease circumstances.

Conventional means of controlling major livestock diseases include vector control, vaccination, slaughter of infected stock, and other management practices (including grazing management and controlled movements). Vector control requires continuous application of pesticides. These are often unaffordable to farmers in developing country. Moreover, where these drugs or pesticides are used, resistance by parasites is often encountered and reinfection following administration of drugs against parasitic diseases usually occurs.

Immunisation remains one of the most economical means of preventing specific diseases. An effective vaccine can produce long-lasting immunity. In some cases, vaccination can provide lifetime immunity. Moreover a small number of doses is usually required for protection. Level of infrastructure and logistical support required for a large-scale vaccination programme is such that a successful vaccination campaign can be implemented in remote rural areas. In general, vaccines offer a substantial benefit for comparatively low cost, a primary consideration for developing countries.

3. STATUS OF ANIMAL GENETIC RESOURCES OF RAJASTHAN, CONSERVATION STRATEGIES AND BREEDING POLICY FOR THEIR IMPROVEMENT

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Rajasthan, the largest state of India (3,42,239 Sq.km.) situated in the northwestern part of the Indian Union (23˚30′ and 30˚12′ North latitude and 69˚30′ and 78˚17′ East longitude) is largely an arid state for most of its part. One of it district, Jaisalmer is almost equal to Kerala State (38401 sq. kms). More than 60% of the state's total land area is desert, characterized by extreme temperature, low rainfall, and sparse habitation. Temperature in most other parts of the state reaches the 40C mark during the summer months. Winters are mild in Rajasthan with the temperatures ranging between 22C and 8C. In Rajasthan, Animal Husbandry is not merely a subsidiary to Agriculture but it is a major economic activity specially in arid and semi-arid areas, thus providing the much needed insurance against prominently occurring scarcity conditions. Income from live stock accounts for 30 to 50% of the rural households' income, with wide variation in region and households.

Livestock in Rajasthan have been developed over hundreds of years through selection and thus have born various traits of economic and environmental importance. However, to meet the needs of growing population, exotic breeds have been used in crossbreeding that result on gradual decline in genetic variability. Hence, livestock production system may become unpredictable with environmental changes, adverse nutritional conditions, disease and parasites. Though there is high potentiality of indigenous livestock for the sustainable production, many important livestock species are in the verge of extinct. So, there is a need to facilitate effective management of livestock bio-diversity, and sustainable use of indigenous genetic resources and endangered breeds of livestock in Rajasthan.

The state of Rajasthan has a vast animal genetic resource with a wide variety of indigenous breeds. Representing a hub of domestic animal diversity, Rajasthan has proud possession of 8 cattle breeds, 8 sheep breeds, 3-4 goat breeds, 4 camel breed and also endowed with thorough bred horses. The important breeds of cattle traded in the State are Rathi, Kankrej, Nagouri, Tharparkar, Haryana, Malvi, Gir and Mewati. Regarding buffalo breed, Murrah buffalo is the only preferred breed found in Rajasthan. Sheep also occupy an important place in animal husbandry sector of the State. The important breeds of sheep are, Nali, Magra, Chokla or Shekkavati, Marwari, Jaisalmeri, Malpura, Sonadi and Pugal. The important goat breeds in the State are Marwari, Jakhrana, Sirohi and Jamnapari breeds, which are reared for milk and meat.

Table 1: Status of Different Livestock in the different district of Rajasthan

	Region/zone	District covered	Species/breeds available
1	Bikaner Division	Bikaner, churu, Ganganagar, Hanumangarh	Cattle: Rathi, Tharparpar, Nagouri, Hariana Buffalo: Murrah Sheep: Chokla, Magra Goat: Marwari
2	Jodhpur Division	Jodhpur, Pali, Jaisalmer, Jalore and Barmer	Cattle: Tharparlar, Kankrej Buffalo : Murrah Sheep: Magra, Jaisalmeri Goat : Sirohi, Marwari
3	Jaipur Division	Jaipur, Bharatpur, Alwar, Dholpur, Sikar, Jhunjhunu and Dausa	Cattle : Gir, Hariana, Mewati Buffalo : Murrah Sheep : Chokla, Malpura Goat: Jakrana

4	Ajmer Division	Ajmer, Bhilwara, Nagour and Tonk	Cattle: Gir, Nagauri, Malvi, Hariana Buffalo: Murrah Sheep : Chokla, Magra, Malpura Goat: Sirohi
5	Udaipur Division	Udaipur, Chittorgarh, Dungarpur Banswara and Rajsamand	Cattle : Gir, Buffalo : Surti Goat : Sirohi
6	Kota Division	Bundi, Jhalawar, Kota, Baran, Sawaimadhopur and Karauli	Cattle : Gir, Malvi Buffalo : Murrah, Magra Goat: Sirohi

The livestock population in the state is very large in numbers but its productivity is very low as compared to other parts of the country. As per the livestock census 2012, there are 512.05 million lacs livestock (which include Cattle, buffalo, Sheep, Goat, Pig, Camel, Horse and donkey) and more than 50.12 lacs. poultry in the State. Rajasthan has about 7% of cattle, 11.94 % buffalo, 13.95 % sheep, 16.03 % goat, 81.37 % camel and 2.31 % pig country's population and contributes over 10% of total milk production, 30% of mutton and 40% wool produced in the country. Rajasthan is first in Wool production while third in milk production. Animal Husbandry contributes about 13% in the G.D.P. of the State (Livestock cense, 2007). The Sheep and Camel population showed a decreasing trend over last decade, whereas the cattle and buffalo population showed an increasing trend, Goat population showed a fluctuating trend and mule population showed abrupt increasing trend. The total livestock population increased simultaneously similar to the increase of buffalo and cattle population, whereas the sheep and Camel population decreased. There are slight downward variations in goat population in comparison with other animals. This sector has a great potential for rural self employment at lowest possible investment per unit.

Table 1: Status of Livestock population during various years in Rajasthan (In lacs).

Livestock	**1977**	**1983**	**1988**	**1992**	**1997**	**2003**	**2007**	**2012**	% of change over 2007	% share in 2012 of country population
Cattle	128.96	135.04	109.21	116.66	121.41	108.54	121.20	133.24	12.05	6.98
	(31.18%)	(27.20%)	(26.69%)	(24.08%)			(21.38%)	(23.08%)	(9.94%)	
Buffalo	50.72	60.43	63.44	77.75	97.70	104.14	110.92	129.76	18.84	11.94
	(12.26%)	(12.17%)	(15.50%)	(15.98%)			(19.58%)	(22.48%)	(16.99)	
Sheep	99.38	134.31	99.32	124.91	145.85	100.54	111.90	90.80	-21.10	13.94
	(24.03%)	(27.05%)	(24.24%)	(25.78%)			(19.75%)	(15.73%)	(-18.86%)	
Goats	123.07	154.8	125.78	152.85	169.71	168.09	215.03	216.66	1.63	16.03
	(29.76%)	(31.18%)	(30.79%)	(31.55%)			(37.95%)	(37.53%)	(0.76%)	
Camel	7.52	7.56	7.19	7.46	6.69	4.98	4.22	3.26	-0.96	81.37
	(1.82%)	(1.52%)	(1.76%)	(1.53%)	(1.22%)	(1.01%)	(0.75%)	(0.56%)	(-22.79)	
Pigs	1.30	1.79	2.07	2.53	3.03	3.37	2.09	2.38	0.29	2.31
	-	-	-	(0.52%)	(0.55 %)	(0.68 %)	(0.37%)	(0.41%)	(13.96%)	
Others	2.64	2.57	2.16	2.29	2.16	1.70	1.27	1.23	-0.04	0.21
	(0.95%)	(0.88%)	(1.02%)	(0.47%)	(0.39 %)	(0.39%)	(0.22%)	(0.21%)	(-3.15%)	
Total	**413.59**	**496.50**	**409.17**	**484.45**	**546.55**	**491.36**	**566.63**	**577.32**	**1.89 %**	**100**

A. CATTLE POPULATION

Cattle population of Rajasthan is estimated at 13.32 million contributing 6.98 % of Country cattle population and ranks fifth amongst the states of the India. As against thirty two well defined breeds of cattle in the country, the state is endowed with eight breeds with finest drought hardy milch breeds (Rathi, Gir and Tharparkar), dual purpose breeds (Kankrej and Hariana) and the famous draught breeds of Nagouri and Malvi.

1. Rathi

Rathi cattle are named after a pastoral tribe of Rajasthan called Raths who lead a nomadic life. The home tract of this breed lies in the heart of Thar desert i.e. Bikaner, Jaisalmer and Ganganagar district of Rajasthan. The population of Rathi cattle is estimated as 9.24 lac as per livestock census, 2007. The animals are of medium size with a symmetrical body and a short and smooth body coat. The animals have brown colour with white patches and some animals with complete brown or black coat colour with white patches are also found. Horns are short to medium curving outwards, upwards and inwards, ears are of medium size, voluminous dewlap and large naval flap. Their udder and teat are well developed with a prominent milk vein. The females are docile and good milkers (1325 to 2593 kg per lactation). Calving interval ranges between 445 and 617 days. The average age at first calving (AFC) ranges from 1388.44 (Singh, 1996) to1601.4 days (Nehra, 2004) and inter calving period ranges from 450 to 620 days.

2. Tharparkar

It is an important cattle breed raised primarily for its milking potential .The original habitat of this breed is Tharparkar district in the Province of Sind, Pakistan. The breed is also found in the adjoining tracts in Rajasthan State in India, particularly around Jodhpur and Jaisalmer where excellent milch specimens are found. The population is estimated as 5.58 lac as per Livestock census, 2007. This is a medium-sized compact breed. The males are also good draught animals. The milk yield in cows ranges from 1800 to 2600 kg per lactation, age at first calving is from 38 to 42 months and the inter calving period is from 430 to 460 days. Lactation length is 285 days and dry period 140 days. Milk fat is about 4.88 % and SNF 9.2 %

3. Kankrej

The home of this breed is Gujarat and found in adjoining part Rajasthan (Barmer and Jodhpur district). It is one of the heaviest breed in India. The colour of the female is silver gray, iron or black. The males are darker than the females. The forehead is broad slightly dished in the center. The horns are thick, strong and curved. The base of the hornsare covered with skin. The body is powerful, with broad chest. Straight back, well developed hump, pendulous sheath in males, and tail is of moderate length with black switch extending below the hock. Dewlap is thin and pendulous and hump is large and prominent. In cows udder is well shaped and slightly developed and carried more forward than behind. The average weightof the male is 455 to 682 kg. and of the female is 409 to 455 kg. The average milk yield is 1750 kg. and milk fat is around 4.8 %. The lactation length averages 295 days and the calving interval

4. Hariana

The breeding tract of this breed encompasses large parts of Rohtak, Hisar and Gurgaon district of Haryana State and is found in Alwar, Bhartpur district of Rajasthan. The colour of the breed is white or light grey. Hariana cattle are characterised by a long and narrow face, flat forehead and well marked bony prominence at the centre of the poll. The muzzle is usually black. This eyes are large and bright expressive but not prominent in mature bulls. The horns are short and fine or moderately long, and they are generally 4 t0 9 inches, long thinner in females than in males. Dewlap is small without flashy folds and large in males. The chest is well developed. The udder is capacious and extends well forward with a well-developed milk vein. The teats are well developed, proportionate and medium sized. Good specimens of cows yield up to 1500 kg of milk per lactation. The age at first calving is 40 to 60 months depending on management and feeding conditions. The inter calving period varies from 480 to 630 days is around 490 days. The age at first calving is 36 to 42 months.

5. Gir

Although, the breed is native of Gujarat, it is also found in Maharashtra and Rajasthan States in India. The peculiar features of the breed are a protruding-broad and long forehead, and pendulous forward turned ears. The popular colour is white with dark red or chocolate-brown patches distributed all over the body. Entire red animals are also encountered although it is usually mottled with yellowish-red to almost black patches. The animals are medium sized with proportionate body. The head is moderately long, massive and the forehead bulging. The face is narrow and clean. The muzzle is square and black. The eyes are placed higher up in line with root of ears. Ears are large and pendulous. The horns are black, medium sized, shapely round medium heard, well set apart, and peculiarly curved. They take a down ward and backward curve and inline a little upwards and forwards taking a spiral inward sweep, finally ending in a fine taper. Dewlap is thin and hanging not pendulous. Chest is deep, full and well developed. Legs are well proportionate and muscular. The hump is medium sized. The barrel is deep, long and proportionate. The back is long, strong and wide. The tail is long touching the ground. The udder is of medium size. Average weight of the male and female is 545 kg. and 386 kg., respectively. Gir cows are good milkers and milk yield ranges from 1200 to 1800 kg per lactation. The age at first calving varies from 45 to 54 months and the inter-calving period from 515 to 600 days.

6. Nagouri

The Nagouri cattle from the "Swalak" area in Nagaur district (250 mm mean annual rainfall) is very famous as a draught breed and used to be exported to Multan, Sind and other regions. It was developed by Jat farmers to resemble a horse rather than a cow with a very light body and has no superfluous fleshy hangings at dewlap, prepuce, or testicles (Akhil Bharat Krishi Goseva Sangh 1981). This particular phenotype was achieved by both selective breeding and specific management practices. The young calf is starved from milk so that it will never develop fat cells and always remain lean. Later its access to roughage is also restricted to prevent the rumen from expanding. A normal diet is started only after the rumen has been stunted. (Akhil Bharat Krishi Goseva Sangh 1981). A pairs of Nagauri bullocks for draught were still very popular and purchased by customers from Punjab and Uttar Pradesh for top prices (more than Rs.20.000/-). Currently this breed is very much in decline because the demand for fast bullocks has decreased.

7. Malvi

The breed is found in Malwa tract in Madhya Pradesh and Rajasthan. The bullocks are known for their draft qualities and the cows are poor milkers. The colour of the animals is white to light grey, with black markings on neck, shoulders, hump and quarters. The colour changes with age. The head is small and the face dished. The body is deep, short arid compact with short legs and the tail touching the fetlocks. Ears are short and alert. The sheath in the male and navel flap in the female are short. The horns are massively built. Black, upright and pointed at tips.

8. Mewati

Mewati cattle are reared for milk production as well as for agricultural operations but due to fast growing farm mechanization in the area, the draft utility of the breed is reducing. The animals of this breed possess white coat and skin colour , black muzzle, eyelids, tail, hoof and horns. The orientation of horns was outwards, upwards, inwards and pointed tips or outwards and upward with pointed tips and comparatively smaller in size whereas ears had horizontal orientation. The forehead was straight, broader and slightly concave; Hump and dewlap was medium, naval flap was small and basic temperament was moderate. The fore and rear udders were bowl shaped and shape of teats was cylindrical with rounded teat tips and medium milk vein. The average milk production was found as 6.2 liters per day but in some elite animals it may go up to 12 kg per day with a lactation length of 150-210 days. The age at first calving varied from 3.5 to 4.0 years and inter calving period varied between 14 months to 2 years. The breed is declining in population and needs immediate attention for conservation and improvement. (P K Singh and Pundir)

9. Nari Cattle

One breed that has been overlooked is the **Nari cattle**. It is another strain of cattle estimated to be around 10 thousand in number and located in Sirohi and surrounding areas towards south of Rajasthan state This breed is kept by the Raika in Sirohi district in migratory production systems. This breed is extremely hardy, gives good milk yields, and is also suitable for draught. The cows give small amount of milk and are maintained mainly for cow-dung which is sold for livelihood. Young calves for sale is another source of income. The herd grazes on open common land in the nearby jungle. This system – organic by default – continues without much intervention from outside. Dung collected is largely used as Bio-fertilizer. Fertilizers or pesticides or even veterinary medicines are unheard of by the community members maintaining Nari cattle.

B. Buffalo

Rajasthan buffalo's population was 89-9 million in 1997. This is about half the buffaloe population of the world and about 19 per cent of the total livestock of India. Buffaloes thrive best in areas of warm and humid climate. Buffaloes are reared mainly for milk but some buffaloes are used as draught animals in certain parts of the country.

1. Murrah

The breeding tract of Murrah breed is Rohtak, Hisar and Jind districts of Haryana and Nabha and Patiala districts of Punjab but the animals are distributed throughout Rajasthan. The animals are noted for milk and fat production. The breed has a massive body; neck and head are comparatively long, horns short and tightly curved. The hips are broad, and fore – and hindquarters drooping. The tail is long reaching up to the fetlocks. The colour is usually jet black with white markings sometimes found on tail, face and extremities. The skin is soft and smooth. Ears are small, thin and pendulous. The udder is well developed with prominent veins and good sized teats. The average milk yield per lactation is 1500 to 2500 and the milk fat percentage is about 7-9 %. On an average the daily milk yield is found to be 8-10 Kg. The age at first calving is 45-50 months in villages but in well managed herds it is 36 to 40 months. The inter calving period is 450-500 days. The bodyweight of an adult female ranges from 430 to 500 kg and that of a male 530-575 kg.

2. Surti

The breeding tract of this breed is Kaira and Baroda districts of Gujarat and the animals are distributed to Udaipur division of Rajasthan. The body is well shaped and medium sized; the barrel is wedge shaped. Because of their medium size, Surthi buffaloes are economical producers. The head is long and eyes are round and bulging. The back is straight. The horns are sickle shaped, moderately long and flat. The tail is fairly long. The colour is black or brown. The peculiarity of the breed is that there are two white collars, one round the jaw and the other at the brisket. The milk yield ranges from 900 to 1300 Kg. The peculiarity of this breed is very high fat percentage in milk (8-12per cent). The average fat percentage of milk is about 7.5%. The age at first calving is 40 to 50 months with an inter calving period of 400 to 500 days. The breed is famous for early maturity and efficiency of milk production. The bullocks are good for light work. Also used for the grading up of inferior local buffaloes.

SHEEP

With 90.07 million sheep (2012), Rajasthan stands 3rd in sheep population in the country after Andhra Pradesh and Karnataka. More than 13.95 per cent of the India's sheep are reared in Rajasthan. The sheep population has been a small increase in population between 2003 and 2007. However there has been a decrease (18.86 %) in the population from 2007 to 2012. About 36% of total sheep population is slaughtered annually for meat purposes. The wool production has also remained constant at about 45 million kgs out of which around 4 million kgs is of fine quality while the remaining of medium and coarse quality. The requirement of industry is estimated at around 35 to 40 million kgs of fine wool, which is met mainly through imports. Most of the sheep are raised in regions which are too dry, too stony or too mountainous to be too good for agriculture or for cattle rearing.

The important sheep breeds of north western semiarid and arid regions are Chokla, Magra, Nali, Pugal, Marwari, Malpura, Sonadi, Jaisahneri, Patanwadi and Muzzaffamagri. Further, in the major sheep rearing areas, specially in North-Western districts of Rajasthan, grazing and stock watering resources are available only for few months in a year compelling shepards to lead a nomadic life. Migration and grazing practices have an impact on the present status of sheep husbandry in the state.

1. Magra

Magra is an important sheep breed of north-western arid and semi-arid region of the country. It is distributed in Bikaner, Jaisalmer and Chru district of Rajasthan and produces most lustrous wool suitable for carpet manufacturing. They are medium to large size animals, with a white face with light brown patches around the eyes, which is characteristic feature of this breed. The skin colour is pink, ears are small to medium and tubular. Age at first breeding is 18 months for ewes and 20 months for Ram. Lambing percentage is about 45 and the litter size is mostly single. The average annual fleece weight is 2.18 kg with an average fibre diameter of 32 micron and a medullation percentage of 48. According to 18th Livestock Census of 2007 there are 313004 Magra sheep in the country.

2. MaIpura

Malpura sheep are found in Jaipur, Tonk, Sawaimadhopur and adjacent areas of Ajmer, Bhilwara and Bundi districts in Rajasthan. The animals are fairly well-built, with long legs. Face is light brown. Ears are short and tubular, with a small cartilaginous appendage on the upper side. Both sexes are polled. Tail is medium to long and thin. The fleece is white, extremely coarse and hairy. Belly and legs are devoid of wool. The overall least square means for 1st six monthly and adult annual GFY were 551 and 810g respectively and least square means of birth, 3, 6 and 12 month's weight of lambs were 3.02, 15.41, 20.80 and 25.60 kg, respectively under farm conditions. The average fibre diameter was 41.67μ with medullation of 75.9 %. Staple length was 4.9cm.

3. Marwari

Marwari sheep, one of the important breed distributed in Jodhpur, Jalore, Nagaur, Pali and Barmer districts extending up to Ajmer and Udaipur districts of Rajasthan. The animals are medium size with black face, the colour extending to the lower part of neck. Ears are extremely small and tubular. Both sexes are polled. Tail is short to medium and thin. The fleece is white and not very dense. The wool produced by Marwari is approximately 7.2 million kg per annum and is very good for carpet manufacture. The overall least square means for 1st six monthly, adult six monthly and adult annual were 607.16, 631.25 and 1260.50g, respectively and least square means of birth, 3, 6, 9 and 12 month's weight of lambs were 3.05, 14.74, 19.33, 22.85 and 25.90 kg, respectively under farm conditions. Average fibre diameter, medullation and staple length were 31.9μ, 50.8 % and 5.35cm respectively (Gohil, 2010).

4. Nali

The Nali sheep is found in Ganganagar, Churu and Jhunjhunu districts of Rajasthan, southern part of Hissar and Rotak districts of Haryana. The animals are medium-sized. Face colour is light brown and skin colour is pink. Both sexes are polled. Ears are large and leafy. Tail is short to medium and thin. Fleece is white, coarse, dense and long-stapled. Forehead, belly and legs are covered with wool. The overall means for 1st six monthly and adult annual were 1.01 and 2.84 Kg, respectively and means of birth, 3, 6, 9 and 12 month's weight of lambs were 2.43, 10.74, 14.93, 17.13 and 19.64 kg, respectively under farm conditions. Average fibre diameter, medullation and staple length were 29.89μ, 41.14 % and 6.79cm respectively.

5. Pugal

Pugal sheep is found in Bikaner and Jaisalmer district of Rajasthan. The breed produces wool is suitable for carpets and has long migratory capability. The population of this breed is declining continuously. The flock size and number of pure Pugal animals varied from farmer to farmer and village to village. The animals are fairly well built. Face is black with small light brown stripes on either side above the eyes; the lower jaw is typically light brown. The black colour may extend to neck. Ears are short and tubular. Both sexes are polled. Tail is short to medium and thin. The fleece is white.

6. Chokla

Chokla is one of the famous carpet type wool-producing sheep of Rajasthan and well suited for the regions where migration is a common practice. The wool produced from Chokla sheep is suitable for carpet manufacturing and have good lustre quality. Chokla sheep prevails in a limited area at the junction of Churu, Nagaur, and Sikar districts of Rajasthan. The purity with respect to purebred Chokla type sheep in the flock ranged between 40-70%, which is further dwindling. The Chokla sheep distribution area is characterized by high temperature and long periods of severe droughts accompanied by high wind velocity and low humidity. Migration is a common practice. The Chokla flocks start migration to the neighboring state of Haryana in February/March and return to their homestead in July with the onset of monsoon.

7. Sonadi

Sonadi sheep are found in Udaipur, Chittorgarh, Rajsamand, Bhilwara and Dungarpur districts of Rajasthan and part of north Gujarat. The breeding tract of Sonadi sheep has land area of 42360 sq. km, which is 12.38 per cent of the total geographical area of the state and contains 17.05 per cent livestock population of the state. The animals of Sonadi breed have well built body, long legs, prominent nose, large dropping ears, long tail and white or light brown face. The average body weight of the animals at 12-months and 18-months was reported as 23.31 ±0.12 and 28.01±0.10 kg, respectively. The shearing of wool is practiced thrice a year and the wool production ranged from 200–400 g per head per shearing (Talior at al., 2006).

8. Kheri

Bohra et al. (l993b) identified a new breed of sheep viz. Kheri evolved under the field conditions in the migratory flocks of using black faced (Marwari/Jaiselmeri) rams on local sheep breed. Kheri sheep are reared for meat and wool production. This breed was evolved and developed directly in the farmers' flocks due to the need felt by the migratory sheep breeders for sturdy and more tolerant of heat and drought conditions. The breed is believed to have originated from a crossbred base with unknown levels of inheritance of Marwari, Malpura and Jaisalmeri sheep of Rajasthan. The animals are medium to large with light-brown face and pink skin. Both sexes are polled. Ears are medium (11-13 cm) and tubular, tail is short to medium (21-23 cm) and thin. Forehead, belly and legs are covered with wool. Average flock size is 70. Most of the farmers kept one or two breeding rams. The average body weight, body-length, height at wither, chest girth and paunch girth of rams and ewes were 38.85±1.49 and 31.38±0.30 kg; 68.95±0.91 and 64.17±0.25 cm; 69.16±0.82 and 64.39±0.24 cm; 80.03±0.99 and 78.03±0.99 cm, and 81.14±1.20 and 78.02±0.38 cm in that order. Lambing is about 80 to 100% with lambing interval of 12-18 months. Age at first lambing varied between 18-24 months. Litter size is mostly single with twinning of about 2%. An ewe produced 4-8 lambs in its lifetime. Daily milk yield varies from 300-500 ml. Lactation length varies from 120-180 days. Age at first breeding in males varies from 12-18 months with a breeding life of 5-6 years. Average greasy wool production ranges between 1.5-3.0 kg per annum. (Gurmej Singh and Anand Jain, 2005).

GOAT

Goat is called the poor man's cow because it can be cheaply reared on meagre grass of poor quality. It is the major supplier of mutton along with milk, hair and skins. The goat population of Rajasthan is around 216.66

million (Livestock Census 2012), which is almost 16.03 % of India's total goat population and the highest among all the states of the country. Goat population in Rajasthan during the last four decades has increased at the fastest rate amongst various livestock species, in spite of the fact that nearly 41% of goats are slaughtered annually The increase in goat population from 47.2 million in 1951-52 to the current level of 216.66 million show that it offers great potential in terms of population growth making it most important species of animal for meat production. Rajasthan is having 3 well known breeds of goats viz.: Jakharana, Sirohi, and Marwari breeds. Goat rearing was a traditional activity and a way of life for most farmers, and was adopted as a subsidiary or main enterprise to utilize the family labour and ensure livelihood for the family. Family of goat the keeper earned a net annual income of Rs. 1302 to Rs. 1873 per goat in different categories. The goat rearing was a major source of income for women of the household, especially in small size category.

1. Marwari

Marwari is a desert goat breed of India and is found in Marwar region of Rajasthan, comprising Jodhpur, Pali, Nagaur, Bikaner, Jalore, Jaisalmer and Barmer districts. It is well known for its tolerance of hot and cold climates, disease resistance and thriving in very harsh nutritional conditions. It is a hairy black coloured goat. The means of the body length, body weight and ear length were estimated as 54 cm, 83 cm and 20 cm in males and 49 cm, 72 cm and 16 cm in females. Males have larger and stronger horns than females. The average adult body weight in males and females is 46 and 30 kg, respectively. The overall milk yield at 200 days is 98 kg. The kidding percentage in field conditions is 79.3 percent and multiple birth is about 19 percent. The Marwari is an early maturing breed as the average age of puberty is 306 days. The mortality in kid is 3.3 percent and in adults 3.5 percent in field conditions.

2. Jakrana

The goats are distributed in Jhakrana and a few surrounding villages near Behror, in the Alwar district of Rajasthan. Jakhrana is a valuable milch breed and also used for meat due to its compact and large size body. Black coat colours with white patches on ears are typical characteristics of Jakhrana goats. It is a medium size, dairy breed of goat with good potential for milk production and prolificacy. The average body weight at birth, 3, 6 and 12 months were 2.54±0.11, 12.28±1.50, 16.47±1.89 and 25.30±3.01 kg respectively. The average milk yield and lactation length were 152.87±0.19 kg and 143.0±3.2 days in semi intensive system and 107.39±0.11 kg and 118.0±2.3 days in extensive system of management, respectively. The average age at first kidding, kidding interval and twinning rate were 561.24±8.23 days, 287.78±6.89 days and 1.54±0.16 in semi-intensive and 632.35±5.83 days, 332.86±6.34 days and 1.32±0.12 in extensive management system respectively.

3. Sirohi

Sirohi goat found in the Sirohi, Ajmer and Udaipur districts of Rajasthan. The animals are of medium body size and weight and are reared for milk and mutton purpose. Three types of colour variants viz. light brown spots with dark background and dark brown spots with light background, large spots on body but with white face of animal and uniform light brown colour, are observed. Ears are flat and leaf like, medium sized and drooping. Both sexes have small horns, curved upward and backward.The flock size varies from 10 to 80. Animals are kept on pasture grazing. Stall fed animals are rarely seen. The females show maturity at about 12 to 18 months of age. The breeding seasons are March– April and September- October. Goats kid once in a year. Twining is only in well fed goats (10-20%). Milk yield varies from 0.5 to 2.0 kgs. On average, birth weight is ranged from 2.14 ± 0.02 kg (Pathodiya *et al.*, 2004) to 3.12 ± 0.05 kg (Gowane *et al.*, 2011). The age at first kidding is 19-20 months and the litter size is one kid per birth. The breed is well suited for stall feeding.

4. Jamnunapari

Usually found in the Etawah district of UP, and in the tracts lying between Jamuna & Chambal rivers. The bucks of Jamunapari breed of goat are being reared at Cattle Breeding farm, Kumher, in Bharatpur District. These bucks are distributed in Bharatpur, Dholpur, Karauli, Alwar and Sawai Madhopur districts under the goat development program. Animals are large sized, tall, leggy with large folded pendulous ears and prominent Roman nose. They carry long and thick hair on their hind quarters and has a glossy goat. Horns are short flat. The body weight of adult bucks and does varies from 65 to 86 kg and 45-61 respectively. The average daily milk yield in 2.25 to 2.7 kg. The milk yield in a lactation period of, 250 days varies from 250 - 300 kg with 3.5 percent fat content.

.Camel

India has the third largest camel population in the world and the camel has long represented an important component of Rajasthan's agro-biodiversity and cultural heritage. The state is having the 81.37 percent of camel population of the country. The people most closely associated with the camel in Rajasthan are the Raika, who earlier took care of the camel breeding-herds of the Maharajas. Originally the Raika acted as guardians of the camels and never sold female camels outside the community, as well as abhorring the idea of selling camels for meat. But due to ever increasing pressure, these social mechanisms and cultural beliefs are now breaking down. Camel numbers in the state are plummeting. As per the Livestock Census data, 668000 camels were recorded in 1997 which has gone down to 498024 in 2003. This means 25 percent decrease in a period of five years. By 2007, the number of camels had further decreased to 430426, a further 13.5% decrease. In the Livestock census 2012 data, the population of camel remain 23 percent to 325713. To save India's dwindling camel population, the government of Rajasthan has declared the camel an official State Animal and has drafted legislation, the Rajasthan Camel Bill 2014, to protect it.

The country has four major breeds of camel; the Bikaneri, Jaisalmeri, Kachchhi and Mewari. (Kaura, 1961; Rathore, 1986 and Report of the Camel Development Committee, 1988). Bikanneri, Jaisalmeri and Marwari are the common breed of camel found in the state. The Mewari breed of camel is adapted to the hilly terrain of the Aravali hills of Mewar in south Rajasthan which is considered to be the major breeding tract of the breed (Rathore, 1986;Kohler-Rollefson, 1992 and Khanna, 2004). Jaisalmeri camels are predominantly bred in Jaisalmer, Barmer and part of the Jodhpur district of Rajasthan state and are well known for their riding and race potential (Rathore, 1986 and Rai et al.,1992). Bikaneri breed of camel is one of the major camel breeds found in India. The breed derives its name from the city Bikaner which was established by Rao Bika in the 15th century and is known for better draught potential.

Conservation Strategies

There are thirty seven recognized breeds of cattle, 12 breeds of buffalos, 42 breeds of sheep and 20 breeds of goats in India, in addition to large number of non-descript livestock. In recent times, several of the indigenous breeds suffered decline mainly due to their becoming uneconomical. Draught breeds utility has decreased because of mechanization in agriculture. Most of the wool produced in the region is of36 to 48s quality suitable for carpet manufacturing. The conservation has been recognized as an increasing national concern. Genetic characterization is the first step in prioritization of breeds for conservation.

The local breeds have following merits over exotic breeds viz:

1. Better disease resistance than exotic breeds
2. More suitable for low input management system
3. Survive better in local environment
4. Suitable for draught work

In addition, existence of superior indigenous breeds can provide valuable research inputs for developing superior breeds. It is therefore important that Indigenous breeds of cattle are conserved, developed and proliferated.

Conservation Strategies

(A) Breeding Policy

The existing breeding policy of the State emphasised the conservation and genetic improvement of defined indigenous livestock breeds through selective breeding, upgrading and improvement of non-descritive stock through crossbreeding

(i) Indigenous Breed Improvement Programme

To preserve and develop the well recognized indigenous breeds of cattle of the state, the indigenous breed improvement programme is being operated in the native tract of cattle breeds viz. Gir (Ajmer), Tharparkar (Barmer), Rathi (Bikaner), Kankrej (Jalore) and Nagauri (Nagaur district). The frozen semen of the selected bulls of these breeds is provided for artificial insemination in animals of the respective breeds and genetic improvement is achieved by selective breeding / upgradation of the animals in the respective breed tract.

The state breeding policy envisages upgrading of indigenous germ plasm on priority through selective breeding within indigenous breeds, whereas non-descript cattle will be up graded with high yielding indigenous native breeds. Selective breeding of indigenous breeds of Gir, Haryana, Malvi, Rathi, Kankrej, Nagauri, Sahiwal and Tharparkar cattle will be carried out in native tracts where these animals are found in their true forms. Under the breed improvement programme scrub bulls and calves which are not considered suitable for breeding purpose shall be castrated.

(ii) Sheep Breeding Programme: - To improve the sheep population of the state genetically by providing superior breeding males (rams) to the sheep breeders, State is running a Sheep Breeding Farm at Fatehpur (Sikar). According to the sheep breeding policy, the crossbred animals of the farm has been sold and replaced by indigenous breed i.e. Nali and Marwari. The indigenous rams will be distributed to the Sheep breeders at the subsidized rates. The farm also has 84 exotic sheep (49 ewes, 5 rams and 30 lambs) of Rambouillete breed.

(iii) Goat Breeding Program: The programme for goat development is mainly aimed to help in improving the weaker sections of society. There are goat farms of the department working at Ramsar in Ajmer district, Cattle Breeding Farm, Nagaur and Kumher at Bharatpur District. Goat development programme is aimed to develop Sirohi goats in ten districts of South-Western regions of the State viz.: Ajmer, Pali, Sirohi, Bhilwara, Rajasmand, Chittorgarh, Dungarpur, Banswara, Nagaur and Udaipur. Sirohi breed kids of about 4-6 months age are selected from the home tract and are reared at Ramsar farm Ajmer and Cattle Breeding farm, Nagaur. The bucks of Jamunapari breed of goat are being reared at Cattle Breeding farm, Kumher, in Bharatpur District. These bucks are distributed in Bharatpur, Dholpur, Karauli, Alwar and Sawai Madhopur Districts.

(iv) Pig Breeding Programme: - The pig is one of the most efficient animal having a great food conversion efficiency among domesticated livestock, and can play an important role in improving the socio-economic status of the weaker sections of the society. The state has established one Piggery Development Training Center at Alwar where 5 days training programme is being conducted free of cost. With an idea to provide breedable exotic Pigs to local pig breeders and to encourage the Scientific pig breeding in the state a Pig Breeding Farm is functioning at Alwar. Unit of pig (3 male + 1 female) is being supplied in the Alwar and Bharatpur districts specially to the Schedule Caste, Tribes and marginal farmers. This Pig unit (3+1) is being distributed to the Socially Backward Classes on subsidized rates i.e. @ Rs. 5000 per Unit.

(B) Implementation of the Breeding Programme

1. The State developed region specific and breed specific breeding strategies, programmes and plans to implement the conservation programme.
2. In the districts of Jaipur, Jodhpur, Bikaner, Kota, Ajmer and Bharatpur division, Murrah breed shall be the breed of choice for buffalo breeding. In the districts of southern belt of the Udaipur division, breeding

by Surti breed shall be the breed of choice for buffalo breeding. Use of Murrah bull / semen in this part of the division shall be done only on specific demand of the livestock owner / animal breeder. Non-descript buffalo shall be required to be improved/upgraded by using Murrah / Surti bulls or it's semen specified for that area.

3. Region wise policy for breeding Cows

SN	Name of District	Breeding Policy	Breeds proposed for propagation
Jaipur division			
1	JAIPUR	SB/UG/CB	Gir / Haryana / Exotic / Crossbred
2	ALWAR	SB/UG/CB	Haryana / Gir / Exotic / Crossbred
3	DAUSA	SB/UG/CB	Haryana / Gir / Exotic / Crossbred
4	SIKAR	SB/UG/CB	Gir / Haryana / Exotic / Crossbred
5	JHUNJHUNU	SB/UG/CB	Gir / Haryana / Exotic / Crossbred
AJMER DIVISION			
6	AJMER	SB/UG/CB	Gir / Exotic / Crossbred
7	BHILWARA	SB/UG/CB	Gir / Exotic / Crossbred
8	TONK	SB/UG/CB	Gir / / Exotic / Crossbred
9	NAGAUR	SB/UG/CB	Nagauri/ Tharparkar / Exotic / Crossbred
10	JODHPUR	SB/UG/CB	Tharparkar/ Exotic/ Crossbred
11	PALI	SB/UG/CB	Kankrej /Gir/Tharparkar / Exotic/Crossbred
12	SIROHI	SB/UG/CB	Kankrej / Exotic/Crossbred
13	JAISALMER	SB/UG/CB	Tharparkar / Exotic/Crossbred
14	JALORE	SB/UG/CB	Kankrej / Exotic /Crossbred
15	BARMER	SB/UG/CB	Kankrej/Tharparkar/ Exotic /Crossbred
UDAIPUR DIVISION			
16	UDAIPUR	SB/UG/CB	Gir / Exotic/Crossbred
17	CHITTORGARH	SB/UG/CB	Gir / Exotic/Crossbred
18	DUNGARPUR	SB/UG/CB	Gir / Exotic /Crossbred
19	BANSWARA	SB/UG/CB	Gir / Exotic /Crossbred
20	RAJSAMAND	SB/UG/CB	Gir / Exotic /Crossbred
21	PRATAPGARH	SB/UG/CB	Gir / Exotic /Crossbred
BIKANER DIVISION			
22	BIKANER	SB/UG/CB	Rathi / Tharparkar / Exotic / Crossbred
23	CHURU	SB/UG/CB	Rathi/ Tharparkar / Exotic/Crossbred
24	GANGANAGAR	SB/UG/CB	Rathi / Sahiwal / Tharparkar /Exotic /
25	HANUMAN-	SB/UG/CB	Rathi / Tharparkar / Sahiwal / Exotic / CB

Note: SB: Selective Breeding; UG: Up Grading; CB: Cross breeding

(C) Promotion of Breeders organization

1. Breeding Farms

The existing State/University breeding farms of indigenous breeds should be declared as germplasm repositories and used for production of bulls. Only pure breeding should be practiced at these farms

2. Gaushala

Conservation efforts have mostly limited to institutional farms with small herd sizes, leaving larger parts of the breeding tract totally neglected. There are large number of Gaushala have quite sizable populations of purebred animal of Indigenous breeds but do not have the resources for maintaining and improving these animals. Such Gaushala may be supported to maintain indigenous breeds so that they can supply improved quality of germplasm for breeding. They should be provided with scientific and technical inputs and training for genetic evaluation

Out of about 4000 Gaushalas in the country, 677 Gaushalas are registered in the Rajasthan State. A few of these Gaushalas maintain herds of pure indigenous breeds and are providing quality indigenous / crossbreds heifers and bulls. These can be rich source of identifying superior germplasm and their multiplication. In order to plan and assign a grater role to Gaushalas and using them for cattle development, there is a need to conduct a nationwide survey to have baseline information about the total number of Gaushalas available in each State/UTs. The survey should generate required information about the number and breeds of the cow and her progeny maintained in the available Gaushalas, size of agriculture farm land, capacity and number of biogas plants, facilities for research and development on value added products from cow dung and urine and man power available to manage the Gaushalas scientifically. Based on this information, a criterion needs to be evolved for declaring a Gaushala as a conservation unit for a particular breed. The selected Gaushalas thus identified should be encouraged to maintain purebred superior germplasm of indigenous breeds and strengthened to have state of the art facilities for animal maintenance and germplasm production and multiplication. A long term breeding programme could be developed for selected indigenous breeds, which may be undertaken by individual (large) or group (medium size) of Gaushalas in associated manner to act as "bull mother farms".

(D) Role of voluntary organization

1. Breeder Association – without involvement and participation of farmer's it is not possible to conserve the breed. Improvement of Indigenous breeds can be taken up in collaboration with Breeders' association through selection of outstanding animals true to their breed types.
2. These Breeders' association can be encouraged to form a Federation at the State/District level to take up issues relating to conservation and development of respective indigenous breeds.
3. States may consider having State level awards for Breeders' associations and for progressive farmers who have contributed to conservation and development of recognized indigenous breeds.

(E) Use of Science and Technology

Since the introduction of cross breeding programme, most of the techniques and methodologies for breed improvement have been used to produce cross bred cattle. The application of such technologies for propagation and improvement of indigenous breeds is a relatively rare phenomenon, one of the reasons for which may be the reluctance of the farmers, owning these breeds to accept new and established techniques for reproduction.

1. Technologies such as artificial insemination, Frozen semen production, progeny testing, embryo transfer technology should be used, after proper evaluation where ever required
2. National gene bank should maintain the germplasm in the form of semen & embryo. Regional gene banks should meet the requirements of National gene bank

(F) Data Base

1. A reliable data base should be developed with regard to all the details of Indigenous breeds, including their breeding tracts, numbers, characterization, gene make up, the institutional farm where they are being preserved and /conserved.
2. The national level data base for cattle and buffalo developed by NDDB may be utilized for this purpose.

3. A breeding network should be set up by computerizing and net working all AI outlets, semen stations, breeding farm and Gaushala

(G) Creation of Public Awareness

1. Available information on different breeds should be published in the form of pamphlets, books, calendar etc. This will create awareness and motivate farmers to conserve the important breeds.
2. Some farmers are the proud owner of the popular breeds of their area. Such farmers, if encouraged through financial & veterinary help will help in preservation of breeds
3. Breeds shows should be arranged for local breeds and owners should be rewarded for maintaining pure local breeds. Publish success stories on local breed conservation and innovative utilization.

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4. CRYOBANKING OF ANIMAL GENETIC RESOURCES – OPTIONS AND CHALLENGES

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Extinction of mammalian species is part of natural process of evolution and is irreversible, but now it is taking place at a much higher rate. In the last few decades *ex-situ in-vitro* conservation strategies were developed by cryopreservation of gametes, embryos, testis, ovarian tissues, somatic cells etc. This is an overview of current status of the technology and the challenges for the future.

Need for Cryobanking

The goal of cryoconservation are (i) to keep genetic variation as gene combinations in a reversible form and keep specific genes of interest (Printice and Anzar, 2010) (ii) to minimize inbreeding and genetic drift in small populations (iii) to quickly redirect the genetic trend of a selected population (iv) to store foundation stock with rare/extreme breeding value (v) as an Insurance against climate change, disease, selection errors, unforeseen catastrophic events etc. (Meltdown of Nuclear reactor at Chernobye in 1986, Foot and Mouth Disease epidemic UK in 2001, Civil war in Rwanda in 1990 etc) and (vi) to provide multi generations samples for scientists performing DNA research (Mara *et al.* 2013).

Sample Collection

The standard recommendation is that a conserved population (including a newly reconstituted breed) should have an effective population size (Ne) of 50 individuals, so that the rate of inbreeding can be held at 1% per generation (FAO 1998). This could be met by 25 unrelated sires with frozen semen or by 25 unrelated parental pairs with frozen embryos. These may be increased in practice for a margin of safety depending on reproductive success (FAO 2011). For DNA, it is recommended that if fewer than 25 individuals are available in one sex extra individuals from the other sex should be sampled to make the total no. of DNA samples stored up to 50.

Stopping the Biological Time

Cells can endure storage at low temperatures such as -196° C for centuries (Mazur, 1984). No thermally driven reactions occur in aqueous systems at liquid nitrogen (LN_2) temperature (-196°C). One reason is that liquid water does not exist below -130 ° C. The physical states that do exist are 'crystalline' or 'glassy'. In both states, the viscosity is so high (◎10^{13} poises) that diffusion is insignificant. Moreover at -196°C there is insufficient thermal energy for chemical reactions. The only possible reaction in frozen aqueous system at -196°C is formation of free radicals and breaks in macromolecules as a direct result of 'hits' by background ionizing radiation or cosmic rays.

The dose ionizing radiation that kills 63% of cultured mammalian cells and room temperature is 200-400 rads. Because of terrestrial background radiation in some is 0.1 rad/year, it ought to require some 2000-4000 years at -196° C to kill that fraction of mammalian cells (Mazur, 1984). Therefore stability of stored biological material for centuries requires a constant temperature below -130° C.

Freezing Rates

Slow Freezing (Controlled Rate Freezing)

i) Diluents containing cryoprotectants are used to minimize ice crystal formation and to increase solute concentration during freezing. In slow freezing lower levels of cryoprotectants are used. Spermatozoa can tolerate a wide range of freezing rate 0.5 -100° C/min. On the contrary, oocyte and embryo are highly sensitive to drastic reduction in temperature. Hence, a very slow rate of fall in temperature (0.3 – 0.5

°C/min) is employed by using a computerized programmable freezer. Semen and embryo are routinely frozen using slow freezing rates.

Ultra Rapid Freezing (Vitrification)

ii) In vitrification, both ice crystal formation and chilling injury are avoided. It is a physical process by which aqueous solution forms in to an amorphous 'glass like' state rather than crystalline. This phenomenon is achieved by adopting a cooling rate of 2500° C/min or even higher by directly plunging the vial in to LN$_{2..}$ A very small volume of freezing media (0.6-02 µl) is used. Only problem is use of very high concentration of cryoprotective agent (40-50%), which is toxic if exposed for longer time. This method is becoming more popular for its advantages like simple and rapid procedures, no requirement of costly equipment and user friendly for on-farm procedures. Apart from oocytes and embryos, vitrification has been successfully used in cryobanking of organs like kidney, liver, heart, organ slices, tissues blood vessels, cartilages, skin, cornea etc. Attempts to vitrify spermatozoa have not been successful.

Cryobanking of Semen

Semen is stored as a method for reviving a breed through back crossing. With four back cross generations it is possible to reconstitute over 90% (4 generations ~94%, 5 generations ~97%) of the conserved breed or population genome. However the mitochondrial genome of original breed is lost, where only semen is used. Semen is one of the most practical means of storing germplasm due to its abundant availability and ease of collection. Variability between bulls for cryoresistance is a major concern. Though this technique is in vogue for more than 60 years still there is need to improve fertility of frozen semen. Cryoinjury affects several structures of the spermatozoa resulting in compromised fertility. Therefore, only the best samples to be taken up for long term storage.

Ram and Buck semen freezing protocol is more or less similar. In sheep very low level of fertility (10-30%) is obtained when frozen semen is used for cervical insemination (Curry, 2000). However, with laparoscopic deposition, 70-80% lambing rate is reported (Paulenz, et.al. 2004). This technique needs well experienced technicians and costly equipment. In goats, fertility ranges between 50-60%, since anatomical structure is different and deposition of semen is easy. However, in some cases, mixing of seminal plasma and diluents containing milk or egg yolk has detrimental effect on spermatozoa lowering the fertility of frozen semen.

Swine has complicated cryotechnology because of large volume of fractioned ejaculate. Cryosurvival is consistently low in comparison to other species. The procedure is time consuming, costly and yields few doses per ejaculate (Rodriguez and Wallgren, 2010). Individual variation among boars for cryosurvival is significant.

In **Stallions,** processing the semen for cryopreservation is complex as the gelatinous portion of semen has to be removed by filtration. Individual variation for freezability between stallions is significant. The success of cryopreservation is lower than other farm animals and the motility/fertility ranges between 35-40% (Blottner et al, 2001).

Sperm Sexing on the basis of differences in DNA content between X and Y sperm has become a reality with the flow cytometer with an accuracy of 90%. Sexed semen will have more application in *in-vitro* production of embryos. Unbalanced sex ratio, especially excessive male birth can play havoc with small population in wild life.

Cryobanking of Embryo

Embryos are the best choice, if complete genotype of a breed is to be conserved for later regenerations. Storing embryos enables conservation of mitochondrial genome. The main advantage is the speed with which breed could be reconstructed (in less than 5 years). However embryos are significantly more expensive to collect and require greater technical competence (Mara et al. 2013). Sufficient no. of embryos has to be stored to generate at least 10-20 females to reconstruct mitochondrial DNA. The calving rate in cattle under ideal circumstances is 45-50%.

In several species, the most convenient stage for embryo freezing is the expanded blastocyst (6-7 days) (Sommerfld and Niemann, 1999). The success rate for embryo freezing is 40%, 35%, 40% and 10 to 20% in sheep, goat, horse and pig respectively. Cryopreservation of pig embryo has long been a problem due to extreme chilling sensitivity and high lipid content of pig embryo. The *in-vitro* produced embryos have lower success than *in-vivo* produced embryo (Mermillod, 2001).

Cryobanking of Oocyte

The Major advantages of oocyte storage are (i) the mitochondrial genes are not lost (ii) when stored with semen no back crossing is required. However, cryopreservation of mammalian oocyte in general has several problems. They are extremely sensitive to chilling (Printice and Anzar, 2010). And the damage to cryoskeletal system results in aneuploidy. However, vitrification has shown encouraging results. Oocytes can be frozen either at germinal vesicle (GV) or metaphase II (MII) stage. However, equine and porcine oocytes undergo significant changes during freezing.. Limited studies have been undertaken in small ruminants. In sheep, poor developmental rates have been reported following vitrification. In goats, acceptable levels of survival and cleavage have been reported.

Tissue Graft Banks

The aim of ovarian testicular tissue preservation is to store primordial follicles and spermatogonial cells respectively. Xenografting of the thawed ovarian tissue of monkey, African elephant, cat, cow into immune deficient mice has resulted in antral follicle development. Isolated sperm nuclei supporting embryonic development has been recorded in cattle and human (Andrabi and Maxwell, 2007). Whole ovary of sheep cryopreserved, thawed and auto transplanted has been reported (Revel et al, 2004).

Somatic Cell Nuclear Transfer (SCNT) has been used to produce offspring from cattle, goat, pig, horse, mule, cat etc. Overall success rate is very low and gestational and neonatal developmental abnormalities have been reported. Dermal fibroblast cells are the most common source for donor cells Somatic cell preservation is a low cost way of establishing gene bank. The current levels of success in the cryopreservation of gametes and embryo are summarized in the following table.

Table 1. Current Levels of Success Rate of Cryopreservation of Gametes and Embryos

Species	Semen	Oocytes	Embryos
Bovine	Good	Difficult	Good
Ovine	Good	Difficult	Good
Caprine	Good	Difficult	Good
Swine	Difficult	Difficult	Difficult
Equine	Difficult	Difficult	Difficult

(Source: Mara et al, 2013)

Biosafety in Cryostorage

Contamination with pathogens can occur from animals, during collection and handling, storage etc. Direct exposure to Liquid nitrogen as in vitrification or imperfect seal can lead to contamination. Several organisms survive LN_2 temperature *viz. T.fetus, L.Pomana, Foot and Mouth disease virus* etc. Whenever there is a breach (freezing injury/ICSI/sexing/embryo cloning/gene transfer) on the zona pellucida, the protective covering, there is an increased risk of infection (Bielanski, 2007).

Hence care should be taken to comply with sanitary and veterinary regulations of IETS, OIE, HASAC, MSP of Govt. of India. Major importance is the ethical and technical excellence of those responsible for these procedures.

Management Safety in Planning

- Objectives of programme to be clearly defined.
- Adequate funding to be allotted.
- Collaboration and skill sharing are essential.
- Concept of single centre storing huge stock of multiple species is unrealistic
- Legal frame work, rights of disposal to be defined.
- Samples to be stored at regional and national level to overcome any eventuality.
- Regular supply of liquid nitrogen and adequate back up containers are to be provided.
- Dewars are to be replaced after 10 years.
- Storage tanks to be connected to alarms system to monitor liquid nitrogen level.
- Data base and complete documentation is essential.

A gene bank without consistent documentation is worthless.

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5. GOAT GENETIC RESOURCES OF INDIA:STRATEGIES FOR THEIR IMPROVEMENT AND CONSERVATION

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Introduction

India is home to 135.17 million goats, 23 recognised breeds and many lesser known but important genetic resource ready for description as breed. Goats share about 26.4% of livestock population of India.The 12th livestock census however, showed negative annual population growth rate (<1%) which might be due to very high demand (slaughter rate is 64%) and rapidly depleting grazing resources and other factors yet to be analysed. Goat has huge potential to meet the food security requirements and play vital role in rural development because of its affiliation with resource-poor farmers. Goat farming has been extremely important means of family farming in particular, landless, marginal and small farmers and income generation. It has proven record of eradicating hunger, and poverty, providing food and improving livelihood in sustainable manner even in disadvantageous regions. Presently, goats have become driving force of livelihood and employment security of rural households and also possess huge exportpotential. It contributes 8.4% of the total value of output from livestockin Indian economy through meat, milk, skin and manuresand generate about 4.2% of total of rural employment.Goat possesses an important mechanism for coping up extreme climates because of better adaptability compared to crops and large ruminants. Because of low input farming system,productivity of these goats are lower than their actual genetic potential. Lower productivity can also be attributed topoor adoption of management practices &technologies (breeding, feeding, health care, market andinadequatefarmers participatory genetic improvement programmes) and depletion of grazing resources.More than 24 indigenousbreeds have been developed in different regions to cater the multi-facet needs of people in different regions of the country. The caprine diversity presently available in the form of different breeds/strains is the outcome to thousand years of deliberate selection and breeding efforts made by our ancestor to address the variable need of human being of different agro-climatic regions.This diversified germ-plasm is critical to meet-out future challenges and to sustain most of agro-ecosystem and production system. The potential future value of a trait in a breed could not be determined and if the available genetic resource, breed or strain is lost then that could not be retrieved and revived. Moreover, the genetic diversity and variability in the form of different breeds is necessary for system resilience and enhancing productivity in variable production environments. Since, food is essential component of livelihood security therefore,conservation of animal genetic resources (sustainable utilization and improvement) is critical for sustenance of livelihood of people.

Goat Genetic Resources of India

India is rich source in goat genetic resources as 24 breeds with great diversity are available. These genetic resources possess potential for production of meat, milk, fiber, delicate skinsand climatic resilience. All the 24 Indian goat breeds are great performer in their habitat under adequate feeding and bear great degree of resistance for disease and climatic fluctuations. Some of the breeds show overlapping characteristics which might be due to intermixing among the breeds in a region (s) where two or more breeds exist.Indigenous goat breeds, however, low in production potential because (a) these breeds were subjected to selection in the past for adaptability to the climatic stress and tropical diseases, rather than improving the genetic production potentials for production (b) poor expression of their production potential due to in-adequate feed, fodder, housing, health measures and harsh climatic conditions (c) lack of long term structured fieldgenetic improvement programmes.

The goat breeds on the basis of broad agro-climatic regions are described as

1. **Northern Temperate Region**: Chegu, ChangthangiGaddiandPantja are the important breeds of the region. Chegu and Changthangiare distributed in northern upper Himalaya region (Laddakh and Kashmir) above 3500 MSL, are medium in size and produce finest quality of under coat hair called 'Cashmere' or 'Pashmina' beside

quality meat. Prolificacy, milk yield and body growthrate however is low. Gaddi is habitat of medium Himalaya region (Jammu, Himachal and Uttrakhand)medium in size, produce coarse fibre beside chevon. Pantja is recently developed goat breed developed found in lower regions and foothills of Uttrakhand. It is a is a medium size breed with good prolificacy.

2. **North-WesternRegion:**This region has maximum caprine biodiversity with 11 breeds i.e. Beetal, Jamunapari, Barbari, Sirohi, Marwari, Jakhrana, Surti, Gohilwadi, Kutchi, Zalawadi, Mehsana. These goats are medium to large in body size, dual purpose with special attribute of higher milk yield (150-350 liter/lactation). Body weight at 12 month (20-40 kg), Prolificacy (liter size1.3 to 1.7) and kidding rate (1.3 to 1.6) of breeds of this region is also moderate to high. Many breeds (Beetal, Jamunapari, Sirohi, Zakhrana, Barbari etc.) are candidate breed for grading up of non-descript goat of arid and semi-arid regions of India.

3. **SouthernRegion:** Goats in the Southern and Peninsular part of the country, though of dual utility but low in milk yield as compared to goats of North-Western region and possess better traits for meat breed. Sangamneri, Osmanabadi, Kanna-aidu, Malabari, KonkanKanyal, Berari and Black Attapady are the main goat breeds of the region. These goats possess good ability for prolificacy (40-80%)

4. **Eastern Region:** Bengal or Black Bengal is main breed of eastern region of India. It is a dwarf size meat goat breed and has great recognition for prolificacy (>80% females produces multiple birth), skin and carcass qualities however, low in milk yield. Body weight at 12 month varies from 10-34 kg thus bear great scope of improvement through selection. Ganjam is another localized medium breed of this region. These goats have great value for climatic resistance, rear on low quality community grazing resources thus low in milk, growth rate and prolificacy.

Goat breeds according their major function are classified as:

Milk:1. Beetal, 2.Jamunapari, 3. Jakharana4. Surti

Meat: 1.Barbari 2.BlackBengal 3.Gaddi 4.Ganjan 5.Gohiwadi 6.Kannai Adu 7.Kutchi 8.Malabari 9.Marwari 10.Mehsana 11.Osmanabadi 12.Sirohi 13.Sangamneri 14.Zalawadi 15.Black Attapady 16.KonkanKanyal17. Pantja 18. Assam Hill

Fiber: 1.Changthangi2.Chegu3.Gadddi

Lesser Known Goat Genetic Resources

Several goat strains/genetic groups have been developed by the goat keepers in different regions. These breeds/strains are developed by crossing goats of two or more breeds or up grading local goats. Bundelkhandi and Rohilkhndi are found in large area and probably developed by crossing local goats with Beetal or Jakhrana far ago and subsequently inter-se mating. Whereas, Battisi (Maiwati), Totapari, Sojat, Karoli, Nagfani etc. are found in localized area and developed by goat keepers initially through cross-breeding and sub sequentially inter-se or selective breeding focusing certain morphological, adaptability and production characteristics, particularlyexploringEid market and major attention is given for coat colours, body height and growth rate. Goat developed in Assam Hill in upper Assam region and Shingery in Sikkim are such modified strains of Bengal. Nostrils of goats of these strains are relatively broad with long hair on coat, liter size is relatively low as compared to Bengal goat and white coat is predominate colour in these goats. Some strains have also developed in Orissa crossing local goats or Ganjam with Bengal such as Malkangiri, Badavihana, Dalua and Narayanpatna.

Threatened Goats breeds

A breed classified as endangered is dependent upon number of factors i.e. the actual number of animals, the rate of decline in the population size, the closeness of relationship between individuals within the population, the geographical range and the rate of reduction of that range, special threats from introduced species, rapid changes in the environmental conditions, predators and parasites (Hensen, 1992). Generally the range of numbers used to determine the point at which a population is in need of conservation. It varies from European estimates in the hundredsto FAO estimates in thousands (Hodges, 1990). It is because Europeanestimate are based on the minimum number of animals needed to maintain viablepopulation where as FAO estimates are based on minimum numbers needed tomaintain a population or breed in which future selection and improvement can becarried out. For goats, a breed will be included if there are less than 500 breedingfemales and four or less distinct male lines as defined. Breeds were listed if therewere less than 500 breeding females.Rich caprine diversity of India has been in danger and mainly attributed to indiscriminate cross-breeding on account of sale/castration of superior male, lack of clearly defined breeding policy and it's faulty implementation, poor adoption of improved management practices, degraded eco-system and lack of marketing infrastructure. Due to above said reasons not only population of many well-known goat breeds (Jamunapari, Beetal, Surti, Barbari, Changthangi, Sangamneri) but also their genetic variability, adaptability for climatic fluctuations and productivity etc. has been declining. Goat breeds mentioned are vulnerable to the extent that either the populations are declining numerically or their security is not secure, or the populations are of adequate size but security is depend upon special intervention programme.

The well recognized breeds of goats surprisingly facing a greater threat of endanger ness mainly due to improvement of goat increasingly emphasized the development of few breeds at the expense of others, changes in rearing objective i.e. during last 2-3 decades goat rearing for milk has been given low attention by goat keepers, sale of high potential goats without their replacement i.e. in many breeds such as Jamunapari, Jakhrana, Barbari the high producing goats (male and female) were purchased by traders for commercial farming in a region which was not suitable for that particular breed resulted in loss of introduced genotype and also created scarcity of improved animals for multiplication in their respective home-tract.Sale of superior male for slaughter left inferior and impure male to breed the female which has been resulting in negative genetic contribution in productivity, thus reduces profit and population size of a goat breed.Dilution of breeds has emerged a bigger threat pushing many important goat breeds in endangerment such as Barbari has been replacing by Sirohi.So, besides decline in population size purity level of many breeds has also jeopardize.

The international union for conservation of nature (IUCN) has classified the animals in to seven categories on the basis of their viability as (a) Extinct, (b) Endangered (c) Vulnerable (d) Rare (e) Intermediate (f) Insufficiently known and (g) Out of danger. Threatened goat breeds in India are falls under two categories i.e. endangered and vulnerable. A breed is considered as endangered, when the effective population size is too small to prevent genetic loss through inbreeding leading to infertility and lack of survivability resulting in ultimate loss of the population. According to FAO, a breed with a population size of 5000 breeding females or less can be an endangered breed. However, the need for conservation depends upon several factors e.g. (i) rate of decline in the population size, (ii) closeness of relationship between individuals within the population (iv) sex ratio (v) geographical range and its rate of reduction (vi) special threats from introduced breed/species (vii) rapid changes in the environmental conditions (viii) predators, parasites, disease etc. A breed is vulnerable, when the population is rapidly declining numerically or its security is under threat.

Constraints of Goats Genetic Improvement and Conservation:

Major constraint is the non-availability of pure-bred and quality breeding bucks. Goat keepers with small even with medium size flocks do not keep bucks due to fear ofincrease in rearing cost and difficulty in routine management. Absence of large flocks has compelled the goat keepers not only for breed dilution but also mating with low-potential buck. Scarcity of bucks with goat keepers not only is decreasing production potential but also reducing reproduction efficiency of goats. Mostly smallholders even with large flocks sell their potential male kids to butchers to meet domestic needs of their family ie either no replacement or replacement with inferior/impure male for breeding. Genetic variability might also declining of most of the breed particularly of threatened breed on account of high rate of inbreeding due to using a buck for long period of time (>3 years) in a flock and subsequently using male kids for breeding from own flock. Improper breeding practices such as breeding of females before attaining proper age and weight resulted in high rate of abortion, stillbirth, higher kids morbidity and mortality and lower life time productivity of goats. Scarcity of feeding/grazing resources i.e. supplementation of concentrate was not given even to high production goats, thus good genotype of goats (breed) do not fully expressed by them and blamed for poor production efficiency, and also biased the selection of genotype. Pre-requisite of a genetic improvement programme is pedigree and performance data recording which is not being practiced in field. Since genetic improvement programmes acted in additive/cumulative manner and take time to show their impact. However, there is a tendency to show quick improvement impact by development agencies. Statedevelopment/ Bank officials have perception that goats are detrimental to the environment thus do not allow goat keepers to take advantage of loan schemes. All these constraints all together have been leading to selection (improvement of goats) in negative direction, dilution and ultimately threat for a breed.

Approach and Mechanism of Conservation

If the breeds are disappearing in its natural habitat then action to conserve the breed should be taken immediately. The following information (estimate) is necessary in planning conservation strategy.

1. Descriptive information on breeds, production characteristicsand distribution/location.
2. Breed population dynamics.
3. Rate of breed dilution/introgression.
4. Health risk status, epidemics and endemic diseases.
6. Estimate the other risks and natural calamity.

The mechanism for the conservation is dependent upon rate of genetic loss and the increase in homozygosity. The increase in homozygosity within a small population causes the loss of ability to adapt, inbreeding depression and extinction.The maintenance of diversity in a population depends on founder population and effective population size. The population size, birth and survival rates, sex ratio and levels of variation must be taken into account before deciding the manner the breeds will be conserved. Two major approaches *Ex-situ* and *In-situ* have been used for conserving the goat population in India.

In situ: The maintaining animal in its natural habitat or in their adaptive environment as close as possible is called *in-situ* conservation.

Ex Situ: It is the storage of animal genetic resources, which farmers are not currently using in field condition. It includes cryogenic preservation and maintenance of breeds of domesticated animals in farms, zoos and other location away from its home tract. It is the preservation of semen, ova or embryos, DNA segments in frozen blood or other tissues. Both in-situ and Ex -situ methods are equally feasible for conserving Indian goats.

Strategy for Improvement and Conservation of Indian Goat Resources

The programme should be designed in such a manner so as to contribute both immediate production needs and long term improvement programmes in order to take up breed characterization evaluation and utilization. It is necessary that each State Govt. should establish an appropriate infrastructure at the State level with adequate specific allocation of funds for goat development. Central Institute for Research on Goats, Makhdoom, Mathuraand National Bureau of Animal Genetic Resources, Karnal may act as the nodal agency for goat improvement and conservation of Goat Genetic Resources,respectively. State Government to give adequate priority to conservation, Management and Development of goat genetic resources to provide food security and help in poverty alleviation of rural poor. The Scientists and Technicians may be trained in the area of management for breed conservation and improvement.

All Indigenous goat breeds including threatened breeds have an immense production potential and preferred in past for milk and meat purpose. Concerted efforts are necessary to characterize and evaluate under optimum production systemOpen nucleus flock can be established through selecting high productivity goats on the basis of objective assessment from the farmers flock and utilized for producing breeding male through intensive selection and distribution to the co-operating and other farmers. Keeping nucleus flock open would help in reducing in-breeding and increasing selection intensity. Some flocks (covering about one thousand population) of a may be registered to form a goat breeder co-operative with an elite open nucleus flock. The high producing goats of the cooperating herds should be pooled to form a nucleus flock, which will produce proven bucks for the genetic improvement of the cooperating flocks. High performing females (10-20% of strength) from cooperative/ registered goat keepers should be purchase toinclude in nucleus flock. Simultaneously capacity building of goat keepers be done for putting identification marks and recording data on performance traits, supplementation of concentrate ration, vaccination, deworming, following improved breeding practices.

Goats with good milk production such as Jamunapari, Beetal, Jakhrana and Surti etc. of North –Western region; Fibre producing goat of northen region such as Changthangi; Assam Hill and Shingery breeds of north-eastern region need immediate attention for their conservation. The best approach to conserve them is In-Situ through improving their productivity along with adaptability to prevailing climates by long-term structured genetic improvement programme with farmer's participation. Capacity building of goat keepers to increase adoption of improved management practices, support for vaccination and medication, strengthening of feed resources and marketing structures are equally essential activities. Development of local institution such as goat cooperatives, societies and SHG,s would be useful for bringing faster and effective improvement and conservation of threatened breeds. Moreover, nearly 80% goat population is non-descript, which are well adapted therefore such goats should be improved through grading up possibly though supplying of potential breeding bucks of threatened breeds such as Jamunapari, Beetal, Jakhrana, Barbariand Surti etc. in their respective home tracts. Funding and implementing agencies should not withdraw support half-way from programme, otherwise whole programme would become futile. Development authorities should understand that gains due to genetic improvement are permanent cumulative and will contributes hundreds of years. Goat improvement programme should be synergies with other component such as empowerment of goat keepers, development of common resources for fodder, and availability and delivery of vaccines and medicines etc.

Role of All India Coordinated Research Project on Goat Improvement and Conservation

AICRP on Goat Improvement is a long term, multi-disciplinary, structured programme operating in consortia mode to bringing upon genetic improvement and conservation of goat genetic resources of the country in their native tracts. The present approach for improvement being adopted is outcrossing (selective breeding) in their native tract. The major traits of goat improvement are body weight, milk yield, fibre yield, kidding percentage, fecundity, survivability, production life and profit. The programme explores genetic variations in local breeds by supporting technological interventions and financial assistance for systematic animal identification, pedigree and performance recording, preventive health care, selecting superior goats on the basis of performance for multiplication, development and transfer of technologies, capacity building of goat farmersand creating marketing infrastructure. Under 12thplan large weightage has been given through linkagedevelopment with state livestock development agencies, NGO's and Farmersfor breed based genetic improvement for sustainable livelihood and feed security of poor goat keepers. Improvement and conservation of goat resources/breeds of different regions is focused in farmers flock through establishing breed societies, cooperatives multiplier flocks, strengthening marketing structure and capacity building of goatfarmers.Presently, thirteen breeds and five locally adaptive and lesser known genetic groupsare covered through eighteen centers across the country. All the centers are solely concentrating in improvement of villagers goat flocks predominated in tribal and disadvantageous regions of the country. Al most all threatened breeds except Beetal and Jakhrana are included in AICRP and being improved under farmer's flock in their respective home tract.

Goat Improvement and ConservationProgrammes in India

S N	Name of the centers	Breed	Purpose	Starting date
	C.I.R.G., Makhdoom (U P)	Jamunapari	Milk &Meat	1993
	C.I.R.G., Makhdoom (U P)	Barbari	Meat & Milk	1993
	CSWRI, Avikanagar (Raj)	Sirohi	Meat & Milk	1993
	RAU, Bikaner (Raj)	Marwari	Meat	1993
	WBUV&FS, Kolkata	Black Bengal	Meat	1997
	OUA&T, Bhubaneshwar	Ganjam	Meat	1997
	MPKV, Rahuri (MH)	Sangamneri	Meat	1997
	G.A.U., Navsari (Gujarat.)	Surti	Milk & Meat	1997
	KV&ASU, Thrissur (Kerala)	Malabari	Meat & Milk	1997
	MPUA&T, Udaipur (Raj.)	Sirohi	Meat & Milk	1997
	NARI, Phalton (MH)	Osmanabadi	Meat	2009
	HPKVV, Palampur (HP)	Gaddi	Fiber & Meat	2009
	BAU Ranchi (JHK)	Black Bengal	Meat	2009
	AAU,Burnihat	Assam Hill	Meat	2009
	IVRI Campus, Mukteswar	Himalyan Goat	Meat	2014
	SKUAST-K Leh, J&K	Changthangi	Pashmina & Meat	2014
	GBPUA&T, Pantnagar	Pantja	Meat	2014
	CARI, Portblair	Andmani	Meat	2014

Impact of AICRP on Goat in Goat Improvement and Conservation

1. Pure-bred goat's identification of 1500-2000 goats of each breed in farm/farmers flock along with pedigree and performance over years and generations.
2. Estimated genetic and phenotypic component of variance and co-variance.
3. Established 4-6 multiplier flocks of each breed/genetic group.
4. About 10000 superior goats of different goatbreeds were supplied to farmers and development agencies for improvement and conservation.
5. Developed packages of breeding, health, feeding and housing management practices for all agro-climatic regions.
6. Developed low cost technologies for different region such as feed supplementation, feed devices, goat houses, silvi-pasture models and value added goat products from goat milk, meat, fiber, manure, etc.
7. There was significant improvement in body weight (19-43%), milk yield (12-32%), prolificacy (11-29%), kidding rate (15-40) and survivability (up to 200%) of different breeds at different locations over base population.
8. Significant increase has recorded in population of several threatened goat breeds such as Jamunapari, Barbari, Surti, sangamneri and Malabari.
9. Programme has created infrastructure and stored germplasm in the form of semen and ova.
10. The income of goat keepers at different locations in the country was increased up to 300% annually through scientific goat rearing under AICRP.
11. Programme has improved capacity and skill of more than 5000 people in the area of livestock farming.

12. More than 10,000 goat farmers and officials of 12 SAU's & state livestock improvement agencies have been actively associated with this programme.

Breeding Policy and Road map for Goat Improvement and Conservation

1. Selective breeding and grading up are major breeding approach and may be implemented through nucleus ***schemes.*** Up gradation of huge non-descript goat population by improver breed should be seriously implemented.There should be clearly described breeding policy for each breed in every states/regions/ farming system.
2. Evaluation of goat genetic resources with respect to production environment, production attributes, genetic architecture and for end use suitability and, establishment of Inventory of important breed.
3. Formation of goat breeder's cooperative/ societies/SHGs and such groups should be financially and technically supported.
4. Establishment of nucleus farm, kids nursery farm, buck mother farms of initially of threatened breed and subsequently for other breeds to ensure regular availability of elite buck to farmers.
5. Establishment of more number of multiplier flocks of each breed and proper recording of data for ONBS based genetic improvement.
6. Up-gradation of non-descript goat population of that particular region through distribution of elite breeding bucks of threatened breed.
7. Ban on indiscriminate slaughter of elite males of threatened goat breeds.
8. Promoting strategic feeding practices i.e. semi-intensive and intensive goat rearing.
9. Improvement of community pastures, grazing land and water bodies.
10. Promote adoption of prophylactic goat health calendar with ensuring availability of vaccines and essential medicines.
11. Linking goat farmers to supply chain
12. Simplified process of credit facilities to goat keepers to expand their flocks.
13. Promote formation of Goat co-operatives, goat self-help groups, Goat producer groups' companies and markets and their vertical integration.
14. Capacity building of farmers for technology adoption (breeding practices, vaccination, deworming, strategic feeding, goat housing) and for smart marketing etc.

CONCLUSION

Indigenous goat breeds have immense production potential in given climate provided they get congenial environment. Their optimum potential has not expressed due to subsistence production systems and low inputs. While framing breeding strategy for goat improvement traits of local importance (adaptability to climate, disease resistance and irregular and scarce feeds availability etc.) should not be ignored. Improvement objectives of a breed(s) in different region should be well defined along with breed basedimproved package of practices. Management interventions for different farming systems (integrated/specialized/mixed/low or high input) in different regions should be popularized among stakeholders. Critical inputs for goat farming such as bucks, vaccine, medicine, credit etc. should be essentially made available with easy access particularly in the home tractsthreatened goat breeds. Formation of goat breeder's cooperative/ societies/Buck Mother Farm/Multiplier Flocks should be encouraged. Up gradation of non-descript goats should beimplemented in big way.At least 2000 goats of all threatened breeds should be properly tagged and be made part of in-situ conservation programme. Sell of high potential males for slaughter should be minimized by making farmersaware. For effective goat germ-plasm conservation thrust should be given to low cost management interventions, capacity building of goat keepers and participatory field improvement programmes. Organizational initialization and support are essential for sustainable conservation and improvement of local goat breeds in their habitat. More number of breeds with large number of goat keepers representative of entire home-tract of a breed may be included in AICRP on Goat improvement in collaboration of state livestock development agencies. Facilitation access of appropriate goat production technologies, Integrated Farming System Models, technical assistance, credit, linkage of farmers with market through SHGs &Goat producer organizationsand restoration of grazing resources are the key component of holistic goat and poor goat keepers livelihood improvement.

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6. INDIAN RIVERINE BUFFALOES TRANSFORM THE WORLD BUFFALO GENETIC RESOURCES

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Introduction

The **water buffalo** (*Bubalus bubalis)* is found in the Indian subcontinent to Vietnam and Peninsular Malaysia, Sri Lanka and Philippines. The wild water buffalo (*Bubalus arnee*) native to Southeast Asia is considered a different species but most likely represents the ancestor of the domestic water buffalo. Two types of water buffalo are recognized based on morphological and behavioral criteria:

(i). R**iver buffalo** of South Asia and further west to the Balkans, Egypt and Italy.

(ii). Swamp buffalo, found from Assam in the west through Southeast Asia to the Yangtze valley of China in the east.

The original domesticated buffaloes are believed to have been derived from the Indian wild buffalo (*Bubalus arnee).* Riverine and Swamp buffaloes were domesticated almost together (around 2000BC), former in the Indus Valley Civilization and the latter in the Yangtze Valley. Domestic buffalo reached South-East Europe by 12th century; later taken to the Americas and Australia, and Africa in the 20th century. Riverine breed development has largely centered in Indo-Pak subcontinent. Water buffalo (Bubalus bubalis) includes two sub-species known as the riverine and swamp types, which differ in chromosome numbers and morphology. The riverine buffalo has 50 chromosomes while swamp buffalo has only 48 chromosomes due to tandem fusion translocation between riverine buffalo chromosome 4 and 9. However, the two subspecies are inter-fertile and produce progeny with 49 chromosomes. The morphology of two types differs considerably. Swamp buffaloes are small in size and have body weight 300 to 450 kg, while, the riverine buffaloes are generally larger in size (400 to 800 kg). Riverine buffaloes prefer to enter in clean water and are primarily used for milk production, while, swamp buffaloes prefer marshy land habitats and are primarily used for draught and meat production. Satish Kumar et. al. (2007) also studied the phylogeographic and domestication of India river buffalo and reported that the present day river buffalo is the results of complex domestication processes including more than one maternal lineage and a significant maternal gene flow from the wild populations after the initial domestication events. The phylogeographic and domestication study also concluded that the riverine buffalo was likely to be domesticated in western region of India sub-continent, specially the present day breeding tract of the Mehsana, Surti and Pandharpuri breeds.

Population

The buffalo population trend is increasing in the world and according FAO data (FAOSTAT, 2010), the world buffalo population is about 182 million with a positive trend of 8.3% increased in comparison with the 168 million population in 2005. In Asia, according FAO data (FAOSTAT, 2010) there are 174 million buffaloes (95% of total population), with a positive trend (+ 8.1%) as 5 years before the Asian population was161 million (Borghese, 2005). This positive trend is due to the increasing population in India and Pakistan, where milk purpose breeds were selected and buffalo milk market is very strong. In Africa, where the buffalo is found only in Egypt, there are 5.23 million buffaloes (FAOSTAT, 2010),while before six years the Egyptian buffalo population was 3.71 million (Borghese, 2004), with an incredible positive trend of 40.7%. In Europe, the most of population is in Italy with about 400,000 buffaloes, while the European buffalo population is 459,000 (0.25% of world population), less than the buffalo population seven years ago (500,000; 0.30%), Borghese, 2005. The decreasing trend in many Balkan countries as Romania, Bulgaria, Macedonia, Greece, Albania, Serbia, partially balanced by the increasing trend in Italy, link to the expansion of mozzarella market. In America, recent buffalo population reported about 4,227,000 buffalo head, 2.32% of total population, while 11 years ago there were only 3,345,000 buffalo population, with a positive trend (+26.4%) due to the changing from a meat purpose breeding to a dual purpose (milk and meat) livestock.

Buffalo Genetic Resources

In India: India has, in its length and breath, a number of climatic zones with varied natural resources, climatic conditions and differing socio-economic cultural systems. Several of such stable systems have resulted in unique local and genetically stable buffalo breeds and populations that make significant contribution in the local milieu. Indian riverine buffaloes are represented by thirteen well recognized breeds viz. Murrah, Nili Ravi, Bhadawari, Mehsana, Surti, Jaffarabadi, Nagpuri, Pandharpuri, Marathwada, Toda, Banni, Chilika and Kalahandi. The genetic diversity ranges from high yielding dairy type (Murrah, Nili-Ravi, Banni, Mehsana etc) to extensively managed semi-wild Toda. The NBAGR-Karnal and ICAR-New Delhi has registered all the above thirteen buffalo breeds and their accession numbers have been issued. The details of State / Breeding tract, utility and accession numbers are given in Table-1. The population status of all the registered breeds is stable except Bhadawari, Toda and Nili-Ravi.

Table 1: Home tract, accession numbers and utility of 13 registered buffalo breeds.

Sr. No	Breeds	Accession No.	State / Breeding tract	Utility
1	Murrah	INDIA_BUFFALO_0500_MURRAH_01001	Haryana, Delhi & Western UP	Milk
2	Nili Ravi	INDIA_BUFFALO_1600_NILIRAVI_01002	Punjab	Milk & Meat
3	Bhadawari	INDIA_BUFFALO_2010_BHADAWARI_01003	UP & M P	Milk & Fat
4	Mehsana	INDIA_BUFFALO_0400_MEHSANA_01004	Gujarat	Milk
5	Surti	INDIA_BUFFALO_0400_SURTI_01005	Gujarat	Fertility
6	Jaffarabadi	INDIA_BUFFALO_0400_JAFFARABADI_01006	Gujarat	Milk & Meat
7	Nagpuri	INDIA_BUFFALO_1100_NAGPURI_01007	Mahrashtra	Milk
8		INDIA_BUFFALO_1100_PANDHARPURI_01008	Mahrashtra	Milk
9		INDIA_BUFFALO_1100_MARATHWADI_01009	Mahrashtra	Milk
10	Toda	INDIA_BUFFALO_0018_TODA_01010	Tamilnadu	Draught & Milk
11	Banni	INDIA_BUFFALO_0400_BANNI_01011	Gujarat	Milk
12	Chilika	INDIA_BUFFALO_1500_CHILIKA_01012	Orissa	Milk & draught
13	Kalahandi	INDIA_BUFFALO_1500_KALAHANDI_01013	Orissa	---

World Buffalo Breeds Originated from Indian Buffaloes

Murrah buffaloes exported to many countries for improvement of local buffalo populations. Murrah buffaloes are reported to be in China, Ecuador, Guatemala, Indonesia, Malaysia,, Nepal, Philippines, South Africa, Sri Lanka, Azerbaijan, Brazil and Bulgaria (DAD-IS, 2010). In Malaysia, Murrah buffaloes were introduced from India in the early 1900, in China 1957 and used for crossbreeding with local buffalo population. In Bulgaria, Murrah buffalo bulls were first crossed with Bulgarian buffaloes in 1962. The Philippines had a long history of importing Murrah buffaloes and the first time imported in 1918, in 2001 frozen Murrah embryos were imported and last infusion of 2000 Murrah buffalo from Brazil in 2010. Indian Riverine buffaloes exported to different countries for improvement of local populations age given in Table 2.

In Bulgaria the only breed is Bulgarian Murrah, coming from crossbreeding of Indian Murrah on local Mediterranean breed. From Bulgaria, buffaloes were exported in other countries as Romania and Germany and in far countries as Brazil and Venezuela. Murrah buffaloes were exported in Sumatra to increase the availability of milk, as the local breeds are Swamp with low production; the same for many Asian countries where the original population is Swamp type. Murrah buffaloes were exported from India to Brazil for meat purposes. Jaffarabadi breed was chosen by many American countries and selected as meat purpose breed. Now it is possible to find

Murrah and Jaffarabadi pure or crosses in Brazil, Colombia and in other South America countries, where these breeds shown a great adaptability to marsh lands, to different crops and pastures and a high meat production animal. Jaffarabadi was the basis for the creation of Buffalypso breed in Trinidad-Tobago and Cuba.

Riverine Buffalo have been introduced into many countries in the world. The importations have primarily been from India, Italy, Bulgaria, Indo-china and Australia. The first introductions are believed to have been made in 1890, but subsequent importations have mostly been of the breeds from the Indian subcontinent. Initially they were introduced for work and later for meat. They were primarily managed on ranches on extensive system, but presently milk production is in high focus, and the dairy type breeds are stall-fed and kept under intensive management. The breeds of Indian origin are maintained as pure breeds, but they have also been interbred leading to new breeds like Brazil Mediterraneo, Brazil Murrah and Bulgarian Murrah. The buffalo breeds developed in the world with the introduction of Indian buffaloes are given in brief as below:

Bulgarian Murrah: Bulgarian Murrah breed, created on the basis of crossing among the native Bulgarian buffalo and the Murrah breed from India. The new breed was officially recognized in January 2002. From 1962 to 1990, Murrah buffaloes from India were imported into Bulgaria and a new population of buffalo "**Bulgarian Murrah" (**Local Bulgarian Buffalo -25% X Indian Murrah -75%)was created by upgrading the local buffalo.

Egyptian Buffalo: Buffaloes were introduced into Egypt from India, Iran and Iraq approximately during the middle of the 7th Century. It is the most important and popular livestock for milk production in Egypt.

Mediterranean or European Buffalo: The Mediterranean buffalo originates from the Indian buffalo. It was introduced into Europe with the advent of Islam and the Arab occupation in the 8th century in Sicily and in the south of Italy, while in the east Europe, buffalo was introduced later with crusaders in the 12th century and after with Turkish invasion during the Ottoman empire (15th century). The Mediterranean buffalo is present in many countries of South America as particularly Brazil, Argentina, Venezuela and Colombia, where it was introduced to increase the milk and meat capacity. In these countries and in many Asian countries (Turkey, Iran, Azerbaijan, China, Bangladesh, Indonesia), Mediterranean Italian semen was largely used to create F1 crossbreds with higher milk potential. Therefore we can find many million head coming from crossbreeding with Murrah and Mediterranean in the world, from America to Asia. In Bulgaria, Romania, Macedonia, Greece and Albania.

Brazilin Buffalo: In Brazil most of the buffaloes are progeny of the stock imported from Indo-china in 1890; of Murrah, Jaffarabadi, Nagpuri, Surti, Nili-Ravi from Indian subcontinent during 1907-1962; and of Italian buffaloes from Italy. Most of these are used for milk and meat, while carabo's are used for work and meat. These breeds have undergone a period of mixing. At the present time, they are classified as (i) Brazil Murrah derived from imports of Murrah breed of India; (ii) Jaffarabadi derived from Jaffarabadi stock of India and bred pure; and (iii) Mediterrano derived from imported Italian buffaloes and some Murrah admixture currently bred within the stock as purebred. These three breeds are for milk and its products, and for meat production.

Anatolian Buffalo: The Anatolian buffalo has been raised in Turkey for centuries, originating from Indian migration (7th Century), together with the expansion of Islam.

Azeri or Caucasian Buffalo: This breed originates from the Indo valley (Indian buffalo). There is some evidence that buffalo were raised in Lorestan (Iran) in the 9th Century B.C.

Romanian Buffalo: The Romanian buffalo breed originates from the Mediterranean type of water buffalo. Introgression has been made since 1960 from Murrah buffalo stock from Bulgaria.

Buffalypso: Buffalypso is the typical buffalo of Trinidad and Tobago. River type milk buffaloes were imported into Trinidad from India at the beginning of the last century. The first importation of 30 Jaffarabadi to a sugarcane farm occurred on 1905. Afterwards other breeds have been imported from India, such as Murrah, Nili-Ravi, Surti, Nagpuri, Bhadawari, and Swamp Carabao were imported from Australia. Steve Bennet started on 1948 in the

Caroni State farm to cross Bhadawari and Murrah on Jafarabadi and after with other breeds to create a triple purpose breed, meat, milk and draught for working in sugarcane farms, named Buffalypso (Buffalo x Calypso that is Caribesong). Buffalypso is historically the only breed selected exclusively for meat, very muscular animal.

Performance of Buffalo Crosses

(A). Murrah cross with River buffaloes

Bulgarian Murrah: The performance of Bulgarian Murrah and crosses with Murrah buffaloes are given in table 3. The results indicate significant improvement in performance traits of crossbreds and Bulgarian Murrah buffaloes.

Romanian buffalo: Main uses are milk, meat and draught power. Milk yield varies according to season of calving, lactations number, level of feeding, and length of lactation. Lactation milk yield (kg) is between 958-1455 kg. The number of days lactation per year is 252-285; age at first calving is 38-42 months; average lactations number is 6-9; age at slaughter for young stock is 22-24 and 350-400 kg or at 3-4 months and 60-100 kg for males and the females are slaughtered at 500-600 kg, usually after the first lactation or after the productive life. In 2003 the female that was included in herd book had 1831 kg milk, with 136 kg fat (7.48%) and 71 kg (3.93%) protein. Age at first calving was 38 month and 6 days and calving interval of these female was 456 days. The average of calves/year is 0.85.

Buffalypso: Buffalypso is historically the only breed selected exclusively for meat, very muscular animal. The slaughter weight is about 400 kg with dressing percentage of 52.43%, until 450 kg with a dressing percentage of 50.88%; the meat quality is better than correspondent local steer (Rastogi and Rastogi). The milk yield is 611 kg in 192 days of lactation, with 7.15% fat and 4.03 protein (Rastogi and Rastogi). From 1996 the milk production from Buffalipso started too in Cuba, because of the need of milk for human food, obtaining an average 873 kg milk for lactation of 244 days

Average slaughter weight is 250-400 kg, at the age of 12-15 months.

Dairy performance: Lactation duration270 days, Milk yield 900-4000 kg, Milk fat 8.0 percent, Milk protein 4.2-4.6 percent (Mitat, 2011).

(B). CROSSBREEDING RIVER AND SWAMP BUFFALOES

Crossbreeding has been practiced in almost all countries where swamp buffalo predominates i.e. China, Burma, Thailand, Philippines, Malaysia and Sri Lanka with the objective for improving milk yield capacity. China started crossbreeding work in the late 1950, imported Murrah buffalo from India and the Nili-Ravi buffalo from Pakistan in the late 1970. The crossbreds in China had good conformation, a massive body structure with well developed hindquarters and significant improvement in milk yield. The performance traits of swamp, Murrah and their crosses are given in Table 4. The success of crossbreeding between swamp with Murrah buffalo in China, lead the transformation of Swamp buffalo population and the research on crossbreeding of swamp buffaloes with the riverine breeds, specially the Murrah, has been conducted in different countries, e. g. Philippines, Malaysia, Vietnam, and Thailand. Reports on crossbred performance in various countries reported by various workers (Eusebio, 1975), Liu, 1975, Jalatge, 1980 and Keshary and Shrestha, 1980) are given in Table No 4 to 8.

In Philippines the milk production of Phil-Murrah F1 and Phil-Ravi F1 was reported an increase of 32 percent in birth weight, an increase by 100 percent in weight at 18 months (average 300 kg) and a 3 to 4-fold increase in milk yield (1200 1 in 300 days) than the native carabao. These reports revealed genetic potentials of crossbreeding to improve the swamp buffalo for milk and meat.

Table 2: Indian Riverine buffaloes exported to different countries for improvement of local populations.

Sr. No.	Country	Breed Imported	Year of Introduction
1	Brazil	Murrah	1890 /1895
		Jaffrabadi	1907
2	Trinidad	Murrah	1900
		Jaffrabadi	1924
		Nagpuri	1938
		Surti	1949
		Bhadawari	---
		Nili-Ravi	---
3	Argentina	Murrah	1980
		Jaffrabadi	1983
4	China	Murrah	1957
5	Philippines	Murrah	1918
		Frozen semen	1980
6	Vietnam	Murrah	1970
7	Bulgaria	Murrah	1962, 1972
8	South America	Murrah	1895
		Jaffrabadi	1895
9	Australia	Water Buffalo	1824, 1849, 1886
10	Malaysia	Murrah Buffalo	20th century
11	Sumatra	Murrah	1850
12	Nepal	Murrah	1967 and 1971
13	Egypt	---	7th Century
14	Iran	---	7th Century
15	Iraq	---	7th Century
16	Europe	---	8th and 12th Century
17	Turkey	---	7th Century
18	Sri Lanka	Murrah	1939, 1941 to 1991.

Table 3. Performance of Murrah, Bulgarian and Bulgarian Murrah crosses

Breed / Crosses	Traits			
	300-d milk yield (kg)	Fat %	L L (days)	Fat yield (kg)
Murrah (M)	1823	7.95	306	145.2
Bulgarian)B)	1198	7.59	296	091.4
F1 M X B	1492	7.64	288	113.9
Bulgarian Murrah	1845	7.40	274	135.6

(B). Murrah cross with swamp buffaloes

Table 4. Performance of Swamp buffaloes and its crosses in China

Crosses	No. of Records	Milk Production Traits				
		LL (days)	LMY (kg)	ADMY (kg)	SLMY (kg)	APY (kg)
Swamp (S)	70	280.4 ± 20.2	1092.8 ± 207.4	3.79	----	6.60
Murrah (M)	237	324.7 ± 73.6	2132.9 ± 578.3	6.57	2117.1 ± 430.0	17.40
F1 MXS	241	280.1 ± 76.1	1233.3 ± 529.7	4.40	---	16.50
F2MXS	54	303.2 ± 83.1	1585.5 ± 620.6	5.22	---	13.00
NXMXS	168	317.6 ± 78.4	2294.6 ± 772.1	7.22	2348.0 ± 533.2	18.80

Table 5: Performance of Philippines Carabao, Murrah and their crosses in Philippines

Breed / Crosses	Traits	
	LMY (kg)	L L (days)
Phil Carabao	259.40 (21)	200.81 (21)
Murrah	1804.40 (21)	348.48 (21)
F1 Murrah X Phil	705.60 (29)	259.45 (29)
F1 Ravi X Phil.	623.10 (12)	233.67 (12)

Table 6: Performance of Murrah buffaloes and its crosses in Taiwan

Traits	Genetic Groups		
	Murrah	F1 Cross	G1 Backcross to Murrah
Birth weight (kg)	33	32	32
Total milk yield (kg)	1518	824	1015
Lactation Period (days)	240	240	240
Daily milk yield (kg)	6.3	3.4	4.2
Peak Yield (kg)	8.0	4.6	6.0

Table 7. Performance of Swamp, Murrah and its crosses in Vietnam

Traits	Genetic Groups		
	Swamp	Murrah	F1 Crossbred
Milk yield (kg/day)	1.50	5.55	3.50
Lactation Period (days)	210	236	292

Table 8. Performance traits of buffaloes across breed in Nepal

Traits	Breeds		
	Hill Buffalo	Murrah Crossbreds (50%)	Murrah Crossbreeds (75%)
305 DLMY (lit)	874.7±30.7(234)	1222.7±41.8(93)	1560.3±51.3(61)
Fat contents (%)	7.0± 0.2 (234)	7.0± 0.2 (90)	6.7± 0.3 (61)
L L (daya)	351.3± 9.8 (223)	354.9±14.4 (88)	379.9±17.6 (57)
AFC (months)	52.9± 0.8 (215)	56.6± 1.2 (86)	55.5± 1.6 (53)
Calving to 1st service (days)	197.8±14.0 (202)	189.1±20.8 (76)	201.9± 3.0 (45)
Calving interval (days)	495.9±16.4 (188)	446.4±25.4 (63)	500.6±29.7 (47)

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ABSTRACTS

TS-II-01

MARKER ASSISTED SELECTION CAN MINIMIZE THE RISK OF MASTITIS DEVELOPMENT IN DAIRY CATTLE

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Mastitis is the most common inflammatory disease of dairy cattle characterized by physical and chemical changes in the milk and pathological changes in the mammary gland. Mastitis is the most costly disease of lactating animals affecting animal health and welfare, and is important due to its public health concerns. Somatic cell count (SCC) is a useful indicator of udder health and has highly positive genetic correlation (r_g=0.84) with clinical mastitis. Numerous therapeutic, prophylactic and management strategies are being used as control measures for bovine mastitis; however, a widely proposed strategy is based on improving the host genetics through marker assisted selection. Lymphocyte-activation gene-3 (*LAG-3*) is located on bovine chromosome 5 and plays crucial role in inflammatory condition. The genetic effects of single nucleotide polymorphisms (SNPs) in *LAG-3* gene were investigated on some serum cytokines and mastitis indicator traits in a population of 268 Chinese Holstein cattle. Pooled DNA sequencing revealed three novel SNPs including one (SNP 1) in exon 4 and two (SNP 2 and SNP 3) in 3′ flanking region of *LAG-3*. Fixed effect model considering the effects of SNPs, parity, herd, season and year of calving was used by general linear model (GLM) procedure of SAS 9.1. Genotypic frequencies of these SNPs in the population were in Hardy–Weinberg Equilibrium (HWE) (P>0.05). SNP in exon 4 was missense that was predicted to cause amino acid substitution from threonine to proline. The results of association study showed that SNP2 was significantly associated with SCC, whereas SNP3 was significantly associated with SCC, SCS and IL-10 (P<0.05). The combination of SNP2 and SNP3 showed significant effect on SCC and SCS (P<0.05). As for mRNA expression analysis, the homozygous wild type genotype in SNP3 showed higher expression level and were significantly different from the heterozygous genotype (P<0.05). The results imply that *LAG-3* gene can be considered as useful candidate gene, and the identified polymorphisms could be potentially strong genetic markers to select dairy cattle for genetic resistance against mastitis. Thus improving the host genetics eventually can minimize the public health hazards associated with mastitis.

TS-II-02

UNVEILING HIDDEN TREASURES IN ZAMBIAN INDIGENOUS CATTLE USING MICROSATELLITES

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Selection has created a range of diverse breeds, important for breeding and conservation programs. Yet, during the recent past, there have been concerns to losing this unique genetic diversity. Studies have been conducted to evaluate genetic diversity in cattle, but this has not been undertaken in Zambia. The aim of this work was to evaluate genetic diversity, population structure and degree of admixture in Zambian indigenous cattle, to provide information for genetic improvement strategies and conservation programs for local well-adapted cattle. Therefore,

genetic information from 32 microsatellite DNA markers in 72 Zambian indigenous cattle of three *Bos indicus* breeds (Angoni, Tonga and Barotse) were used to assess genetic diversity and population structure. Blood samples were collected from Zambia and DNA extraction and analysis was conducted in Australia, University of Adelaide. A total of 274 alleles (N_a) were detected and only 74 alleles were unique. The results demonstrated that Angoni and Barotse breeds exhibited a slightly excess average observed heterozygosity (1.0% and 0.9%) respectively, while Tonga breed exhibited a slight deficit observed heterozygosity of 3.6%. The global heterozygosity deficit across all populations (F_{IT}) was 4.2%, significantly different from zero ($p<0.001$), because of observed inbreeding within breeds (F_{IS}) was 1.0%). Breeds showed only slight genetic differentiation (F_{ST}) of 3.2%, but still significantly different from zero ($p<0.001$). High gene flow (11.3%) was evident between populations. Although, Zambian indigenous cattle breeds did not exhibit a high and unique breed's purity, cattle exhibited a higher level of genetic diversity within breeds than between breeds, despite evidence of a close gene flow between the three populations. Inbreeding was largely insignificant going by Bayesian cluster at K=2 and this may be an evidence of existing divergent and multi-loci genetic admixtures between and within breeds. If accurate, the uniqueness of the population clustering offers valuable information on the gene pool available for selection within breeds for genetic improvement and conservation in Zambia.

TS-II-03

GENETIC CHARACTERIZATION OF BELAHI (*BOS INDICUS*) CATTLE FROM NORTH INDIA

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Genetic characterization of local population and breeds is important as it allows the evaluation of genetic variability, a basic component for working out conservation and genetic improvement programs with optimal utilization of available genetic variability present in a breed. Microsatellite markers are best suited to characterize the genetic variability, within and between populations, because of their high variability, distribution throughout the genome, co-dominant inheritance and neutrality to selection. Microsatellites have been effectively exploited to evaluate genetic diversity. The aim of the present study was to assess the genetic variation in Belahi cattle and to establish the relationship amongst the indigenous cattle breeds of North India using bovine-specific microsatellite markers. Within-breed diversity indices were estimated in Belahi cattle and between-breed diversity was compared with Sahiwal, Gir, Tharparkar, Rathi, Nagori, Mewati and Kankrej breeds of cattle. The 16 microsatellite loci were found to be polymorphic with five or more than five alleles per locus in Belahi cattle. The estimated mean allelic diversity in Belahi cattle was 9.31, with a total of 149 alleles and polymorphism information content (PIC) varied from 0.31 (TGLA227) to 0.87 (CSSM33) with an average PIC of 0.71. On an average deficiency of 3.37% of heterozygotes existed in Belahi cattle. However, Belahi cattle revealed presence of genetic diversity within population, and the population was deviating from mutation drift equilibrium with no significant heterozygosity excess indicating the absence of genetic bottle neck in the recent past. The global F_{ST} estimates demonstrated that approximately 85% of the total genetic variation was contributed by within-breed genetic differentiation, while only 15% genetic variation was present across different breeds. In the UPGMA-based phylogenetic tree constructed from the Nei's genetic distances, Sahiwal and Belahi cattle were grouped together in one cluster and were found to be closely related breeds, thus indicating the milk potential of this lesser known cattle genetic resource from North India

TS-II-04

SISTER CHROMATID EXCHANGE IN CATTLE AFFECTED WITH ARSENIC

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In present study cytogenetic study was conducted on 21 arsenic affected cattle from Nadia district of West Bengal which is considered to be heavily arsenic infected zone and six normal ones to know the effect of arsenic on frequencies of Sister Chromatid Exchange (SCE) along with the number and morphology of metaphase chromosomes. The result showed that the frequency of SCE in arsenic affected cattle is significantly ($p \leq 0.005$) higher than the normal cattle. The mean SCE frequencies in normal and arsenic affected cattle were found to be 3.367 and 6.245 respectively. Chromosomal evaluation of selected animals by SCE staining revealed normal karyotype ($2n = 60$, XX) without any chromosomal gaps, breaks and fragments in both normal as well as in arsenic affected cattle. Morphological study showed that from the centromeric position all the 29 pair of autosomes was found to be acrocentric or telocentric and the sex chromosomes (XX) were sub-metacentric in both normal and arsenic affected cattle.

TS-II-05

A1 AND A2 MILK: IMPORTANCE OF CONSERVATION OF NATIVE BREEDS

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A1 and A2 are the two types of cow milk available for consumption. On consumption of A1 milk, people are exposed to the risk factor for Type 1 diabetes mellitus, coronary heart disease, arteriosclerosis, sudden infant death syndrome, neurological impairment, including autistic and schizophrenic changes. A2 milk is safe for consumption and beneficial for health. Indian cows yield less milk as compared to crossbreds, it has amino acid, which makes the milk protein easily digestible and good for the kidney. It is also a rich source of vitamins B2, B3 and A, which help increase immunity and reduce acidity. Milk from native cows also reduces the chances of peptic ulcer and colon, breast and skin cancer. The original 'A2' milk is generally produced by cattle in Africa, Asia, France and Guernsey. Cattle in other countries generally produce mainly 'A1' milk. "The A2 allele in Indian milch breeds of cows and buffalos are 100 per cent, while in foreign breeds, it is around 60 per cent". Frequency of this allele in Indian milk breeds is 1.0 (100 per cent), while in exotic breeds, it was nearly 0.6 (60 per cent) or less. There is only one genetic difference between A1 and A2 milk, being the amino acid at position 67 in the chain of 209amino acids that make up beta-casein protein in milk. In the case of A1 beta-casein the amino acid at position 67 is histidine, whereas with A2 beta-casein it is proline. This small difference results in the milk having quite a different chemical and physiological effect.

TS-II-06

EXPLORING POLYMORPHISMS IN FEW OF THE GENES AFFECTING MILK TRAITS IN ONGOLE CATTLE

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The candidate gene approach provides tools for searching causative polymorphisms affecting quantitative traits that lead to production variability in cattle. *STAT5A*, *DGAT1*, and *CYP19* are some of the genes having possible effect on milk traits in cattle through different physiological pathways. In the present study *STAT5A/Ava*I, *DGAT1/CfrI* and *CYP19/Pvu*II polymorphism was investigated with PCR-RFLP in Ongole cows (n=135) and their association with milk production traits. *STAT5A* and *CYP19* were found to be polymorphic and *DGAT1* was monomorphic in Ongole cattle. Of the three genotypes reported for *STAT5A* only *CC* and *CT* genotypes were observed and the gene frequencies of *C* and *T* alleles were 0.97 and 0.03 respectively. *DGAT1K232A* polymorphism revealed the fixation of $DGAT1^K$ allele (lysine) in Ongole population. *CYP19/Pvu*II revealed the presence of all the three previously reported genotypes *viz*. *AA*, *AB* and *BB* with allele frequency of 0.77 and 0.23 of '*A*' and '*B*' alleles respectively. The PCR-RFLP variants of the three loci were confirmed by Sanger sequencing. Association analysis of *STAT5A* genotypes with milk production revealed that *CC* genotype was higher (528.40 ± 22.10 kg) than *CT* genotypes (396.37 ± 76.17 kg). The genotypes did not influence any of the milk constituent traits except for fat per cent; *CT* genotypes recorded more fat per cent (4.36 ± 0.58) than *CC* genotypes (3.52 ± 0.17). The analysis on *CYP19* genotypes revealed that *BB* genotype is associated with higher mean milk yield (590.85 ± 92.29 kg) and SNF content than the other genotypes. The *AB* genotypes showed higher fat (4.09 ± 0.33) and protein (3.53 ± 0.16) content. However, none of the associations were found to be statistically significant (P>0.05). The study suggests the need for exploration of additional genetic variants at these loci in Ongole cattle.

TS-II-07

ASSOCIATION OF SINGLE NUCLEOTIDE POLYMORPHISM IN THE LACTOFERRIN GENE WITH MASTITIS IN VRINDAVANI CROSSBRED CATTLE

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Lactoferrin (*Lf*) gene is one of the most important candidate genes for mastitis. Lactoferrin is produced by the mammary gland and is having anti-bacterial and anti-inflammatory activities. In the present study, two single nucleotide polymorphisms (SNPs) located on *Lf* gene viz., g.3879_3880insG and g.4432 T>C were analysed for their association with somatic cell score (SCS). SCS is an indirect indicator of mastitis because both are positively genetically correlated (r=0.7). Milk and blood samples were collected randomly from 100 lactating Vrindavani crossbred cattle maintained at Cattle and Buffalo Farm, Indian Veterinary Research Institute, Bareilly, U.P, India. SCS and california mastitis test (CMT) were carried out for grouping the animals in two categories i.e. affected and non- affected. The genomic DNA was isolated and its quality and purity were checked. Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) was used for SNP genotyping. Gene fragments of 125 bp (g.4432 T>C) and 712 bp (g.3879_3880insG) were digested using *Sty*I and *Mwo*I enzymes, respectively. The

SNP g.4432 T>C was found monomorphic, while g.3879_3880insG showed polymorphism. The allelic frequencies of g.3879_3880insG gene were found to be 0.56 and 0.44. However, the genotypic frequencies were 0.23, 0.67 and 0.1 for wild, heterozygote and mutant genotypes, respectively. The average heterozygosity and polymorphism information content (PIC) were 0.494 was 0.37, respectively. The chi-square value indicated that the population is not in Hardy-Weinberg equilibrium. Association study of g.3879_3880insG and SCS using regression analysis showed that the mutant genotype was significantly associated with mastitis. Hence, g.3879_3880insG SNP can be used as a possible candidate for marker assisted selection (MAS).

TS-II-08

IDENTIFICATION OF SINGLE NUCLEOTIDE POLYMORPHISMS IN BOVINE CARD15 GENE AND THEIR ASSOCIATION WITH SOMATIC CELL SCORE IN VRINDAVANI CROSSBRED CATTLE

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Mastitis is one of the most economically important disease affecting cattle in particular and mainly the crossbred cattle. Somatic cell score (SCS) is most often used as an indirect indicator of mastitis. Now these days, emphasis has been laid down in the selection programme on marker assisted selection (MAS) using single nucleotide polymorphisms (SNPs). The bovine Caspase Recruitment Domain 15 (CARD15) gene is located on *Bos taurus* chromosome 18 (Bta18). CARD15 is involved in the signaling events associated with recognition of different pathogen associated molecular patterns (PAMPs). In the current study, milk and blood samples were randomly collected from 100 lactating Vrindavani crossbred cattle maintained at the Cattle and Buffalo Farm, Indian Veterinary Research Institute, Bareilly, U.P, India. The california mastitis test (CMT) and SCS of these animals were ascertained and the genomic DNA was isolated. Three SNPs viz., rs43710287, rs43710289 and rs43710290 located on the CARD15 gene were genotyped using tetra-primer ARMS-PCR procedure. The SNP rs43710287 was monomorphic, whereas SNPs rs43710289 and rs43710290 were found to be polymorphic. The SNP rs43710289 showed C and A alleles with the frequencies of 0.7 and 0.3, respectively. The population studied showed three genotypes namely CC, AC and AA with genotypic frequencies as 0.44, 0.51 and 0.05, respectively. The allele frequencies of C and T alleles of SNP rs43710290 were 0.55 and 0.45, respectively. Similarly, three genotypes namely CC, CT and TT were also observed for this SNP with the frequencies as 0.16, 0.78 and 0.06, respectively. The average heterozygosity and polymorphic information content (PIC) were 0.426 and 0.334 for rs43710289 and 0.497 and 0.372 for rs43710290, respectively. Both the loci studied were found not to be in Hardy-Weinberg equilibrium. No significant association of these loci with SCS were found by regression analysis.

TS-II-09

PCR-RFLP AND SEQUENCING OF PARTIAL CODING REGION OF METALLOTHIONEIN ISOFORM-2 OF ZEBU CATTLE

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Metallothionein is important due to its function of binding tightly to heavy metals for decreasing their toxicity. DNA was isolated from approximately 30 toxic metal exposed and unexposed animals. The designed primer was used to amplify coding region of 489 bp size of Metallothionein Isoform-2 (MT-2) in zebu cattle. This amplified MT-2 PCR product (489 bp) was further used for PCR-RFLP and DNA sequencing analysis to reveal DNA polymorphism. MT-2 *TaqI* PCR-RFLP revealed homozygous genotype (AA) except E23 animal (AB). The frequency of AB genotype was found to be 0.033 in exposed group, whereas frequency of AA genotype was 0.967. DNA sequencing was carried out for toxic metal exposed sample (E23) and control sample (C13). The obtained nucleotide sequences of E23 and C13 samples were edited to get 420 bp sequences. The alignment of edited sequence revealed 150 nucleotide substitutions consisting 70 transition and around 80 transversion type mutations. Chromatographic verification for each nucleotide substitution revealed nature of nucleotide substitutions as 14 heterozygous and 09 homozygous. DNA sequencing based on random sampling was carried out for E21 and C13. Alignment analysis of E21 and C13 sample revealed 38 nucleotide substitutions consisting equal number of transition and transversion. Chromatographic verification revealed 17 heterozygous and 12 homozygous mutations. Results of DNA sequencing followed by PCR-RFLP for MT-2 revealed higher number of nucleotide substitutions (150) for AB genotype of E23 as compared to AA genotype (38) of E21. The proportions of transversion mutations in AB genotype were higher as compared to MT-2 AA genotype. The comparison of MT-2 of zebu cattle with *Bos taurus* cattle reference sequence revealed 46.7% identity. BLAST analysis revealed 89% identity with *Bos taurus*, 85% identity with sheep, 98% buffalo and 100 % with goat. The phylogenetic tree revealed that partial MT-2 zebu cattle coding sequence was in closer proximity with sheep metallothionein sequence. Overall findings of present study revealed DNA sequence variation in coding region of MT-2 gene of zebu cattle which can be utilised as identification marker for heavy metal homeostasis in zebu cattle.

TS-II-10

CYTOGENETIC STUDIES IN MALNAD GIDDA CATTLE

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Cytogenetic investigation was carried out in two breed groups of cattle, viz. Malnad Gidda (B.indicus) and Jersey (B.taurus), in an effort to compare the karyomorphological pattern between Malnad Gidda cattle and Jersey. Blood samples were collected from Malnad Gidda cattle maintained by farmers of Malnad region of Chikmagalur District of Karnataka and from Jersey cattle maintained at Livestock Breeding and Training Centre, Dharwad, Dept. of A.H & V.S, Govt. of Karnataka. Metaphase spreads were obtained by short term whole blood lymphocyte culture using standard techniques. A normal chromosomal complement of 2n=60 (58 autosomes and 2 sex chromosomes) was observed in all Malnad Gidda and Jersey cattle. The X- chromosome was sub-metacentric in both breeds and Y-chromosome was acrocentric in Malnad Gidda and metacentric in Jersey cattle. The X-chromosome was the longest chromosome, while first autosome was second longest and Y-chromosome was shortest chromosome in both Malnad Gidda and Jersey cattle. The relative length of autosomes progressively decreased from 4.85 ± 0.05 to 1.85 ± 0.03 per cent and from 4.95 ± 0.05 to 1.58 ± 0.03 per cent in male and female Malnad Gidda cattle, respectively; and from 5.00 ± 0.07 to 1.80 ± 0.04 per cent and from 4.76 ± 0.08 to1.83 ± 0.05 per cent in male and female Jersey cattle, respectively. The X-chromosome contributed 5.09 ± 0.05 and 5.15 ± 0.05 per cent in male and female Malnad Gidda, respectively; and 5.12 ± 0.05 per cent and 4.86 ± 0.09 per cent in male and female Jersey cattle, respectively, whereas the Y- chromosome contributed 1.70 ± 0.03 and 1.69 ± 0.05 per cent towards total genome in male Malnad Gidda and male Jersey cattle, respectively. The mean centromeric index of X-chromosome was 0.32 ± 0.01 and 0.33 ± 0.01 in Malnad Gidda and Jersey cattle, respectively. The mean centromeric index for Y-chromosome in male Jersey cattle was 0.41 0.01. The mean arm ratio (AR) for the X-chromosome was 2.11 ± 0.07 and 2.23 ± 0.11 in Malnad Gidda and Jersey cattle, respectively and that of Y-chromosome of male Jersey cattle was 1.54 ± 0.09. The G-banding pattern of Malnad Gidda cattle was almost similar with minor differences to that of Amrithmahal, Hallikar and Deoni cattle, reported earlier.

TS-II-11

MOLECULAR CHARACTERIZATION OF LYSOZYME GENE AND ITS ASSOCIATION WITH MILK PRODUCTION IN SAHIWAL CROSSES

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Lysozyme, an anti-bacterial enzyme mostly found in the body fluids, various tissues and secretions of animals and humans, confers immunity against a wide range of bacterial species. In the present study the gene sequence of this enzyme was elucidated in Sahiwal x Holstein Friesian crossbred cattle and genetic polymorphism was explored. The association of this gene with milk production traits was accessed. The total length of lysozyme cDNA was found to be 447 bp. The similarity with *Bos taurus*, human, pig, monkey, gorilla, mice, rat, chicken, dog and sheep was estimated as 99.1, 85, 81.0, 85.2, 84.3, 77.9, 77.9, 41.4, 40.5 and 24.6 per cent, respectively. Polymorphism study of two fragments, extended exon1 including promoter, exon 1 and partial intron 1 (268 bp) and extended exon 2 including partial intron1 and 2, and exon 2 regions (287 bp) of milk lysozyme gene was carried out by employing PCR-SSCP in 200 DNA samples from above mentioned crossbred cattle maintained at Instructional Dairy Farm, Pantnagar, Uttarakhand. In the extended exon 1 fragment, three alleles namely A, B and C with frequencies of 0.59, 0.28 and 0.12, respectively and in the extended exon 2 fragment, three different alleles i.e. P, Q and R with respective frequencies of 0.61, 0.38 and 0.01 were observed. A total of eight haplotypes were found in this population where the most predominant one was h1 (0.52). Genotypes of exon 1 extended fragment showed significant association with total milk yield, daily milk yield and peak yield ($P < 0.05$) while that of exon 2 extended fragment had significant association only with total lactation milk yield. Haplotype combinations also revealed significant association with total milk production, where h1h1 homozygote showed highest yield during first lactation.

TS-II-12

LEPTIN GENE POLYMORPHISM WITHIN THE INTRON REGION IN HILL CATTLE OF UTTARAKHAND

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Leptin, a 16 KDa protein secreted by adipose tissue, is involved in regulation of feed intake, energy balance, fertility, immune functions, and the neuroendocrine axis in rodents, humans and large domestic animals. The physiological properties of leptin gene stands in support to consider it as a strong candidate gene for evaluating genetic polymorphism, which has been further associated with reproductive performance, body growth, milk yield and other economical traits in livestock. This study was conducted to identify genetic polymorphism of the intron region of leptin gene in a hitherto unexplored Hill cattle population of Uttarakhand using the PCR-RFLP technique and to estimate gene and genotype frequencies of different restriction fragments. A total of 50 unrelated individuals of hill cattle of Kumaon region of Uttarakhand were considered for the study from different pockets including those maintained at Instructional Dairy Farm (IDF), G.B. Pant University of Agriculture and Technology, Pantnagar. Genomic DNA was extracted from whole blood following standard phenol–chloroform extraction method. A 422 bp fragment within intron 2 was amplified employing PCR. Digestion of PCR products with *Sau3AI* enzyme revealed two alleles *viz.*, allele A (390, 32) and allele B (390, 87, 32). Three genotypic patterns were observed with frequencies 0.5041, 0.4118, and 0.0841 for AA, AB and BB respectively.

TS-II-13

ISG15 EXPRESSION AND ITS CORRELATION WITH PROGESTERONE PROFILE FOR EARLY PREGNANCY DETECTION IN DEONI CATTLE

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One of the major constraints in the dairy industry is inability to identify the pregnant cows as early after insemination and if some diagnosticswhich can accurately distinguish pregnant cows, it can save both the time and associated economic lossto the farmers. Even though, bovine conceptussynthesize large amount of Interferon tau (IFNT) during maternal recognition of pregnancy period, its production and circulation is mainly limited to the endometrium. However circulatory leukocytes responds to IFNT by expressing Interferon stimulated gene 15 (ISG15) which is an important factor determining the uterine receptivity and conceptus development. The present study was carried out with the aim to analyse the expression levels of ISG 15 mRNA from PBMC in Deoni heifers during early pregnancy using qRT-PCR method and simultaneous monitoring of plasma progesterone level by ELISA. Sixteen Deoni heifers maintained at the cattle yard of SRS, NDRI were selected for the study. Deoni cows were synchronized for timed AI by CIDR-Ovsynch protocol and six animals were kept as non-pregnant control (without AI). Blood samples were collected from each animal on day 7, 14, 16, 18, 21, 30 and 45 days post AI for PBMC and Plasma separation. qRT-PCR was done to observe the expression pattern of ISG15 mRNA and data were analysed (SAS 9.3). Similarly plasma progesterone levels on different days of pregnancy were estimated by ELISA. A significantly ($p<0.05$) high expression of ISG15 mRNA was found on day16 and day18 of pregnancy in Deoni heifers whereas average progesterone concentration was observed significantly high (>3ng/ml) on day 21 in pregnant heifers compared to non pregnant control. Sensitivity and specificity of pregnancy prediction based on ISG 15 gene expression level on day 18 of pregnancy was found to be 90% and 50% with positive predictive value of 90% and negative predictive value of 50%. Whereas sensitivity and specificity of pregnancy detection based on plasma progesterone level was found to be 75% and 100 % with positive predictive value of 100% and negative predictive value of 50%. The results of the current study conclude that up regulated expression of ISG15 gene on day 18 of pregnancy can be used as an effective method of pregnancy diagnosis in heifer.

TS-II-14

SINGLE NUCLEOTIDE POLYMORPHISM OF LACTOFERRIN GENE PROMOTER AND ITS ASSOCIATION WITH MASTITIS IN SAHIWAL AND KARAN FRIES CATTLE

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Mastitis is the inflammation of mammary gland of dairy cattle. It is common in high yielding cows, causing high economic loss to the dairy industry. Selection of animals with higher innate levels of antimicrobial proteins in their milk could be a solution for improving the health of dairy cattle.Lactoferrin is one of the proteins having antimicrobial properties, which exerts several functions related to innate immunity and host defence. Lactoferrin concentration in milk and serum changes during mastitis, indicating that there is some association between lactoferrin and mastitis, resulting from change in expression of lactoferrin gene in cattle. Therefore an attempt was made to screen the lactoferrin gene promoter by PCR-RFLP, to study association between lactoferrin gene promoter variants and mastitis incidence. A total of 350 cows, Sahiwal (n=200) and Karan Fries (n=150) were considered in the study. All the cattle were screened for the presence of lactoferrin gene promoter polymorphism. The detection

of allelic variation at SNP sites were based on the electrophoretic pattern of the restriction enzyme treated PCR products. In both Sahiwal and Karan Fries cattle, lactorferrin gene promoter was polymorphic. Three genotypes were identified viz. GG, GH and HH in both Sahiwal and Karan Fries cattle. Association analysis using Chi square test revealed a significant association of these genotypes ($p \leq 0.05$) with mastitis incidence. The effect of lactoferrin genotype on mastitis incidence in Sahiwal and Karan Fries cattle could be due to varied level of expression of lactoferrin gene. The GG genotype showed higher resistance to mastitis incidence whereas, the HH genotype showed higher susceptibility towards mastitis incidence. This information can be used for early selection of cattle against mastitis and can be used efficiently in breeding and management decisions in dairy cattle.

TS-II-15

EVALUATION OF FECUNDITY GENES IN DAMS OF TWINS OF CATTLE USING PCR-RFLP TECHNIQUE

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Multiple ovulations in mammals is a complex trait influenced by genetic and environmental factors. The present investigation was carried out for evaluation of fecundity genes in cattle, comparing DNA fragments between dams, which had given birth to twin and singletons, to see inheritance pattern of these fragments in their twin progenies. Animals of Sahiwal, Hariana, Karan Swiss, Karan Fries, Holstein Friesian crosses and other crossbreds of unknown lineage were used. Molecular level study (PCR-RFLP) of the genome was carried for three fecundity genes, BMPR-1B, BMP-15 and GDF-9 using six primers on the DNA of 51 animals out of which 20 were dams of twins (experimental), 6 were dams of singletons (control) and 25 were twin progenies. PCR-RFLP analysis of Exon 6 of the BMPR-1B (Boorola) gene using *Ava*II revealed monomorphic band pattern of the wild-type allele in the dams (experimental and control) and twin progenies. Two of the BMP-15 mutation alleles FecX^{G} and FecX^{I}investigated using *Hinf*I and *Xba*I revealed monomorphic pattern of the wild type allele for both dams and their related twin progenies. Exon 1 of the GDF-9 gene amplified to produce 462bp fragment was subjected to *Hha*I and *Hin6*I restriction enzyme revealed homozygous pattern of the mutant allele. The observations showed presence of monomorphic pattern of the three fecundity genes such as BMPR-1B, BMP-15 and GDF-9, irrespective of twinning. In conclusion, the animals used in this study gave birth to twin only one time, which could be due to sire effect. In order to validate the gene/s of fecundity and twinning trait, a large number or dams, which gave twins all the times or frequently is neededfor validation.

TS-II-16

DRB3 GENE - A CANDIDATE GENE FOR RESISTANCE TO MASTITIS IN CROSSBRED CATTLE

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The bovine lymphocyte antigen (BoLA)-DRB3 gene encodes cell surface glycoprotein that initiates immune response by presenting processed antigenic peptides to CD4^{+} T helper cells. The present investigation was proposed with the objectives to elucidate allelic variants of DRB3 gene and to find its association with mastitis in crossbred cattle. DNA was isolated from blood samples of randomly selected 200 crossbred (Jersey×HF×Sahiwal) cattle maintained at IDF, G.B.P.U.A. &T., Pantnagar, Uttarakhand. DNA fragments were amplified using suitable primers spanning over the exon 2 of DRB3 gene. SSCP patterns of the amplified fragments were studied by PAGE.

Six alleles were identified as A, B, C, D, E and F having frequencies 0.2675, 0.245, 0.12, 0.2525, 0.0825 and 0.0325, respectively and twelve genotypes as AB, AD, AE, AF, BB, BC, BD, BE, CD, DD, DE and EF having frequencies 0.23, 0.215, 0.06, 0.03, 0.04, 0.11, 0.04, 0.03, 0.13, 0.04, 0.04 and 0.035, respectively. Genotypes had significant effect on mastitis. Animals with AB, AD, AF, BC and CD genotypes were found more prone to mastitis highlighting the presence of A or C or D allele in the genotype affecting more to mastitis and therefore could be considered for marker assisted selection (MAS).

TS-II-17

POLYMORPHISM OF LEPTIN GENE AND ITS ASSOCIATION WITH GROWTH, PRODUCTION AND REPRODUCTION TRAITS IN CATTLE

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The present investigation was carried out to study two polymorphisms in leptin gene by PCR-RFLP and to examine the possible association of the identified genotypes with growth, production and reproduction traits in crossbred cattle population (½Holstein Friesian X ½Hariana). One fragment of 330 bp comprising of partial intron 2 and exon 3 and another fragment of 94 bp comprising of partial exon 2 of leptin gene were amplified and digested with HphI and Kpn2I restriction enzymes, respectively, for identification of genotypes. The frequencies of mutant homozygotes were very low for both the RFLPs. Least-squares analysis was performed considering sire as random effect. The HphI-RFLP-CT and Kpn2I-RFLP-AV genotypes had significantly ($P<0.05$) higher birth weight than the HphI-RFLP-CC and Kpn2I-RFLP-AA genotypes, respectively. The HphI-RFLP locus was found to have significant ($P<0.05$) effect on body weight at 12 months of age, age at first calving and average daily milk yield, while, Kpn2I-RFLP had significant ($P<0.05$) effect on first lactation milk yield and average daily milk yield. It may be suggested that these mutations, which have caused changes in amino acid sequence of leptin protein, are responsible for some functional loss of this protein.

TS-II-18

MOLECULAR CHARACTERIZATION OF PROTAMINE1 GENE IN GIR CATTLE

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The present study was carried out with an aim to characterize Protamine1 (PRM1) gene which affects male fertility and to reveal possible polymorphism at specific restriction sites in Gir cattle. The genomic DNA from blood samples of 30 male Gir cattle were taken for study. Specific primers were designed to amplify segments of genes encoding PRM1 using Primer3 software. The 518 bp segment amplified by PCR was subjected to PCR-RFLP at restriction sites by digesting with *Hae*III, *Alu*I and *Bst*XI restriction enzymes and electrophoresed on agarose gel that revealed the monomorphic restriction pattern.Sequencing of the amplified product revealed that the ORF was 156 nucleotides long encoding a 51 amino acid protein. Gir cattle PRM1 had variation at one nucleotide, i. e., at 1108 bp as compared to *Bos taurus*. This did not result in to any change in the amino acids encoded by the gene as it lied beyond the exons. Sequence characterization of Gir cattle revealed sequence homology to *Bos taurus* PRM1 gene. Cross-species alignment of nucleotide sequences as well as amino acid sequences revealed that PRM1 of

different species was somewhat conserved at both nucleotide as well as amino acid level. The BLAST analysis of PRM1 gene of Gir cattle revealed nucleotide sequence identical to *Bos taurus* sequence. It revealed 81.7%, 80.4%, 78.2%, 75.8% homology to *Canis familiaris*, *Eqqus caballus*, *Mus musculus* as well as *Rattus norvegicus* and *Felis cattus*, respectively. Least identity of 69.2% was found with *Homo sapiens* Protamine1. The PRM1 protein was found 98.1% identical to *Bos taurus* PRM1 protein both evolving from same ancestor. It has 80.4% identity with dog, 78.4% with horse, 74.5% with cat, 69.2% with house mouse, 63.5% with Norway rat and least 51.9% with human PRM1 amino acid sequence.

TS-II-19

STUDY OF TRANSITION NUCLEAR PROTEIN1 GENE IN GIR CATTLE

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Transition Nuclear Protein1 (TNP1) is the Sperm Nuclear Basic Protein and is an important candidate gene affecting male fertility. The present study was carried out to characterize TNP1 gene of Gir cattle and to identify polymorphism in the coding as well as non-coding regions of the gene. DNA was extracted from blood samples collected randomly from 30 male Gir cattle. Specific primers were designed to amplify segments of genes coding for TNP1 using Primer3 software encompassing 2 exons and one intron. The 597 bp PCR product was digested with *Hae*III, *Alu*I and *Rsa*I restriction enzymes, each separately that generated monomorphic restriction patterns. The PCR products were sequenced to study sequence variation with taurine sequence of the gene. Multiple alignment of sequences of Gir cattle with *B. taurus* sequences (NCBI accession number X65041) revealed a total of two silent mutations. At 1286 bp position, there is addition of G and at 1370 bp position there is a substitution of A by G in Gir cattle. These mutations are non-synonymous leading to no change in the protein structures. Basic Local Alignment Search Tool (BLAST) analysis of Gir cattle TNP1 revealed nucleotide sequence homology of 100% with *Bos taurus*, 89.9% homology to *Eqqus caballus*, 89.3% homology to *Canis familiaris*, 88.1% with *Homo sapiens*, 87.5% with *Felis cattus*, 85.7% with *Rattus norvegicus* and 84.5% with *Mus musculus.* Gir cattle TNP1 protein has 85.7% identity with horse, dog as well as Norway rat, 78.6% with cat, 83.9% with house mouse and 82.1% with human TNP1 protein. *Bos taurus* and *Bos indicus* TNP1 evolved much earlier than any other species and from common ancestor sharing maximum similarity with each other.

TS-II-20

DNA POLYMORPHISM IN SLC11A1 (NRAMP1) GENE IN THARPARKAR CATTLE

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Solute linked carrier 11A1 (SLC11A1), a transmembrane protein (also referred as Natural Resistance Associated Macrophage Protein 1, NRAMP1), is one of the potential candidate genes that confers innate resistance against various intracellular pathogens. Several studies have been initiated to identify DNA polymorphisms and to ascertain its association with the host resistance/susceptibility against different intracellular pathogens in various species including livestock and human. The present study was undertaken to identify polymorphism in 650 bp fragment of SLC11A1 gene in Tharparkar cattle of different agro-climatic regions. Blood samples were collected

from IVRI, Suratgargh and Jhanshi Farms of Tharparkar cattle and DNA was isolated. A 650 bp fragment of exon 8 of SLC11A gene was amplified using a set of forward (F: 5′-TGG ACT GGA GGG TAA GAA CG -3′) and reverse (R: 5′-AGG GAG GAA TGC AGG TAG ATG-3′) primers. The amplicons were digested with *BPU10I* restriction enzyme for identification of genotypes. Three genotypes (CC, CG and GG) and two alleles (C and G) were identified. The farm-wise genotype frequencies were found to be 67.90, 32.10 and 0.00 in IVRI Farm and 81.80, 18.20 and 0.00 in Suratgargh Farm and 15.00, 65.00 and 20.00 in Jhanshi Farm for CC, CG and GG genotypes, respectively. The farm-wise allele frequencies were found to be 0.84 and 0.16 (IVRI farm), 0.90 and 0.10 (Suratgargh farm) and 0.48 and 0.52 (Jhanshi farm) for C and G alleles, respectively. These results show that there is variation among Tharparkar population of different agro-climatic regions. The CC genotype is more predominant in Suratgarh population and very low in Jhanshi Poulaion of Tharparkar cattle. The sequencing data of these populations are being analysed in order to find out possible genetic effect of climate on this breed.

TS-II-21

IDENTIFICATION OF POTENTIAL INTERNAL CONTROL GENES IN PERIPHERAL BLOOD MONONUCLEAR CELLS OF CATTLE POPULATIONS ADAPTED TO NORMOXIA AND HYPOXIA ENVIORNMENTS

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High altitude environments present a number of physiological challenges for animals by posing a lower partial pressure of oxygen (pO2) and lower ambient temperatures compared to low-altitude environments at similar latitudes. The native species of high altitude environments, lead to physiological changes which are contributed by hypoxia tolerance depict the genetic basis of adaptation that has evolved under natural selection. Thus, the mechanisms of physiological evolution can be better understood by identifying the genetic basis of hypoxia tolerance. Understanding expressed genes pattern is critical to provide insights into complex regulatory networks and mechanism of adaptation to extreme environments. Use of internal control genes (ICG) or housekeeping genes (HKG) that have constant expression in response to experimental treatment or physiological state is an effective mean for normalization of expression data to account for the experimental variations. The quantitative PCR (qPCR) technique requires normalization of expression data as the technique is prone to analytical variations. The objective of the study was to evaluate known reference genes from different functional categories that could serve as suitable appropriate ICG in the cattle (Leh local cattle, HF crosses and Jersey) from higher altitude (hypoxic) and the animals (Sahiwal, Murrah, KF and HF) adapted to tropical (normoxic) environment. For this study, a total of 36 PBMC samples from both the groups were isolated for RNA extraction and cDNA synthesis. A total of 10 candidate reference genes *viz*., *GAPDH*, *RPL4*, *EEF1A1*, *RPS9*, *HPRT*, *UXT*, *HMBS*, *B2M*, *RPS15* and *ACTB* from different functional categories were evaluated for their expression stability in the two groups of samples. Three different statistical algorithms: geNorm, Normfinder and BestKeeper were used for identification of best stable reference genes in the PBMC samples. In geNorm analysis, all the candidate genes exhibited expression stability (M) values below 0.5. On the basis of relative gene expression stability and stepwise exclusion of the gene with the highest M value, genes were arranged in descending order of stability: *RPS9=RPS15>HMBS >GAPDH>B2M >RPL4 >EEF1A1 >UXT >ACTB > HPRT*. Similar to geNorm, Normfinder also identified *GAPDH* and *RPS15* as most stable and *HPRT* as least stably expressed genes. There was a good agreement between geNorm and Normfinder outcome, albeit slight variation was observed in the ranking of other genes. The Bestkeeper algorithm was used to calculate gene expression variation based on Ct values. Each of the 10 candidate reference showed consistent expression levels. *RPS9, GAPDH, HMBS* and *RPL4* exhibited higher coefficient of correlation (r) to the bestkeeper index, lower coefficient of variance and standard deviation, pointing towards their expression stability. In the present investigation, all three algorithmic methods have demonstrated that *GAPDH*, *RPS15*, *RPS9* and *HMBS* are the most stable internal control genes and geometric means of these 4 ICG could be used for the normalization of expression data in PBMC of animals adapted to normoxic vs. hypoxic conditions.

TS-II-22

ASSOCIATION BETWEEN SNPs IN TLR2 GENE AND BOVINE MASTITIS

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The objective of this study was to understand the association between SNPs reported in the TLR2 gene of cattle and bovine mastitis. Allele specific-PCR (AS-PCR) was developed for the detection of six SNPs (rs55617172, rs111026127, rs68268256, rs68268260, rs68343170 and rs68268268) which were reported to be responsible for change in amino acid present on the LRR-functional domain of TLR2 gene. Fifty well characterized mastitis cases in terms of California Mastitis Test, bacterial culture and PCR, and fifty age-matched controls confirmed to be free from mastitis were selected from Puducherry region, India. DNA was isolated from blood samples of the above animals. AS-PCR was performed with the custom designed primers and genotypes determined. The genotypes detected were further confirmed by sequencing and sequence analysis which had proved the efficiency of AS-PCR developed for the detection of SNPs in TLR2 gene. Statistical analysis of association between genotypes detected with the cases and control resulted in the identification of association (*p*=0.0328) between TT genotype for SNP T◎G at 385 mRNA position with the control and heterozygous genotype, CT for SNP C◎T at 2010 mRNA position (*p*=0.0006) with the mastitis. Odds Ratio (OR) analysis with 95% confidence intervals (CI) further confirmed significant (OR=5.76; 95 % CI=2.07-15.97) association between the CT (C◎T at 2010 mRNA position) heterozygous genotype and mastitis.

TS-II-23

SEQUENCE BASED STRUCTURAL ANALYSIS AND EXPLORING THE GENETIC VARIATION IN TOLL-LIKE RECEPTOR-6 GENE OF BUFFALO (*BUBALUS BUBALIS*)

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Toll like receptors (TLRs) are family of pattern-recognition receptors (PRRs), mainly expressed by immune cells, recognizing and responding to broad range of molecules called pathogen associated molecular patterns (PAMPs) of bacterial, viral and fungal pathogens. Out of the 10 mostly recognized TLRs in mammals, TLR-6 is expressed on the cell surface, recognizing Gram-positive bacterial and fungal ligands in association with TLR-2, signaling to generate innate followed by adaptive immune responses. In this study, approximately 2.4 kb long genomic sequence of TLR-6 covering the entire coding region of the gene, was characterized in the Indian buffalo. Sequence data was generated by both end sequencing of overlapping fragments and a contig of entire coding region was constructed. Sequence analysis revealed a 2382-nucleotide long open reading frame (ORF) of buffalo TLR-6, encoding 725 amino acids of exon-1 and 68 amino acids of exon-2, similar to that of cattle. Further analysis of sequence data generated in different riverine and swamp buffaloes revealed, presence of 18 Single Nucleotide Polymorphic sites in this region (SNPs). Out of these, 11 SNPs were found to be non-synonymous (10 in exon-1 and 1 in exon-2) and seven were synonymous (4 in exon-1 and 3 in exon-2). SMART analysis revealed one amino acid change in the trans-membrane domain and four amino acid changes lying in the LRR domains of buffalo TLR-6. The Polyphen analysis showed three non-synonymous SNPs (15V>I, 381T>P and 498S>F) to be possibly damaging the structure and function of the protein. Further, the binding sites of three microRNAs *i.e.* bta-miR2417, 654 and

2300 were observed in buffalo TLR-6. However, none of the targeted miRNAs sites were found in the polymorphic sites identified in the present study. The identified polymorphism might be helpful in finding its association with disease resistance traits in buffalo.

TS-II-24

DETECTION OF ALLELIC VARIANTS OF β_2M GENE IN BUFFALO DAMS AND THEIR ASSOCIATION WITH COLOSTRAL IgG CONCENTRATION

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Neonatal calves have little or no detectable circulating immunoglobulins at birth. They are dependent on passive transfer of immunoglobulins, via maternal colostrum, for antibody-mediated immunity early in life. It has long been recognized that failure of passive transfer (FPT) is strongly associated with increased calf mortality due to infectious disease. Indications of relatively high heritability for both colostral IgG and post-suckle calf serum IgG have been reported, suggesting that passive transfer is influenced by the genotype of both the dam and the calf. We attempted to detect SNPs in β_2M gene in buffaloes and ascertain their association of colostral IgG levels. 40 newly parturated Murrah buffaloes which were maintained at Livestock Production Management (LPM) Section of IVRI, Izatnagar, were included in the present study. Two pairs of primers for amplification of fragment I (206 bp: full exon 1) and fragment II (296 bp: partial intron 1) in the DNA samples of these buffaloes were designed on the basis of sequences of cattle (*Bos taurus*) in public database at NCBI with the help of Primer3 online computer software. Genomic DNA was extracted from blood. Polymerase chain reaction-single stranded conformational polymorphism (PCR-SSCP) technique was used to explore the polymorphism in $\beta_2 M$ gene of Murrah buffaloes. 15% PAGE were prepared for each fragment and the gels were resolved by silver staining for SSCP analysis. Further different banding patterns were identified and sequencing was done. The PCR-SSCP analysis revealed polymorphism in fragment I of $\beta_2 M$ gene and sequencing of different patterns of fragment I revealed two alleles A and B which differed at nucleotide positions 45 and lied in 5`UTR region. The genotype frequencies of genotype AA and BB were 95 and 5 % respectively in dams. The SNP viz. C45G transversion was present in untranslated region. The PCR-SSCP analysis did not reveal polymorphism in fragment II. All the genotypes were AA type in buffalo dams. Indirect ELISA was done to estimate IgG concentrations in colostrum (first milking) whey. IgG levels in colostrum ranged from 11.22 to 185.1 mg/ml and mean IgG concentration in colostrum was 51.71 ± 5.99 mg/ml. The effect of different haplotypes was evaluated on IgG concentrations. The least-squares analysis of variance revealed a non-significant effect of dam haplotype on colostral IgG concentrations.

TS-II-25

EVIDENCE FOR A COMPLEX AND MULTIPLE DOMESTICATION OF RIVER BUFFALO (*BUBALUS BUBALIS*)

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The river buffalo (Bubalus bubalis) is one of the important livestock species in southern Asia for milk and agricultural purposes. It has been believed based on the archeological studiess that the domestic river buffalo was derived from the wild buffalo Bubalus arnee a few thousand years ago during Indus Valley civilization. However, the domestication history of the river buffalo has been the subject of debate for many decades mainly due to the divisive conclusions of the genetic studies. But none of the genetic studies have included neither wide range of samples nor wild buffalo samples. Therefore, in order to understand the evolutionary history and genetic relationship among the various river buffalo populations we analyzed 492bp mtDNA control region sequences of 414 river buffaloes sampled from India, Pakistan, Egypt and Iran (those countries were thought to be the important place for river buffalo domestication). Based on phylogenetic analyses along with the archeological evidences we propose three important findings (i) The river buffalo was domesticated at least twice in the past, (ii) The river buffalo was domesticated at least 6000 years ago and (iii) The river buffalo was first domesticated in the Northwestern region of India from which it was spread to other parts of Asia and elsewhere.

TS-II-26

CYTOGENETIC ANALYSIS ON PREVALENCE OF CHROMOSOMAL FRAGILE SITES IN MURRAH BUFFALO CALVES

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Chromosomal fragile sites are considered to play a key role in karyotype evolution, chromosomal rearrangements and disease etiology related to productive and reproductive efficiency of farm animals. Extensive studies have been undertaken on the fragile sites in several species of bovidae regarding different methods of induction, and their clinical and biological significance. The present investigation was carried out to search fragile sites in buffalo calves through cytogenetic analysis and further confirmation by R-banding. The cytogenetic analysis was carried out in 20 Murrah buffalo calves (11 females and 9 males) from an organized herd at Cattle Yard, National Dairy Research Institute, Karnal. Chromosome preparations were made by short-term lymphocyte cultures in RPMI-1640 medium supplemented with aphidicolin. A total of 1243 metaphases or 50-100 cells per individual were analyzed. In female calves, fragile sites were ranging from 5.45 to 41.67% of metaphase plates with a mean of 19.39% and in male calves, the range of fragile site occurrence was varying from 8.33 to 37.93% with a mean of 22.21%. Moreover, fragile sites were found in 20.67% of total screened metaphase plates. Fragile sites on chromosomes were further confirmed by conventional R-banding technique. The revealed fragile sites could be associated in future with reproductive problems like repeat breeding, abortion or still birth for early screening of buffalo calves resulting substantial reduction of time spent in raising them on the farm.

TS-II-27

PCR-SSCP PATTERNS OF LACTOFERRIN GENE AND THEIR ASSOCIATION WITH MILK LACTOFERRIN CONTENT AND SOMATIC CELL SCORE IN MURRAH (*BUBALUS BUBALIS)* BUFFALOES

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Lactoferrin is an iron binding glycoprotein which plays an important role in antimicrobial defence and a potential candidate gene in dairy cattle. In the present investigation, polymerase chain reaction-single strand conformation polymorphism (PCR-SSCP) study was carried out in 100 lactating Murrah (*Bubalus bubalis*) buffaloes

to detect SNPs of lactoferrin gene and to analyse the association between the observed polymorphisms with milk lactoferrin content and somatic cell score (SCS). PCR-SSCP analysis revealed a total of 11 different variants in the entire coding region of the lactoferrin gene. PCR-SSCP analysis of exon 10 of lactoferrin gene revealed three and that of exons 4, 5, 13 and 16 revealed two each unique patterns, while all other exons exhibited monomorphic pattern. Comparison of nucleotide sequences of lactoferrin gene of the Murrah buffaloes with taurine ENSEMBL (accession number ENSBTAG00000001292) reference sequence revealed a total of 23 point mutations, 16 of which were found to be in coding region. Conceptualized translation of nucleotide sequence revealed 11 amino acid changes. SSCP variants of exon 10 had significant ($P<0.01$) effect on milk SCS. The SSCP variants of exon 16 were found to have significant ($P<0.05$) effect on lactoferrin content. The SCS and lactoferrin content in Murrah buffaloes was highest in 4th and above parity group. Stage of lactation had highly significant ($P<0.01$) effect on both milk SCS and lactoferrin content. The observed association between SSCP variants in lactoferrin gene with milk SCS and milk lactoferrin content can be used as prognostic markers for selection of animals for high lactoferrin content and low somatic cell score, thus Murrah animals who are less susceptible to mastitis.

TS-II-28

GENETIC DIVERSITY AT MHC-DQA AND DQB LOCI INDICATES POSITIVE SELECTION IN INDIAN SWAMP BUFFALO

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Swamp buffalo (*Bubalus bubalis carabanesis*), a bovine specific to North-East region of India is reared mainly for meat and draft. These buffaloes seem to be different genetically as well as phenotypically from major riverine type buffaloes of India and supposed to be more close to the wild ancestors. Due to their geographical isolation, the diversity in thesepopulations is presumed to be low, albeit, the animals might possess certain unique alleles and genotypes, specific to their adaptation and immune response. As an attempt to assess the genetic diversity and fitnessof swamp buffaloes, we studied Major Histocompatibility Complex (MHC), a group ofimmune response lociin local swamp buffalo populations from NE region. To assess genetic diversity at MHC class II loci, about 930 and 290 nucleotides long genomic regions corresponding to DQA and DQB genes, encompassing exon 2, were amplified in 90 Assamese swamp buffaloes. Amplified products of both the genes were digested with *Hae*III and *Hinf*I restriction enzymes. PCR-RFLP analysis of DQA gene for both enzymes revealed a total of seven allelic patterns, whereas DQB gene had six and seven restriction patterns for *Hinf*I and *Hae*III, respectively. Based on PCR-RFLP analysis, PCR samples from eight animals having different haplotypes of DQA and DQB genes were cloned, for further study. Colony PCR-RFLP was carried out to identify the clones having different alleles and plasmid of selected clones was isolated and sequenced. A total of 13 DQA alleles were identified in swamp buffaloes, which corresponded to two major groups, DQA1 (11 alleles) and DQA2 (2 alleles). For DQB, total 16 alleles were identified corresponding to three major groups i.e. DQB1, DQB2 and DQB3. Presence of more than two different clones of DQA and DQB from an individual as well as their phylogenetic analysis confirmed the duplication of DQ genes in swamp buffaloes. Further, high ratio (more than 1) of dN/dS for DQA and DQB alleles overall, indicated positive selection for MHC class II diversity in Swamp buffaloes. Moreover, most of the amino acid variations were seen at the peptide binding sites. Results revealed high allelic diversity as well as duplication of DQA and DQB loci in indigenous swamp buffaloes, indicating higher fitness of the population under positive selection.

TS-II-29

MOLECULAR PATHWAYS ASSOCIATED WITH HEAT STRESS RESPONSE IN MAMMARY EPITHELIAL CELLS OF RIVERINE BUFFALOES (*BUBALUS BUBALIS*)

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An attempt was made to identify the pathways that are overrepresented in buffalo mammary epithelial cells (MECs) in response to heat stress. Use of heterologous bovine Agilent microarray expression chip in the present study was successful in dissecting the transcriptome profile of heat stressed and unstressed buffalo MECs. The study has identified several genes from different functional classes and biological pathways which could be termed as heat responsive in buffalo MEC. Additionally, genes related to chaperons, immune function, cell proliferation and metabolism *etc.* were also identified that are known to be affected by heat stress. The pathway analysis was carried out based on transcriptome data generated as it is difficult to extract a unifying biological theme from a large list of individual genes. Thus, in order to put differentially expressed genes (DEG) into biological context; we carried out pathway analysis to know in which biological pathways a significant enrichment of genes of interest are present. Considering the fact that number of pathways getting affected within cells will always be smaller than the number of DEG genes, the transformation of data from a gene-centric view to a pathways-centered view will reduce dimensions. Such a reduction allowed us to interpret and understand the data in a manner that was not possible at the individual gene level. The overall DEG data set across all time points at 3 fold change (>2000 genes) were applied to identify pathways categories that were significantly affected in buffalo MECs due to heat stress. The pathways were identified by comparing each time point data with unstressed (CTR) data. The metabolic pathways most impacted were *viz.*, electron transport chain and cytochrome P450 pathways while most enriched signaling pathways were; apoptosis, IL2 signaling, MAPK, FAS and stress induction of HSP regulation, delta notch signaling pathway, apoptosis modulation by HSP70, EGFR1 signaling, cytokines and inflammatory response, nuclear receptors, oxidative stress, TNF-alpha and NF- kB signaling and GPCRs pathways. In conclusion, the present work presented a suitable strategy to characterize the transcriptomic responses of buffalo mammary epithelial cells to heat stress. Our present data thus provides the strong clue about the coordinated transcriptional response of buffalo mammary epithelial cells to heat stress. In future, such studies could be extended in evaluating the impact of hyperthermia and other physiological stressors in tissue / cell damage and related gene regulation studies to understand buffalo mammary functions.

TS-II-30

COMPARATIVE TRANSCRIPTOME PROFILING OF BUFFALO PBMCS IN REPSONSE TO SUMMER AND COLD STRESSES

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In the present study, for the first time, the detailed transcriptome profile of buffalo PBMCs during summer and winter season was delineated. This study was designed to provide comparative baseline data to understand the underlying alterations in cellular tolerance towards heat stress during hot summer and cold winter in dairy animals. The experiment was conducted to study the effect of environmental stress during hot summer (average

temp 40±1°C) and cold winter (average temp 10±1°C) on dairy animals. A total of 6 buffalo PBMCs, 3 each from summer and winter periods were analyzed using bovine microarray chip from Agilent Technologies. Total RNA was extracted by Trizol reagent (Invitrogen, CA, USA). The RNA quantity was assessed using Experion Bioanalyzer (Bio-Rad).The heterologous bovine specific microarray chip (Agilent Technologies) was successfully utilized to identify the genes/transcripts that are differentially expressing during summer and winter periods in buffaloes. An effort was made to generate the microarray based transcriptome profile of buffalo PBMC harvested during peak summer and winter periods. A total of 1970 transcripts were found to be differentially expressed across two seasons in buffalo PBMCs at $p<0.05$. Further with cutoff criteria of signed fold change ≥2 or ≤2, a total of 1736 genes were found to be significantly differentially expressed across the two seasons. In comparison to winter, a total of 921 genes were up- and 835 genes were down-regulated during summer. Hierarchical clustering approach was followed to partition the normalized transcriptome profile to have a biologically meaningful interpretation of the data. An effort was made to mine transcriptome data to identify genes that were specifically induced or repressed across during summer and winter seasons in buffalo PBMCs. As expected, the whole set of genes related to heat shock protein family; chemokines apoptosis, immune and oxidative stress response etc. were up-regulated during summer season in comparison to winter season in buffalo PBMCs. On the other hand, during winter season, several ribosomal proteins, eukaryotic translation elongation factor 1 alpha 1 *etc*. were upregulated. This kind of effort would help to determine the molecular pathways and genes most significantly influenced due to seasonal stress in different cattle types and buffaloes.

TS-II-31

GENETIC DIVERSITY AND BOTTLENECK ANALYSIS OF MADRAS RED AND MECHERI SHEEP BREEDS BASED ON MICROSATELLITE DATA

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Madras Red and Mecheri sheep populations variability and structure were analysed using FAO recommended microsatellite markers. Genetic variation at 10 microsatellite loci, population structure, and genetic bottleneck were studied to provide genetic information for their conservation strategies and breeding programmes. A total of 98 and 86 alleles were scored for Madras Red and Mecheri sheep respectively. The polymorphism information content ranged from 0.609 to 0.902 for all the microsatellite loci. The overall observed and estimated heterozygosity for all loci combined were 0.972 and 0.785 for Madras Red and 0.982 and 0.774 for Mecheri respectively. The overall mean heterozygosity was 0.779, total heterozygosity was 0.821 and the co- efficient of gene differentiation was 0.049 between the breeds. Apart from these, 10 and 7 loci in Madras Red and Mecheri sheep respectively showed breed-specific alleles which are critical in terms of conservation. Three different tests, viz., Sign rank, Standardized differences and Wilcoxon tests using three models of microsatellite evolution (IAM, TPM and SMM) were utilised to investigate whether the Madras Red and Mecheri sheep populations have undergone recent bottleneck or are in mutation drift equilibrium. The tests revealed no genetic bottleneck in recent past and this was confirmed by mode shift test which gave a normal L-shaped distribution for proportion of alleles.

TS-II-32

NUCLEOTIDE DIVERSITY IN EXONS 4 AND 5 OF GROWTH HORMONE (*GH*) GENE IN INDIGENOUS SHEEP BREEDS

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Growth hormone affects many of the important characteristics of animal production, including growth rate, fatness and lactation. It affects the partitioning of nutrients among tissues in sheep and cattle, increasing bone growth and milk production, and decreasing fatness. In bovines, a single nucleotide polymorphism (**SNP**) in exon 5 (at codon 127) changes leucine to valine in the mature GH molecule. Nucleotide variations in the growth hormone gene have also been associated with decreased milk protein yield, carcass conformation and fat in cattle. There is a conspicuous lack of such information on indigenous sheep. Therefore, the exons 4 and 5 of ovine growth hormone (GH) gene were PCR amplified, sequenced and screened for identification of possible SNPs across a panel of 10 indigenous sheep breeds namely Bandur, Chokla, Deccani, Ganjam, Nellore, Madgyal, Magra, Malpura, Muzzafarnagri and Nali. Sequence alignments, comparisons and haplotype data analyses were carried out using various software programmes. Allele and genotype frequencies were estimated for the identified SNPs. The exons 4 and 5 region of GH exhibited more than 98% identity with homologous regions in the ovine reference sequence (Oar3.1). Analysis of the aligned sequence data with reference sequence revealed several singleton variations in exons 4 and 5 of GH gene. Two SNPs (g.1674A>T and g.1792A>C) were identified in the exon 5, both of which were observed to be heterozygous in nature. The allele frequency of the A allele in g.1674A>T and g.1792A>C SNPs was observed to be 0.674 and 0.860 respectively. The haplotype and nucleotide diversities were estimated to be 0.837 and 0.026 respectively for the GH locus. The effects of these SNPs on production traits in indigenous sheep need to be confirmed by further studies.

TS-II-33

POLYMORPHISM OF *FEC*-G (GDF9) GENE IN BALANGIR, SHAHABADI AND BONPALA SHEEP BREEDS OF INDIA

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The present study was designed for screening polymorphism of *Fec*G (GDF9) gene in Balangir, Shahabadi and Bonpala breeds of sheep by employing forced PCR-RFLP technique. Genomic DNA was isolated from 100 blood samples of Balangir and Shahabadi and 50 blood samples of Bonpala sheep breeds. The 139bp fragment of *Fec*G (GDF9) gene amplified by forced PCR-RFLP from genomic DNA of sheep breeds and digested with *DdeI* restriction enzyme revealed bands at 105bp and 34bp in all three Indian sheep breeds. Band patterns were observed in 3.5% metaphore agarose gel and genotyped. All three Indian sheep breeds were homozygous (FecG^{HH}) for *Fec*G gene with gene frequency of H allele being unity. This indicates that the *Fec*G gene is fixed in the Balangir, Shahabadi and Bonpala population in the natural habitat. Sequencing of representative samples of *FecG* gene from each breed showed presence of point mutation at 105th position. Litter size of Balangir and Bonpala sheep breeds were single but in Shahabadi sheep twinings were recorded. The overall mean (± S.E) of litter size in Balangir, Shahabadi and Bonpala was 1.00±0.00, 1.41±0.02 and 1.00±0.00, respectively. In the present study all the animals of three breeds such as Balangir, Shahabadi and Bonpala were homozygous for *Fec*G and there was no infertility observed in above mentioned breeds in field condition and organized farm.

TS-II-34

GENETIC CHARACTERIZATION OF REGIONAL SHEEP (PURKY) OF KARGIL DISTRICT BY RAPD MARKERS

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The present study was carried out on a total of sixty sheep including 30 each of Bakharwal and Purky sheep population for genetic characterization of Purky sheep from Kargil district. The local sheep population of Kargil district is known as Purky. The word 'Purky' is derived from two different words "*Pot*" means 'Tibetan' and "*Riks*" means 'Race'. Most of the people of Kargil district belong to Tibetan race and the dialect spoken in this region is also known as Purky. Genomic DNA was isolated from the venous blood samples by Hi PuraTM^{SPP} Blood DNA Kit (Hi-Media). Five primers of 10 base pair each were used for RAPD-PCR technique for genetic characterization. Three primers generated reproducible and distinct RAPD profiles. A total number of 34 loci were found in Bakarwal and Purky sheep. The numbers of loci were 12, 8 and 14 for primer 1, primer 2 and primer 3, respectively, for Bhakarwal and Purky sheep. Nei's gene diversity (h) and Shannon's information index (I) of Bakharwal and Purky sheep were 0.3414 and 0.5171 and 0.3497 and 0.5258, respectively. The genetic identity between Bakharwal and Purky breed was very high (0.923). The present work will provide useful information for future sheep breeding studies in Kargil district to conserve the local sheep Purky in its natural habitat and also from dilution of breed due to extensive crossbreeding with exotic improved breeds.

TS-II-35

MICROSATELLITE MARKER BASED ASSESSMENT OF GENETIC STRUCTURE OF NELLORE SHEEP

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The present study was aimed to characterize and make genetic assessment of Nellore sheep using 12 ovine-specific microsatellite markers recommended by Food and Agriculture Organization. Blood samples were collected from 50 unrelated animals in the breeding tract and DNA was isolated by using phenol-chloroform method. All the 12 loci were found to be polymorphic. The number of alleles amplified at each locus varied from four to twelve with a mean of 7.33 ± 0.47 alleles per locus. A total of 88 alleles were observed across 12 loci studied. Mean polymorphic information content was found to be 0.771 which ranged from 0.637 (CSSM47) to 0.8951 (MAF214). The population departed from Hardy-Weinberg equilibrium at all loci studied. The observed heterozygosity ranged from 0.102 to 0.833 with a mean of 0.433 ± 0.074, while the expected heterozygosity ranged from 0.689 (oarVH72) to 0.889 (MAF214) with a mean of 0.800 ± 0.015 which indicated that substantial amount of genetic variability present in Nellore sheep. The overall with-in population inbreeding estimate (0.302±0.08) reflected presence of inbreeding in the population.

TS-II-36

ASSOCIATION OF GENETIC POLYMORPHISM OF CALPASTATIN GENE WITH GROWTH TRAITS OF BANDUR SHEEP

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Ovine calpastatin gene is considered as one of the potential candidate gene for growth and carcass traits. The present study was conducted to determine the polymorphism of calpastatin gene and its association with growth traits (birth weight, weaning weight, 6- month body weight and ADG) in native Bandur sheep of Karnataka. Blood samples were collected from randomly chosen 100 Bandur ram lambs from Livestock Research and Information Centre (Sheep), KVAFSU, Nagamangala and from different villages in the home tract. DNA extraction was based on Miller's High salt method followed by PCR-RFLP to determine polymorphic variation in the exon 1C/1D (including intron between them) region of ovine calpastatin gene in Bandur sheep. The amplified product of length 622 bp was digested by two restriction enzymes, *viz.,MspI* and *NcoI*. Three genotypes MM, MN and NN with genotypic frequencies of 0.24, 0.59 and 0.17, respectively, were differentiated by *MspI* and *NcoI*. The allelic frequencies were 0.535 and 0.465 for M and N alleles, respectively. Chi-square test confirmed the existence of Hardy Weinberg equilibrium in the studied population. No significant differences ($P > 0.05$) were observed between the three genotypes of Bandur sheep with respect to the different growth traits.

TS-II-37

CHARACTERISATION OF LEPTIN GENE IN SHEEP BREEDS OF TAMILNADU

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Characterisation of leptin (*LEP)* gene was carried out in all the eight sheep breeds of Tamilnadu *viz*.Coimbatore, Kilakarsal, Madras Red, Mecheri, Nilagiri, Ramnad White, Tiruchy Black and Vembur. The *LEP* gene consists of three exons and two introns; exon 1 of 13, intron 1 of 11433, exon 2 of 172, intron 2 of 1838 bp and Exon 3 of 2731 bp in length. The coding sequence begins from a portion of exon 2 and extends up to a portion of exon 3. The exon 2 was amplified with a pair of primers and exon 3 with a set of five primers that resulted in overlapping amplicons of a mean size of 800 bp. The PCR products from a minimum of 12 samples from each breed were sequenced and the FASTA and *.ab1 format were compared with the reference sequence from NCBI (NC_019461 and GeneID: 443534). It was found that 100 bp upstream, in 5' UTR region, all the Tamilnadu breeds had only one copy of 'GTT' segment while the reference had two copies. Just before the start of the coding sequence, a transition 13893 T>C (SNP-L1) was identified in all the Tamilnadu breeds. The allele in the reference sequence was *T*. In the coding region of the exon 2, a transition 14013 C>T (SNP-L2) which resulted in a non-synonymous mutation was identified only in the Tiruchy Black sheep. Analysis of exon 3 revealed three SNPs *viz*., 16973 G>A, (SNP-L3), 17476 C>T, (SNP-L4) and 18082 G>A (SNP-L5). All SNPs were transitions of which, SNP-L3 was found in all the sheep breeds of Tamilnadu. SNP-L4 was breed-specific as it was found only in the Nilagiri breed and SNP-L5 was identified in Mecheri and Kilakarsal breeds. Further studies are needed to identify association of these SNPs with growth traits in these breeds and potential of these SNPs to act as marker in selection.

TS-II-38

GENETIC POLYMORPHISM OF GROWTH HORMONE GENE IN VEMBUR AND KILAKARSAL SHEEP OF TAMILNADU

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Vembur and Kilakarsal, mutton sheep are distributed in southern agro-climatic zone of Tamilnadu, comprising of five districts viz. Thirunelveli, Ramanathapuram, Virudhunagar, Tirunelveli and parts of Thoothukudi. Of these, Kilakarsal has now become endangered and is being maintained at Veterinary College and Research Institute (VC&RI), Tirunelveli and District Livestock Farm, Abishegapatti, Tirunelveli for conservation. The genomic regions consisting of part of intron 3, entire exon 4 and a part of intron 4 (214 bp);and part of intron 4, entire exon 5 and a part of 3′ untranslated region (365 bp) of growth hormone (GH) gene wereanalyzed for polymorphism. Blood samples of Vembur (112 numbers) and Kilakarsal (99 numbers) breeds were collected from their breeding tract and from animals maintained at VC&RI, Tirunelveli respectively, and DNA was extracted. Sequencing of GH gene revealed absence of SNPs in exon 4 and 5. However, it showed complete replacement of nucleotides A with G and G with C in the intron 4 region of the GH gene (214 bp) in all the samples of Vembur and Kilakarsal breeds.It also showed a T◎C transition in Vembur breed of sheep in the 3′ untranslated region of GH gene (365 bp). Genotyping of T◎C transition mutation (T1965C) by PCR-RFLP using EcoP15I endonuclease revealed the existence of two alleles viz., A and B; and three genotypes viz., AA (365 bp), AB (365 bp, 301 bp and 64 bp) and BB (301 bp and 64 bp). Genotypic frequencies for AA, AB and BB were 0.696, 0.223 and 0.080, and allelic frequencies for A and B were 0.808 and 0.192 respectively. The highly significant ($P \leq 0.01$) Chi-square value (8.812) showed that the population is not under Hardy-Weinberg equilibrium. Sequence variation of Vembur and Kilakarsal breeds with other breeds of GH gene may be explored for its potential as molecular marker in breed characterization.

TS-II-39

EVIDENCE THAT GANJAM SHEEP OF ORISSA IS A CARRIER OF THE BOOROOLA MUTATION WITH LOW FREQUENCY

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It is well established that the mutation in the Booroola fecundity gene (BMPR-1B) increases the ovulation and litter size in prolific sheep including the Garole, Kendrapada, and Nilagiri in India. It was speculated that the sheep breeds found near the coastal region might have the chance of FecB mutation due to some unknown factors. Therefore, we conducted a study on Ganjam sheep found near the Chilkalake, Rambha, Khallikote, PunnaChandrapur and Mathura villages of District Ganjam of Orissa in year 2007. A total of 83 individuals of both sexes were selected. Out of that 61 individuals were selected randomly and 22 individuals were selected based on their lambing recods, ewes which had at least one record of twins, their progenies and sires. FecB genotyping was done by forced restriction fragment length polymorphism (Forced-RFLP-PCR). Five individuals had one copy mutation in the BMPR-1B gene (FecB^{B+}; heterozygous), while 78 individuals were found non-carrier (FecB^{++}) for the FecB gene. The allele frequency of the FecB allele was found very low (3%) in the selected population. The presence of the FecB gene in the Ganjam sheep indicated that the FecB gene might have travelled either from Garole or Kendrapada sheep found nearest to the native tract of Ganjam sheep. It is concluded that presence of the FecB gene in the Ganjam is segregating at low frequency and might have travelled in the Ganjam sheep by crossing of the Garole or Kendrapada sheep by the farmers.

TS-II-40

CYTOGENETIC CHARACTERIZATION OF MACHERLA BROWN SHEEP

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Macherla Brown sheep are found in the villages mainly adjacent to the Krishna River flowing through Prakasam, Guntur, Krishna, Nalgonda districts of Andhra Pradesh. The present investigation was undertaken to ascertain information on chromosomal profile of Macherla Brown sheep for characterization as a breed. Blood samples were collected from a total of 80 animals with 20 animals from each district and 10 animals from each sex. Cultures were set up as per short term lymphocyte culture method as described by Mooreheadet *al.* (1960) with slight modifications. The modal diploid chromosome number was found to be 54 (2n = 54, XY). The first three pairs of the autosomes were found to be submetacentric (1-3) and the remaining 23 pairs of autosomes were acrocentric (4-26). The X-chromosome was the longest acrocentric, while the Y-chromosome was the smallest bi-armed chromosome in the karyotype. The mean relative length of autosomes of Macherla Brown sheep varied from 1.78 to 9.85 per cent in males and 1.82 to 9.67 per cent in females. The mean relative length of X and Y chromosomes were 5.05 and 1.57 per cent respectively. The arm ratio of first three bi-armed autosomes of Macherla Brown sheep varied from 1.21 to 1.24 in males and 1.19 to 1.22 in females, while the centromeric index in terms of ratio of short arm to its total length varied from 0.46 to 0.47 in males and 0.45 in females.

TS-II-41

HIGH RESOLUTION MELTING CURVE ANALYSIS FOR RAPID MUTATION SCREENING OF *Fec*B GENE IN SHEEP BREEDS OF TAMILNADU

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A study was carried out to screen for the presence of fecundity gene: *Fec* B among the native sheep breeds (Coimbatore, Mecheri, Niligiri, Trichy black and synthetic Snadyno) of Tamil Nadu with objective of developing a high resolution melt curve (HRM) assay. High resolution melting curve, a new method for DNA analysis is introduced as the simplest method for genotyping, mutation scanning and sequence matching. After PCR amplification, melting curves are generated by monitoring the fluorescence of a saturating dye that does not inhibit PCR. In this present study, single–base genotyping with SYBR Green I are used to differentiate the melting curve. SYBR Green I was included in the reaction mixture before PCR, and high-resolution melting was obtained within 2 min after amplification. In all cases, heterozygotes were easily identified because heteroduplexes altered the shape of the melting curves and the homozygotes are easily genotyped by melting temperatures (T_m) that differ by 0.8–1.4°C. The homozygotes cannot be resolved from each other. In these cases, adding known homozygous wild genotype samples to unknown samples allows melting curve separation of all three genotypes. Heterozygous PCR products were easily distinguished from homozygous samples by a double peak on derivative melting curve plots. Both fluorescence colour and Tm were exploited for multiplex. The HRM results show no mutations in Coimbatore, Tiruchy black and Mecheri sheep breeds, whereas in Sandyno and Nilagiri sheep breeds, the presence of *Fec* B mutations was detected. The frequency of wild, *Fec* B heterozygote (B+) and homozygote (BB) genotypes were 54.71, 35.87 and 9.41 per cent respectively in Nilagiri and, 88.14, 11.86 and 0.00 per cent respectively in

Sandyno. In the HRM assay, *Fec* B mutants can be distinguished from the wild-type strains based on the transition of melt curves, which is more prominent when the profiles are displayed in difference plot. Direct sequencing of *Fec* B gene has also revealed the presence of mutation. In conclusion, HRM analysis allows for rapid screening for mutations at the *Fec* B gene in Sheep breeds. This assay markedly reduced the sequencing effort involved in mutational studies of *Fec* B gene.

TS-II-42

ASSOCIATION OF GROWTH HORMONE POLYMORPHISM ON BODY WEIGHT IN BLACK BENGAL GOAT

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Genetic variation of growth hormone gene and its correlation with body weight was investigated in Black Bengal goats. A 472bp fragment (partial intron 2, exon 3 and intron 3 and partial exon 4) was analyzed for detection of polymorphism expected to be present at this locus. SSCP of 472 bp fragment revealed five genotypes. Sequencing revealed substitution at 6 places i.e. 70th, 91st, 106th, 167th, 233rd and 240th among the alleles, out of which three i.e. 70th, 233rd and 240th are found in intronic region whereas three i.e 91st, 106th and 167th were found in exonic region. Mutation in exonic region lead to variation in polypeptide sequences of three alleles. Substitution at 91st position (C◎T) and 167th position (G◎C) led to substitution of proline to serine and glycine to alanine, respectively in B allele. Similarly, substitution at 106th position of nucleotide sequence (T◎G) led to substitution of tyrosine to aspartic acid in allele C. Least- squares analysis revealed that genotypes had significant effect ($P \leq 0.05$) on body weights at 6-month and 9-month of age. Animals having AC genotype had highest body weight whereas animals having CC genotype had lowest body weight. Animals having AC genotype had 65% more weight than the animal having CC genotype at both 6-month and 9-month of age. The order of performance for body weight at 6 month of age was CC < AA, AB, BB < AC whereas order of performance at 9-month of age was CC < BB < AA, AB < AC. One interesting finding in this study is that both the homozygote AA and CC are having lowest body weight. However, heterozygous condition i.e. AC genotype is having highest body weight. This may be due to heterosis where heterozygous performs better than the both homozygotes.

TS-II-43

PROLIFICACY STATUS OF GOATS OF BIHAR - AN EXAMPLE OF GENETIC UPGRADATION

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Bihar contributes about 9% of India's total goat population.Village goat is mostly of Bengal breed. However, crosses with other breeds like Jamunapari, Barbari, Sirohi and Jakharana are also available. This breed is prolific and has high twinning percentage. In the present study, the crosses available in villages of Bihar were analysed for genetic basis for prolificacy by screening for the BMPR1B gene polymorphism. The study revealed two allelic variants (A=0.48 and G= 0.52) and three genotypes (AA= 0.16, AG= 0.62 and GG= 0.22). It indicated the abundance of mutant type (G) nucleotide in village goats. The study revealed sign of introgression of mutant allele (G) into Jamunapari, Barbari, and Sirohi goats at village level. The variation in litter size among the genotypes revealed the benefits of introgression of FecB mutation in the crosses. The litter size showed variation among

the three genotypes. The proportion of singles, twins and triplets were 69, 29 and 2 per cent in AA genotype, 42, 52 and 6 per cent in AG genotype and 14, 66 and 20 per cent in GG genotype. The study shows that the genetic upgradation for prolificacy in goats is taking place at village level. Meantime, some concerns require immediate attention regarding conservation of native breeds. Bihar is inhabited by Bengal breed of goat, which needs to be conserved. Indiscriminate crossbreeding with other breeds should be checked immediately. However, nucleus stock of superior breed like Jamunapari, Barbari and Beetal should be maintained. State breeding policy on goat should be developed and breed improvement may be done accordingly.

TS-II-44

GENETIC VARIABILITY AND BOTTLENECK ANALYSES OF KANNI ADU GOAT POPULATION USING MICROSATELLITE MARKERS

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In the present study, microsatellite data on 25 loci were generated and utilized to evaluate the genetic architecture and mutation drift equilibrium of Kanni Adu goats reared under low input system of southern Tamilnadu, India. Sufficient allelic diversity was observed with a total of 225 alleles across different loci. The genetic diversity analysis of Kanni Adu goats displayed higher level of within-breed variability in terms of mean number of alleles per locus (11.24 ± 0.87) and heterozygosity values (H_o = 0.677 ± 0.041, H_e = 0.857 ± 0.016). The polymorphism information content (PIC) value ranged from 0.531 to 0.915. These high values of PIC indicated higher polymorphism in this breed. Within population inbreeding estimate (F_{IS}=0.215 ± 0.040) showed moderate level of inbreeding, which warranted adoption of appropriate breeding strategies under field conditions. Three quantitative tests viz. sign test, standardized difference test and Wilcoxon sign rank test and a qualitative test for mode shift distortion of allelic frequencies were employed to evaluate mutation drift equilibrium under three different models of microsatellite evolution. The average observed number of loci with heterozygous excess was 20, 17 and 13 in IAM, TPM and SMM models respectively. The average expected gene diversities observed under IAM, TPM and SMM models were 0.796 ± 0.027, 0.829 ± 0.025 and 0.854 ± 0.023 respectively. The population was found to deviate significantly under IAM and TPM models, while it was reverse under SMM. The qualitative test for mode shift supported the results under SMM model indicating the absence of genetic bottleneck in the recent past in Kanni Adu goats. It suggests that any unique alleles present in this breed may not have been lost. The study indicated that Kanni Adu goats exhibited substantial amount of genetic variation as reflected from the heterozygosity and number of alleles per locus. Avoiding unplanned and indiscriminate mating between individuals can increase the heterozygosity which can be exploited in the improvement of productivity of this breed.

TS-II-45

DIVERSITY IN INDIAN GOAT LEADS TO IDENTIFICATION OF POLYMORPHISM IN CANDIDATE GENE OF REPRODUCTIVE TRAIT

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Arylalkylamine-N-acetyltransferase (*AA-NAT*) is a key enzyme associated with melatonin (MLT) biosynthesis and plays a key role in regulation of the reproductive system of seasonally estrous animals. In view of its biological role, *AA-NAT* is a candidate gene for reproductive traits. The present study envisaged to explore the valuable genetic pool existing in diverse Indian goat breeds with respect to reproductive traits firstly, to obtain the status

of partial *AA-NAT* gene and secondly, to identify intra-species polymorphisms for assessment of variability at molecular level. Polymorphism in exonic region (exon 2 and 3) was identified by generating nucleotide sequence and sequence assembly. Two novel, synonymous SNPs C825T (exon 2) and C1249T (exon 3) were identified. All the three possible genotypes (CC, CT and TT) were identified for C825T mutation, whereas two genotypes were observed (CC and CT) for C1249T mutation. SNPs C825T and C1249T changed recognition site of restriction enzyme *BtsCI* (GGA***T***G) and *AciI* (C***C***GC) and thus can be genotyped by relatively simple and cost effective technique of PCR-RFLP for establishing further association with reproductive traits. This is the first description of the polymorphisms of *AA-NAT* gene in Indian goat breeds which differ in reproductive traits (twinning percentage and age of sexual maturity). Present results add up to the existing knowledge and extend the spectrum of genetic variation of caprine candidate genes of reproductive traits, which may lead to the identification of markers for caprine fecundity and sexual precocity.

TS-II-46

SNPs IN FECUNDITY GENES AS POTENTIAL MARKERS FOR ASSESSMENT OF GENETIC ARCHITECTURE OF INDIAN GOAT BREEDS

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Single nucleotide polymorphisms (SNPs) are the most abundant form of DNA polymorphism which can be used as simple genetic markers for many breeding applications as well as for population studies in livestock. SNPs in fecundity genes viz. Bone Morphogenetic Protein Receptor type 1B (BMPR1B), Growth Differentiation Factor 9 (GDF9) and Bone Morphogenetic Protein 15 (BMP15) were genotyped using simple and economical methods of PCR-RFLP and Tetra-primer ARMS PCR in Indian goat breeds to assess their basic population parameters and genetic structuring. Three hundred and ninety one animals of seven different goat breeds (Barbari, Beetal, Black Bengal, Sangamneri, Osmanabadi, Jakhrana and Ganjam) differing in prolificacy, utility and geographic distribution were studied for diversity assessment at six loci in these *Fec* genes (T(-242)C in promoter region of BMPR1B, C818T, A959C and G1189A in exon 2 of GDF9 and G735A and C808G in exon 2 of BMP15). Four loci were polymorphic in all the breeds with varied allele frequencies. Statistical analysis revealed that breeds differed with respect to genetic variability as the observed heterozygosity varied from 0.163 (Ganjam) to 0.359 (Jakhrana). Sangamneri and Osmanabadi were least differentiated (0.003) whereas Jakhrana and Black Bengal were most differentiated (0.048) on the basis of genetic distance. The genetic distance as well as PCA analysis indicated that breeds are grouped according to their geographical distribution. The genetic diversity based on fecundity genes presented here is an essential step towards future exploitation of the available goat genetic resources of India in research and breeding programmes.

TS-II-47

GENETIC DIVERSITY STUDIES ON LOCAL GOATS OF KARNATAKA BASED ON MICROSATELLITE MARKER ANALYSIS

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A study was conducted with the aim of analysing the diversity status of local goats of Karnataka, based on microsatellite marker analysis. DNA was isolated from blood samples collected from 50 randomly selected

local goat flocks of four different agro-climatic zone of Karnataka. Totally 158 alleles were observed from 23 microsatellite markers with the alleles ranging from 3 to 13 for different loci. The mean observed and expected number of alleles were 6.8696 ± 2.9435 (range 3 to 13) and 4.3335 ± 1.9357 (range 2.25 to 8.40), respectively. The mean observed heterozygosity (H_o) was 0.4698±0.2214 [ranged from 0 (ETH225) to 0.8462 (ILSTS034)] and the mean expected heterozygosity (H_e) was 0.7471± 0.1098 [ranged from 0.5656 (ILSTS005) to 0.9138 (SRCRSP 8)]. The gene diversity as indicated by Shannon Index (I) ranged from 0.9431 (ILSTS005) to 2.3102 (RM 088) with the mean of 1.5608 ± 0.4241. The PIC value ranged from 0.0114 (ILSTS059) to 0.9168 (RM088) with mean of 0.7644±0.1895. A significant deviation ($P<0.001$) from Hardy-Weinberg equilibrium (HWE) was observed in 14 loci (ETH225, ILSTS002, ILSTS005, ILSTS008, ILSTS019, ILSTS030, ILSTS034, ILSTS044, ILSTS049, ILSTS058, ILSTS059, ILSTS082, OarFCB48, RM088). The least genetic distance was observed between the flocks of eastern dry zone and central dry zone with 0.5617, while the widest was between southern transition zone and southern dry zone with a distance of 0.8816, which was consistent with the geographical location of the goat flocks.

TS-II-48

EVALUATION OF CANDIDATE GENES (GDF9 AND BMPR1B) FOR PROLIFICACY IN CAMEROON NATIVE GOATS

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Natural mutations in prolific sheep breeds have shown that the transforming growth factor beta (TGF-β) super family ligands such as growth differentiation factor 9 (GDF-9), bone morphogenetic protein 15 (BMP-15) and their type I receptor (bone morphogenetic protein receptor, BMPR1B) are crucial for ovulation as well as for increasing litter size. Mutations in any of these genes increase prolificacy in sheep. The aim of the study was to understand genetic factors which may affect the litter size variability in Cameroon native goats and eventually to develop a test kit for females with high potential of kidding trait. The bone morphogenetic protein receptor 1B (BMPR-1B) gene and growth differentiation factor-9 (GDF-9) were studied as candidate genes for the prolificacy of goats. These genes of the transforming growth factor beta (TGF-β) super family have vital roles in ovarian follicle development, ovulation rate and fertility. Tissue samples were collected on female goats and DNA was extracted using standard saturated salt method. According to mRNA sequence of ovine BMPR-1B and GDF-9 genes, four pairs of primers and one pair of primers were designed respectively to detect single nucleotide polymorphisms (SNPs) of exons 2, 3, 4 and 10 of the BMPR-1Bgene and exon 2 of the GDF-9 gene in both high prolificacy goats (12 animals) and low prolificacy goats (12 animals) by the simple polymerase chain reaction (PCR) procedure. Sequence detection was performed after amplification of the gene segments. So fa, only the products amplified by primers P1 of the unique exon of GDF-9 and primers P2 (exon 2), P3 (exon 3), P10 (exon 10) of BMPR-1B displayed polymorphisms. For primer P1, four genotypes were detected. These results preliminarily showed that two of the detected loci of the GDF-9 gene had a significant effect in the amino acid products in both groups of animals. For primers P2, P3 and P10, a total of 10 mutations were detected. But none of them caused a change in the amino acid products. Further laboratory and statistical analysis are still going on to process the results and conclude.

TS-II-49

GENETIC RELATION AT MOLECULAR LEVEL BETWEEN THREE INDIAN DAIRY GOAT BREEDS OF NORTH WESTERN REGION

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The world has about 351 goat breeds. Among the Indian population there are 20 well-defined goat breeds apart from many non-descript goats. These breeds vary in their genetic potential for the production of milk, meat and fibre, disease resistance, heat tolerance and fecundity. RAPD is a PCR based technique for identifying genetic variation. Blood samples of Jakhrana (16), Sirohi (15) and Jamunapari (15) goat breeds were collected from goat farm at the Central Institute of Research on Goats, Makhdoom, Farah, Mathura. The genomic DNA was isolated from blood samples and checked for its quality, purity and concentration. Good quality DNA was used for further analysis. Two arbitrary short oligonucleotide primers (10 mer) i.e. OPM 12 and OPM 18 with GC content of 60-70% were used in this study. Primer OPM 12 could detect polymorphism within the Jakhrana, Sirohi and Jamunapari while primer OPM 18 produced polymorphic RAPD profile within Jakhrana and Jamunapari breeds but monomorphic RAPD profile was produced within Sirohi breed. From two polymorphic primers OPM 12 and OPM 18, total bands amplified in Jakhrana, Sirohi and Jamunapari were 24, 19 and 20, respectively. The proportions of polymorphic bands in these three goat breeds were 16.66, 15.78 and 20%, respectively.In total, two polymorphic random primers amplified a total of 24 bands and 10 of these (41.66%) were found to be polymorphic.The between-breed genetic similarity was also measured from band sharing (BS) as well as from band frequency (BF). BS estimates ranged from 0.875 (between Sirohi and Jamunapari) to 0.995 (between Jakhrana and Sirohi) with primer OPM 12; and from 0.932 (between Jakhrana and Sirohi) to 0.959 (between Jakhrana and Jamunapari) with primer OPM 18. However, averaged over both primers, the minimum between-breed genetic similarity was observed between Jakhrana and Jamunaparias 0.917, while Jakhrana and Sirohi showed maximum genetic similarity of 0.964. Jamunapari showed comparatively lower genetic similarity (0.910 to 0.917) with other two goat breeds in comparison to other between-breed genetic similarity (0.964). Between-breed genetic similarity based on band frequency (BF) estimates ranged from 0.975 (between Sirohi and Jamunapari) to 0.995 (between Jakhrana and Sirohi) with primer OPM 12 and from 0.986 (between Sirohi and Jamunapari) to 0.994 (between Jakhrana and Jamunapari) with primer OPM 18. However, averaged over primers, the minimum between-breed genetic similarities was observed between Sirohi and Jamunapari (0.981), while Jakhrana and Sirohi showed maximum genetic similarity of 0.994.

TS-II-50

ASSOCIATION OF NOVEL SNPs IN THE CANDIDATE GENES AFFECTING CAPRINE MILK FATTY ACIDS RELATED TO HUMAN HEALTH

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In the present investigation, 618 milk samples of Sirohi breed of goat were collected, and analyzed for conjugated linoleic acid (CLA, C18:2) and other fatty acids. The CLA in studied goat milk samples was 4.87 mg/g of milk fat and C18:2 cis-9, trans-11 contributes 2.9 mg/g of milk fat and trans10 cis12 contributes 0.82 mg/g of milk fat. The saturated fatty acids in the milk accounted for 69.55% and unsaturated fatty acid accounted for 28.50%. The unsaturated fatty acid was constituted by monounsaturated fatty acid (24.57%) and polyunsaturated fatty acids

(3.96 %.). The major contribution (45.56%) in total fatty acid was of C12:0, C14:0 and C16:0. C18:0 and short chain ones (C4:0, C6:0, C8:0, C10:0) which have a neutral or cholesterol-decreasing effect. The DNA sequence analysis of the genes (DGAT1, SCAP, PPARG, OLR, FABP3 and PRL) in a random panel of 8 Sirohi goats revealed 38 SNPs across the targeted regions. Out of the studied SNPs (38) across these genes, 22 SNPs had significant effect on one or a group of fatty acids including CLA. The genotypes at these loci showed significant differences in the least-squares means of a particular fatty acids or a group of fatty acids including CLA and its isomers.

TS-II-51

STUDY OF KIDDING PATTERNS AND POLYMORPHISM OF FecB GENE IN THE BERARI GOAT

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The data on 141 kidding records comprise of 112 of F_0 and 29 of F_1 generations of Berari goats were collected from different villages of Akola and BalapurTaluka of Akola district spread over the year 2011 to 2014. The kidding pattern shows 20.56% single, 69.50% twin, 9.22% triplet and 0.70% quadruplet births in Berari goats. Twining per centage is found less in F_1 (58.62%) as compared to F_0 (72.32%); similarly only 3.44% triplet and no quadruplet is reported in F_1 which may be because of less number of observations recorded in the F_1 generation. DNA was extracted from blood samples of 34 parental (F_0) and 32 of their progeny (F_1) generations and genotyping was carried out by forced PCR-RFLP using Fec^B primer. In the present study a 190 bp BMPR-1B gene fragment containing an introduced Ava II restriction site (G/GACC) was amplified using primers. All PCR products showed single, intense, compact band of 190 bp on 2 % agarose. On restriction digestion with the enzyme Ava II (Eco471), intact PCR amplified segment, uncut by the restriction enzyme was observed in all samples on 3.5 % agarose. These results indicated that there was no FecB mutation in Berari goat and the population was found to be monomorphic containing only FecB+/ FecB+ i.e., wild type allele. Berari goat population was found to be monomorphic containing only wild type allele. Thus it can be concluded that absence of Fec^B polymorphism in Berari goat even though the breed is having 60% twining does not exclude the probability of presence of any other fecundity genes in large population.

TS-II-52

INVESTIGATION OF THE GALWAY ($FecX^G$) AND INVERDALE ($FecX^I$) MUTATIONS IN BERARI GOAT BREED OF MAHARASHTRA

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The 'Berari' is recently recognized as 23rd goat breed of Vidarbha region of Maharashtra in India. Berari is distributed in all 11 districts of Vidarbha region, and is a prolific, medium sized, low yielding meat type breed with light to dark tan colour. Total of 66 blood samples of 34 parental (F_0) as well as their 32 progeny (F_1) of Berari goat with known history of kidding from different villages of Akola and BalapurTaluka of Akola district were collected from the year 2011 to 2014. DNA was extracted and genotyping was carried out by forced PCR-RFLP using $FecX^G$ and $FecX^I$ primer. The 141 bp fragment from the BMP15 protein gene ($FecX^G$ locus) was amplified in 66 Berarigoat containing a forced restriction site for restriction enzyme Hinf I. All PCR products showed single, intense, compact band of 141 bp on 2% agarose. On restriction digestion by Hinf I enzyme, two segments of 111bp and 30 bp segments were resolved on 3.5% agarose gel. This indicates the absence of $FecX^G$ mutation in the Berari goat and the population was found to be monomorphic containing $FecX^G$+/ $FecX^G$+ i.e. wild type allele. The 154 bp fragment from exon 2 of the BMP15 gene ($FecX^I$ locus) was amplified using primers containing a forced restriction site for restriction enzyme Xba I. Incorporation of a single nucleotide change in the PCR product resulted in formation of a forced restriction site for Xba I restriction enzyme. All PCR products showed single, intense, compact band of 154 bp on 2% agarose. On restriction digestion by Xba I enzyme, uncut segments of 154 bp band were resolved on 3.5% agarose gel. This indicates the absence of $FecX^I$ mutation in the Berari goat and the population was found to be monomorphic containing $FecX^I$+/ $FecX^I$+ i.e. wild type allele.

TS-II-53

UNDERSTANDING ASSOCIATION OF SEXUAL PRECOCITY WITH CAPRINE *JY-1* GENE POLYMORPHISM

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Female sexual precocity is a reproductive trait that has a high economic value for goat production system. Since reproductive traits show low heritability, molecular markers can be employed to reduce the generation interval and increase the genetic gain. Recently, genes of female reproductive tract have been identified to contribute in genetic variability of reproductive traits.The markers identified so far, are related to genes that act as transcription factors in the nervous system or during body growth. *JY-1* is a candidate gene for reproductive traits whichis expressed in the oocyte and is associated with folliculo-genesis and early embryo development. Polymorphisms in the third exon of this gene have been associated with early pregnancy probability in cattle. Similarly, a novel SNP (C15329T) has been identified in 3′UTR of Indian goats. Thus, the objective of the present study was to correlate this polymorphism with age of sexual maturity in goats.Sexually precocious and highly prolific Black Bengal goats were genotyped by designing PCR-RFLP test, *Mlu*CIJY-1.Association analysis was performed between SNP and age at sexual maturity following a linear fix model. Age of sexual maturity in days was obtained by the difference between the date of birth and the date of exhibiting first signs of estrous. The model included fixed effect of genotype, year of birth (2009-11) and season of birth; winter (November to February), summer (March to June) and rainy (July to October). The effect of season of birth, year of birth and genotype was not significant as females of three genotypes attained sexual maturity at almost similar ages. However, since the minor allelic frequencies are not stable in small sample size, further replication is required in future study with a bigger sample size. Further studies investigating other regions of this gene or other genes expressed in tissues of the female reproductive system would be interesting to be performed. The study of genes that are expressed in tissues of the female reproductive system is necessary since their influence on reproductive dynamics has been little explored so farand should be the target of future studies.

TS-II-54

POLYMORPHISM IN 285 BP FRAGMENT OF EXON-2 OF DRBII GENE IN GOAT

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The gastrointestinal parasite reduces the productivity and health of small ruminants worldwide. The increasing prevalence of anthelminthic resistance and growing demand for organic animal products worldwide have encouraged a search for alternative methods to control helminthiasis in sheep and goats. There is ample evidence from studies on domestic livestock for genetic variation in resistance to parasites, specially Haemonchuscontortus, both within and between breeds of animals. Therefore, present study was undertaken with the objective to find out polymorphism in goat population pertaining to Haemonchuscontortus at DNA level. Blood samples were collected from 140 goats of Rohilkhandi breed from Sheep and Goat Farm, Livestock Production and Management Section, Indian Veterinary Research nstitute, Izatnagar and DNA was isolated. A 285 bp fragment of exon-2 of DRBII gene (which was found to be associated with faecal egg count and PCV) was amplified using a set of forward (5′-TAT CCC GTC TCT GCA GCA CAT TTC-3′) and reverse (5′-TCG CCG CTG CAC ACT GAA ACT CTC-3′) primers. The amplicons were digested with BsaIrestriction enzyme for identification of genotypes. Three genotypes (AA, AB and BB) and two alleles (A and B) were identified. The genotype frequencies were found to be 0.74, 0.25 and 0.01 for AA, AB and BB genotypes, respectively. The allele frequencies were found to be 0.87 and 0.13 for A and B alleles, respectively. These results show that there is sufficient variation in the population. The AA genotype is more predominant in this population, followed by AB and BB genotypes. The data are being analysed for possible association of these genotypes with indicator traits viz. fecal egg count (eggs/g) and PCV (%).

TS-II-55

GENETIC SCREENING OF MUCIN 4 POLYMORPHISMS IN LANDRACE AND ITS CROSSES

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Mucins are the glycoproteins in the apical surfaces of epithelial cells in GI and respiratory tracts which form the first line of host defence against enteric pathogens. Mucin 4 gene located at SSC13q41 region is the most extensively studied in relation to ETEC-F4ab/ac susceptibility worldwide. The XbaI polymorphism detects a SNP (g.8227 G>C) at intron 7 with the G allele associated with susceptibility which dominates the resistant C allele and used now-a- days as a genetic test in the Danish pig breeding industry. Another SNP (MUC4-g.243A>G) was also reported to be associated with the susceptibility. A total of 72 numbers of pigs were screened for detection of polymorphism for MUC4-g.8227 G>C as well as MUC4-g.243A>G from three genetic groups (LR, CB 50 % and CB 75 %) in the pigs maintained under AICRP on Pigs, IVRI unit. It was found from the study that while in case of g.8227 G>C polymorphism the genotypic frequencies were found to be 0.25, 0.33 and 0.42 for CC, CG and GG, respectively leading to gene frequencies 0.58 (G allele) and 0.42 (C allele). Similarly, *Hha I* polymorphism at DQ124298:g.243A>G revealed the genotypic frequencies 0.72, 0.19 and 0.09 for AA, AG and GG, respectively with gene frequencies 0.82 (susceptible A allele) and 0.18 (resistant G allele). While the study revealed higher frequency

of unfavorable alleles which may partially explain repeated diarrhea incidence, the presence of possible genetic variability at the same time indicates that reduced diarrhea susceptibility can be targeted in future breeding programmes. However the consistency of the association of these PCR-RFLP markers with the susceptibility to ETECF4ab/ac mediated diarrhea in Indian pig population needs to be evaluated before using them in breeding.

TS-II-56

IDENTIFICATION OF A NOVEL SNP IN PORCINE BETA DEFENSIN-1 GENE

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Porcine beta defensin-1 (PBD-1) gene codes for an antimicrobial peptide that plays an important role in the innate immunity of pigs. The PBD-1 peptide demonstrates direct activity against a wide range of microbes and thus, co-creates an antimicrobial barrier in the oral cavity of pigs. The objective of the present study was to detectpolymorphisms in exon-1 and exon-2 regions of PBD-1 gene in Large White Yorkshire (LWY) and native pigs of Kerala. Blood samples were collected from 100 animals and genomic DNA was extracted using the modified phenol chloroform method. The quantity and quality of extracted DNA was assessed using spectrophotometry and gel electrophoresis, respectively. Exon-1 and exon-2 regions of PBD-1 gene were amplified by PCR and the products were subjected to single strand conformation polymorphism- polyacrylamide gel electrophoresis (SSCP-PAGE). Subsequent silver staining of the polyacrylamide gels revealed three unique SSCP patterns in each of the two exons. The presence of single nucleotide polymorphisms (SNPs) was confirmed by nucleotide sequencing of the PCR products. A novel SNP was found in the 5′-UTR region of exon-1 and a known SNP was detected in the mature peptide coding region of exon-2. In exon-1, the pooled population frequencies of GG, GT and TT genotypes were 0.67, 0.30 and 0.03, respectively. GG genotype was predominant in both the breeds whereas TT genotype was not detected in LWY breed. Similarly, in exon-2, the pooled population frequencies of AA, AG and GG genotypes were 0.50, 0.27 and 0.23, respectively. AA genotype was predominant in LWY pigs whereas GG genotype was predominant in native pigs. The Chi-square analysis indicated a significant difference ($P<0.01$) in the allelic frequencies of the two breeds, in both the exons. These results suggest that a considerable genetic variation exists in PBD-1 locus and further association studies may help in understanding the influence of genetic factors on the innate immunity of pigs.

TS-II-57

GENETIC FACTORS CONTRIBUTING TO GROWTH REGULATION IN CHICKEN

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Knowledge of favourable alleles of genes contributing to chicken growth can be used to improve breeding efficiency. As a first step, often a linkage or association study is performed to map genomic loci contributing to the trait of interest. Reciprocal crosses between the inbred lines New Hampshire (NHI) and White Leghorn (WL77) comprising 579 F2 individuals were used to map quantitative trait loci (QTL) for body weight and composition. The lines NHI and WL77 had been selected for high body weight at the age of 20 weeks and for low egg weight during laying period, respectively. Afterwards, the lines were inbred. Here we examine the growth performance until 20 weeks. Linkage analysis provided evidence for highly significant QTL on GGA1, 2, 4, 10 and 27 which had specific effects on early or late growth. The highest QTL effects accounting for 4.6 to 25.9 % of the phenotypic F2 variance were found on the distal region of GGA4 between 142 and 170 cM ($F \geq 13.68$). The QTL allele of the high weight NHI breed had positive additive effects on growth of up to 141.86 g body mass at 20 weeks. Using body weight as a covariate in the analysis of body composition traits provided evidence for genes in the GGA4 QTL region affecting fat mass independently of body mass. The QTL effect size differed between sexes and depended on the direction of cross. *TBC1D1* and *PPARGC1A* are functional candidate genes in the QTL peak region. The findings in our crosses could be relevant for native breeds; Fayoumi in Egypt and Oh-Shamo in Japan (Chicken QTLdb release 25; http://www.animalgenome.org/cgi-bin/QTLdb/GG/index). The results confirmed known QTL and identified new QTL effects for hatching weight on GGA16, 24 and 28. Our study confirmed the importance of the distal GGA4 region for chicken growth performance. The strong effect of the GGA4 QTL makes fine mapping and gene discovery feasible. The final identification of genes contributes to our understanding of the complex inheritance pattern of growth regulation that will be more emphasized in chicken breeding programs with genomic selection.

TS-II-58

CHARACTERIZATION OF GENETIC POLYMORPHISM OF B-LβII FAMILY ALLELES IN VEN-COBB CHICKENS

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The present study was taken up to study the MHC B-Lβ family (class II) alleles polymorphism and genotyping in Ven-cobb chickens using one of the variants of Polymerase Chain Reaction, the PCR-SSP (Polymerase Chain Reaction with Sequence Specific Primers). A total of 30 Ven-cobb birds were included in the study. Genomic DNA was isolated from blood of each of the birds maintained at experimental poultry unit at College of Veterinary Science and Animal Husbandry, N. D. V. S. U., Jabalpur. A set of degenerating primers was used to amplify a 235 bp, exon-2 region of chicken MHC B-Lβ family. The products of the first round of amplification were subjected to PCR-SSP at the specified annealing temperatures and replication cycles. The primers designated for B2, B13, B15, B19 and B21 amplified the target sequences producing a 222 bp, 141bp, 213 bp, 213 bp and 222 bp fragments, respectively. The present research revealed seven genotypes *viz.*, B2B2, B2B19, B2B21, B13B15, B19B19, B19B21 and B21B21. It was observed that the allele B19 and B2 exhibited predominance in this genetic group while genotypic distribution revealed abundance of B19B19 followed by B2B2 in the selected population of birds.

TS-II-59

MOLECULAR CHARACTERIZATION OF B-Lβ II FAMILY ALLELES IN HUBBARD CHICKENS

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The present study was planned to investigate the polymorphism of MHC B-Lβ II family (class II) alleles and genotyping using one of the variants of polymerase chain reaction (PCR), the PCR-SSP (Polymerase Chain Reaction with sequence specific primers) in Hubbard chickens. Genomic DNA was isolated from blood of 30 Hubbard birds maintained at experimental poultry unit at College of Veterinary Science and Animal Husbandry, N. D. V.

S. U., Jabalpur. A 235 bp, exon-2 region of chicken MHC B-Lβ family was amplified using a set of degenerating primers. The amplicons of the first round of amplification were subjected to PCR-SSP at the specified annealing temperatures and replication cycles. The primers designed for B2, B13, B15, B19 and B21 haplotypes amplified the target sequences producing a 222 bp, 141bp, 213 bp, 213 bp and 222 bp fragments, respectively. The findings of the research revealed nine genotypes *viz.*, B2B2, B2B15, B2B19, B21B21, B15B15, B13B15, B13B19, B19B21 and B21B21. It was observed that the allele B19, B15 and B2 exhibited predominance in this genetic group. Moreover, genotypic distribution also revealed higher occurrence of B15B19 and B2B19 heterozygotes in the selected population of birds.

TS-II-60

STUDY OF EXPRESSION AND EPIGENETIC REGULATION OF MYOSTATIN GENE IN CHICKEN

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Myostatin gene (MSTN) is one of the important growth regulatory genes in chicken. Several studies have proven that the mutation in MSTN gene has resulted in higher growth of skeletal muscles in livestock species but the mechanism of switching off and on of this gene is unknown, present work was carried out with the objectives of exploring expression and epigenetic regulation of Myostatin gene (MSTN) in chicken. This study was carried out on Control Broiler (CB) and Control Layer (CL) at ICAR-Directorate of Poultry Research (ICAR-DPR), Hyderabad. PCR-SSCP and sequencing revealed that MSTN gene promoter was highly polymorphic. SSCP pattern of MSTN gene promoter revealed 16 haplotypes in CB and 12 in CL. Number of haplogroups observed in CB was 28 and in CL was 21. Nucleotide variability revealed 18 SNPs in different haplotypes of MSTN gene promoter. Expression study of MSTN revealed high expression of MSTN gene at d0 and wk2 in CL, but it was very low in CL. As myostatin is negative regulator of the growth, it may be one of the reasons of low growth in CL as compared to CB. Methylation pattern study of promoters of MSTN gene revealed that the occurrence of methylation occurs at only cytosine in genome. Methylation was inversely proportional to the level of expression of the MSTN gene in CB and CL. Some of the haplogroups having highest body weight (h1h16) and lowest body weight (h4h5) at different age intervals have the prospects of being used as marker.

TS-II-61

DIFFERENTIAL GENE EXPRESSION OF TLR3 AND TLR4 GENES AMONG LYMPHOID TISSUES AND BREEDS

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Toll-like receptors (TLRs) play an important role in innate immunity, by recognizing pathogen specific motif and exerting downstream effects through different signaling pathways which in turn controls transcription of cytokine genes which are major players in development of adaptive immunity. Variable expression patterns of TLR genes among tissues and breeds have been reported. Present investigation was carried out to determine the relative mRNA expression of TLR3 and TLR4 genes at basal level in bursa, spleen and thymus tissues of Kadaknath (K), Rhode Island Red (RIR) and White Leghorn (WLH) chickens. Four birds, two of either sex, from three breeds were randomly chosen at the age of 6-8 weeks and relative quantification of mRNA was done by qRT-PCR using DyNAmoColorFlash SYBR Green qPCR Kit® and CFX 96® - Real Time PCR detection system. The data on 40-ΔCt values were analysed by least-squares analysis of variance using JMP 9.0.0 of SAS, 2010 taking genotype as fixed and tissue within genotypes and sex within tissue within genotype as nested effects. Expression of TLR3 and TLR4 genes differed significantly ($p \leq 0.01$) among tissues within genotype. The maximum TLR3 expression was observed in bursa of WLH with mean 40-ΔC_t value as 36.752±0.876, which was statistically similar to those in bursa (35.220±0.876), thymus (34.062±0.876) and spleen (33.642±0.876) of Kadaknath, spleen of WLH (33.410±0.876) and RIR (32.852±0.876). The mean 40-ΔC_t value for TLR4 was maximum in bursa of WLH (39.527±0.782) which was non-significantly different than those in bursa of Kadaknath (38.982±0.782), spleen (38.037±0.782) and thymus of WLH (36.030±0.782), spleen (37.292±0.782) and thymus (36.875±0.782) of Kadaknath, but was more than thymus of RIR (28.647±0.782), spleen of RIR (26.857±0.782) and bursa of RIR (23.457±0.782). The mRNA expression of TLR3 and TLR4 genes differed significantly among genotypes. The mean 40-ΔC_t values for TLR3 gene in Kadaknath (34.308±0.506) and WLH (33.804±0.506) did not differ significantly, but were higher ($p<0.05$) than that in RIR (32.008±0.506). Similarly, the mean 40-ΔC_t value for TLR4 gene in Kadaknath (37.716±0.451) and WLH (37.865±0.451) did not differ but were significantly ($p<0.001$) higher than RIR (26.320±0.451). The study revealed the existence of wide variation in basal expression of TLR3 and TLR4 genes among different tissues and breeds.

TS-II-62

PCR-SSCP AND DNA SEQUENCING OF Mx1 GENE IN JAPASESE QUAIL

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Constant efforts to increase the production potential of poultry compromised their disease resistance traits due to negative genetic correlation. Chicken Mx1 gene which was reported to provide genetic resistance against avian influenza virus was not studied earlier in Japanese quail in India. Our current research work was focused to identify the genetic variations in Mx1 gene in Japanese quail. So the present work was undertaken to identify variations in Mx1 gene in quail. A 148 bp fragment in 5th exon of quail Mx1 gene was screened using PCR-SSCP technique in 170 birds. The SSCP analysis revealed four different patterns i.e. AA, BB, CC and DD. The genotype frequency of BB was highest (0.44), followed by AA (0.24), CC (0.18) and DD (0.14). The allelic frequencies for A, B, C and D were found to be 0.24, 0.44, 0.18 and 0.14, respectively (B allele being predominant). The four alleles (A, B, C and D) of 148 bp fragment of Mx 1 gene of Japanese quail were sequenced. The alignment of the allelic variants showed differences at 7 positions among these alleles depicting the polymorphic nature of Mx1 gene. Hence, there is a need of wide search for detection of polymorphism in different regions of Mx1gene of quail and its possible association with the traits of economic importance.

TS-II-63

GENERATION OF MITHUN-SPECIFIC MICROSATELLITES: NEW BEGINNING OF MITHUN GENETICS

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Mithun (*Bos frontalis*) is considered as the living wealth of the tribals of North Eastern Hill Region of India. Considering the importance of this species, there is an urgent need in the development of genetic markers to estimate genetic diversity in the mithun population, and implement genetic improvement programmes. Microsatellite

markers are very useful because they are usually highly polymorphic, co-dominant and multi-allelic in nature. Genetic characterization of mithuns is being taken up using cattle microsatellite markers. However, to date there are no mithun-specific markers available. Hence, the purpose of this study was to isolate and characterize microsatellites specific for mithuns. Genomic DNA is digested with a four base cutter and purified. Around 20bp adapters were ligated to the purified digested DNA fragments. The DNA is then denatured to produce single stranded fragments, which is hybridized to biotinylated microsatellite probe molecules. Streptavidin coated Magnetic beads are added to the above mixture for enrichment. Since the microsatellite probes are attached to the beads, and any DNA fragments containing microsatellites are hybridized to these probes, the microsatellite DNA is also pulled out of solution. This procedure separates the DNA of interest from the rest of the DNA which does not contain the selected microsatellites. The selected DNA is then amplified using primers designed to the linkers, cloned into a vector, and sequenced. Sequencing of these clones enables primers to be designed for each microsatellite locus. A total of eight microsatellites were generated for mithun in this procedure. These were found to be mithun-specific and their primers, PCR conditions etc were standardized. These eight newly developed microsatellites were submitted to Genbank (KJ458991, KJ458992, KM462188-462193). The amplicon sizes ranged from 74 to 216 bp, while observed heterozygosity values ranged from 0.44 to 0.78 and polymorphic information content (PIC) ranged from 0.39 to 0.76. These are highly polymorphic novel microsatellites for mithun and will be immensely useful for estimation of genetic diversity and population studies of various mithun strains.

TS-II-64

ALLELIC DIVERSITY AT MHC CLASS II LOCI FAVOURS ADAPTIVE FITNESS IN INDIAN YAK (*BOS GRUNNIENS*)

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Major histocompatibility complex (MHC) is the most diversified and evolutionarily important region of the genome in vertebrates. Diversity at the MHC loci directly affects the adaptation and survival of a species and provides a measure of the fitness of the population. As a new thrust in conservation programmes of some of the endangered wild animal species, increasing the MHC diversity in population is being adopted as an important strategy. In this study, the efforts were made to unravel the allelic diversity at MHC (*Bogr*) class II DQ loci in domestic Yak (*Bosgrunniens*), a bovine species of alpine region of India, which seems to be at risk due to its small, scattered and declining population. Genomic regions corresponding to exon 2 of DQA and DQBgenes of indigenous Arunachali yaks (n=37) were amplified and directly sequenced. However, to identify more number of alleles, the PCR productsof DQA and DQB genes with heterozygous condition at DQ loci were cloned. The positive clones having inserts of different alleles were confirmed by colony PCR-RFLP using *Hae*III and *Hinf*I enzymes and further sequenced. At *Bogr*-DQ loci, most of the animals showed very high nucleotide variation between the two alternate allelic forms in heterozygous condition. A total of 13*Bogr*-DQA alleleswere identified. Phylogenetic analysis revealed the clustering ofmost of the alleles into two major sub-groups- DQA1 and DQA2, however, three DQA alleles were found to be most diverged. AtBogr-DQB locus, a total of 18 alleles were identified in yak. The alleles were found to be grouped into two major and highly diverged sub-groups. As an estimate of evolutionary divergence between the alleles, overall average number of base substitutions per site was found to be very high for both kind of loci (0.138 for DQA and 0.078 for DQB). dN/dS values based on variability in exon 2 region for DQA and DQB alleles was much higher than 1, indicating positive and adaptive selection for these loci. Presence of three or four different clones of DQA and DQB in animals indicated duplication of DQ genes in yak. Results revealed higher allelic diversity at DQ loci in indigenous yak, positively indicating the adaptive fitness of the population against the pathogens. Presence of duplicated DQ loci further widens the range of recognition of pathogen-derived antigens thereby increasing the overall fitness.

TS-II-65

MOLECULAR CHARACTERIZATION OF NEW ZEALAND WHITE AND APAU BLACK RABBITS USING MICROSATELLITE MARKERS

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Genetic diversity and phylogenetic relationship were investigated in two genetic groups (New Zealand White and APAU Black) of rabbits with a set of 20 microsatellite markers (12 rabbit specific and 8 cross species). Genomic DNA was isolated from blood, which had a mean optical absorbance ratio (260/280nm) of 1.493 while the mean quantity of DNA was 1.065µg/µl. The results showed that out of 20 microsatellites, 12 rabbit specific markers were successfully amplified by PCR which were highly polymorphic and no positive results were obtained for cross species loci revealing that the primers designed for cattle, buffaloes, sheep and goats utilized in the present study are not amplified in the New Zealand White and APAU Black rabbits. A total of 257 alleles (124 in New Zealand White and 133 in APAU Black) were observed across the 12 loci amplified. Number of alleles ranged from 5 to 14 and 5 to 16 in New Zealand White and APAU Black populations respectively. The overall mean values of observed heterozygosity (Ho value0.554 in New Zealand White and 0.556 in APAU Black), expected heterozygosity (He value 0.870 in New Zealand White and 0.875 in APAU Black), Polymorphic Information Content (PIC value 0.856 in New Zealand White and 0.862 in APAU Black) and the mean effective number of alleles (Ne value 8.629 in New Zealand White and 8.876 in APAU Black) of these two genetic groups were high, which indicated that polymorphisms and genetic diversity of genes were abundant. Out of the 12 amplified loci 7 loci deviated significantly from Hardy - Weinberg equilibrium in New Zealand White and 5 loci deviated in case of APAU Black which may be due to selection followed. The mean F_{IS}, F_{IT} and F_{ST} values over all the population are found to be 0.377, 0.402 and 0.040, respectively.The results suggested that the 12 amplified rabbit specific microsatellite loci were effective markers for analysis of genetic relationships among rabbit populations and supported their suitability for genetic diversity studies and this can be used for designating priorities for their breeding.

TS-II-66

SEX DETERMINATION OF ORNAMENTAL BIRDS BY USING POLYMERASE CHAIN REACTION

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The present study was carried out to standardize sex determination protocol in ornamental birds by PCR based method. A total of 38 feather samples were collected from birds across avian species viz. *Aratinga solstitialis*, *Ara militaris*, *Psittacus erithacus*, *Psittacula cyanocephala* and *Cacatua sulphurea* maintained by the Veermata Jijabai Bhosale Udyan (Mumbai Zoo), pet clinic and private owners in Mumbai, Maharashtra. Genomic DNA was successfully extracted from the feather samples by using two different protocols. The quality of DNA varied depending on the sample type and size. Comparatively higher DNA concentration was obtained from along with huge amount of RNA. The P2/P8 and 2550F/2718R primer sets amplified CHD genes at an annealing temperature of 55 ^{0}C. The primer set P2/P8 successfully amplified the CHD genes in all species except for three samples (two in *Psittacus erithacus* and one in *Aratinga solstitialis*). Two bands approx. of 380 bp and 400 bp sizes were recorded in females,

whereas, single band (approx. 380 bp) in males in all the species was detected, using P2/P8 primers. In all the species except for *Psittacula cyanocephala,* females were identified with two bands (450 bp and 650 bp) and males with single band (650 bp) by using 2550F/2718R primer sets. In *Psittacula cyanocephala,* females showed only single band of approximately 450 bp size (CHD-W) while no amplification of CHD-Z gene was observed in both the sexes with 2550F/2718 primer. CHD gene amplification by P2/P8 and 2550F/2718R primer sets proved to be a convenient and reliable method for accurate sex determination in the species studied.

TS-II-67

DEVELOPMENT OF GENE CONSTRUCT CONTAINING HUMAN TISSUE PLASMINOGEN ACTIVATOR

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The commercial potential for transgenesis is substantial, particularly in the fields of animal and plant agriculture. Transgenesis offers a powerful tool to introduce useful genes selectively from diverse sources into the genome of targeted organism. However, the most visible application of transgenic technology in farm animals has been to produce human proteins of pharmaceutical value, which are required in minute quantities and serve as life-saving drugs. Conventionally these are isolated from the blood or other biological fluids and are very expensive to produce. However, using transgenic technology, it has been possible to make these express in mammary tissue and secrete through milk in large quantity, thereby the cost of production has been reduced dramatically. With the availability of modern technologies, the transgenic animal produced can be cloned to ensure continuous supply of the desired protein now. The human tissue plasminogen activator (htPA) is a protease capable of fibrinolysis and has been shown to have efficacy in the treatment of clotting disorders. In the present investigation, promoter and regulatory elements of ovine beta lactoglobulin (oBLG) gene was chosen to drive the expression of human tissue plasminogen activator (htPA) gene in a mammary gland specific manner. Fresh blood was collected from Sheep and its genomic DNA was extracted using Genomic DNA Extraction Kit (Promega, USA) to obtain high molecular weight DNA template for long-PCR. All primers used in the experiments were designed critically to include appropriate overhang RE sites. Two pairs of PCR primer were designed to amplify oBLG gene using Expand Long Template PCR System (Roche, Germany): 5′UTRF– 5′UTRR and 3′UTRF –3′UTRR. The first pair amplified 3.408 kb of the 5′ flanking region and promoter in addition to transcription unit up to second exon; the second pair of primers amplified 2.507 kb 3′UTR of oBLG gene including part of transcription unit. Both PCR products were cloned separately into pTZ57R/T using InsTAclone PCR Cloning kit. After primer designing and PCR standardization, a 1.709 kb fragment, pertaining to cDNA of htPA gene transcript variant 1, has been amplified with primers tPF and tPR containing appropriate overhang RE sites. The PCR product was verified by agarose gel electrophoresis, purified by gel extraction kit (Qiagen) and cloned into a plasmid vector pTZ57R/T using InsTAclone PCR Cloning kit. All the above cloned fragments viz., 5′UTR, 3′UTR and htPA were subjected to restriction digestion separately with *Asc*I, *Xho*I and *Asc*I, respectively and the resultant fragments were resolved by 1% agarose gel electrophoresis. As anticipated, 6.294, 5.410 and 4.595 kb fragments were obtained corresponding to 5′UTR, 3′UTR and htPA respectively which included the length of each fragment plus vector backbone of 2.886 kb. Cloned fragments were further validated through sequencing and checked for possible mutational error. Finally, different fragments were joined together using optimized strategy.

TS-II-68

SEQUENCING ERROR IN POLYADENINE REPEAT CHROMATOGRAM READINGS OF RXFP2 FRAGMENT

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The sequencing of RXFP2 fragment by single pass method using forward primer used for PCR amplification resulted in good sequencing chromatogram but the reverse primer even on repeated attempts failed to give desirable sequencing chromatogram and showed noisy mixed peaks. The RXFP2-II sequence data just based on forward sequencing revealed a deletion of a nucleotide A (CAAG instead of CAAAG) at 28th nucleotide of the amplicon, which would be major deletion mutation leading to non-functional RXFP2. The same result was obtained for all the samples analyzed. Cloning of the RXFP2-II fragment into pGEMT vector and sequencing with SP6 primer revealed no deletion (CTTTG), indicating the sequencing error in single pass method of sequencing. The error in poly single nucleotide repeat region could be either due to error during PCR amplification or chromatogram reading. Similar results form several samples analyzed ruled out the error due to PCR amplification. Findings support the fact that, the sequence chromatograph reading error is more in A/T run homopolymers rather than G/C runs. The chromatograph in polyA regions tended to become wavy, especially when present within 25-35 nucleotides of the sequencing PCR product. Sequencing through a poly-A in a plasmid usually works better than in PCR. Thus vector cloned sequencing with reconfirmation of the sequence by reverse primer is to be adopted before declaring SNP in the amplified products with poly A tracts.

TECHNICAL SESSION – III

Livestock keepers / breeders′ association and legal framework, policies and programmes for development of AnGR

INVITED PAPERS

1. BIO-CULTURAL PROTOCOLS OF TRADITIONAL LIVESTOCK KEEPING COMMUNITIES AND THEIR ROLE IN THE CONSERVATION OF AnGR

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Abstract

Biocultural Community Protocols (BCPs) are a tool supported by the Nagoya Protocol on Access and Benefit-Sharing under the UN Convention on Biological Diversity (CBD). This paper argues that it is urgent to facilitate BCPs for all Indian livestock keeping communities in order to achieve sustainable livestock development at the national level. It also raises the question whether it would not be more important to focus on the conservation of livestock production systems rather than the conservation of breeds.

Paper

The *Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity* is an international agreement which aims at sharing the benefits arising from the utilization of genetic resources in a fair and equitable way, including by appropriate access to genetic resources and by appropriate transfer of relevant technologies, taking into account all rights over those resources and to technologies, and by appropriate funding, thereby contributing to the conservation of biological diversity and the sustainable use of its components. It was adopted by the Conference of the Parties to the Convention on Biological Diversity at its tenth meeting on 29 October 2010 in Nagoya, Japan. It entered into force in October 2014, 90 days after the 50th ratification.

Small-scale livestock keepers have engaged for more than ten years with questions of access and benefit-sharing of AnGR, going back to the Karen Commitment that was issued by the representatives of pastoralists and indigenous livestock keeping communities in October, 2003 and in which they demand to *benefit equitably from the use of AnGRFA in their own communities and by others* (see Appendix 1).In side-events during CBD COPs 9, 10, and 11, livestock keepers have repeatedly drawn attention to their contribution to animal genetic resource conservation. Making the link between the survival of breeds and the survival of small-scale livestock keepers such as pastoralists, smallholders and family farms in a general policy environment that favours large-scale industrial modes of livestock production, they demand Livestock Keepers' Rights.

The term "Livestock Keepers' Rights" was coined during the World Food Summit in 2002 by civil society attending the Forum for Food Sovereignty to flag the role of livestock keepers in animal genetic resource management. It alluded to "Farmers' Rights" as known from the International Treaty on Plant Genetic Resources for Food and Agriculture that had been recently concluded (Köhler-Rollefson et al. 2010).

Between 2003 and 2007, a large number of grassroots consultations were carried out by and with livestock keeping communities to define the term more closely. These consultations took place in Kenya "Karen Commitment"), India, Italy ("Bellagio Brief") and Ethiopia ("Addis Résumé") and involved about 500 representatives of livestock keeping communities from Africa, Asia, Latin America and Europe. They identified 7 cornerstones of "Livestock Keepers' Rights" that would enable livestock keepers to continue playing their role as guardians of biological diversity (Köhler-Rollefson et al. 2010).

During this process, Livestock Keepers' Rights were elaborated into a much more comprehensive concept than Farmers' Rights. Rather than representing legal rights, they correspond to development principles that would help livestock keepers continue to conserve biodiversity.

Principles and Rights

During a workshop with legal experts held in Kalk Bay, South Africa in December 2008, the rights were further refined and subdivided into principles and rights:

Principle 1:*Livestock Keepers are creators of breeds and custodians of animal genetic resources for food and agriculture.*

Principle 2:*Livestock Keepers and the sustainable use of traditional breeds are dependent on the conservation of their respective ecosystems.*

Principle 3:*Traditional breeds represent collective property, products of indigenous knowledge and cultural expression of Livestock Keepers.*

Based on these principles articulated and implicit in existing legal instruments and international agreements, Livestock Keepers from traditional livestock keeping communities and/or adhering to ecological principles of animal production, shall be given the following Livestock Keepers' Rights:

1. *Livestock Keepers have the right to make breeding decisions and breed the breeds they maintain.*
2. *Livestock Keepers shall have the right to participate in policy formulation and implementation processes on animal genetic resources for food and agriculture.*
3. *Livestock Keepers shall have the right to appropriate training and capacity building and equal access to relevant services enabling and supporting them to raise livestock and to better process and market their products.*

Livestock Keepers shall have the right to participate in the identification of research needs and research design with respect to their genetic resources, as is mandated by the principle of Prior Informed Consent.

Livestock Keepers shall have the right to effectively access information on issues related to their local breeds and livestock diversity.

Declaration on Rights

The Kalk Bay workshop also resulted in a Declaration on Livestock Keepers Rights that references the individual principles and rights to existing international legal frameworks such as the UN Convention on Biological Diversity, the United Nations Convention to Combat Desertification, the Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration on Animal Genetic Resources, as well as the Universal Declaration of Human Rights, the International Covenant on Economic, Social and Cultural Rights, the United Nations Declaration on the Rights of Indigenous Peoples, the Convention on the Protection and Promotion of the Diversity of Cultural Expressions, the Convention (No. 169) concerning Indigenous and Tribal Peoples in Independent Countries, the Declaration on the Rights of Persons belonging to National or Ethnic, Religious and Linguistic Minorities, and other pertinent legal agreements (LPP n.d.).

The Declaration on Livestock Keepers' Rights was signed by a large number of individuals and organizations. Subsequently, the participants of the International Technical Expert Workshop on Access and Benefit Sharing in Animal Genetic Resources for Food and Agriculture that was held in Wageningen in the Netherlands from 8–10 December 2010, recommended that "Livestock Keepers' Rights should be better addressed" (FAO 2011).

As there is currently no international process leading towards a legally binding or voluntary agreement in which Livestock Keepers' Rights could be embedded, livestock keeping communities have started developing Biocultural Community Protocols (BCPs) in which they seek to establish their status as an indigenous or local community stewarding genetic resources under Article8j of the CBD. While the methodology still needs to be improved, the BCPs make visible the linkages between breeds and the communities that have developed them and they also establish breeds as the "prior art" of communities and they therefore represent community claims over animal genetic resources.

"BCPs" comply with the notion of community protocols advanced by the Nagoya Protocol which in its Article 12 states that "Parties shall endeavour to support, as appropriate, the development by indigenous and local communities, including women within these communities, of:

(a) *Community protocols in relation to access to traditional knowledge associated with genetic resources and the fair and equitable sharing of benefits arising out of the utilization of such knowledge;*

(b) *Minimum requirements for mutually agreed terms to secure the fair and equitable sharing of benefits arising from the utilization of traditional knowledge associated with genetic resources; and*

(c) *Model contractual clauses for benefit-sharing arising from the utilization of traditional knowledge associated with genetic resources."*

During a conference about the future of livestock keeping that was held in Bonn on 6-7th September, 2012, one of the working groups discussed "Biocultural Protocols and Approaches to Access and Benefit-Sharing for Animal Genetic Resources" (LPP 2012). This working group noted that livestock in traditional communities has both private and public goods characteristics.As livestock breeds represent specific combinations of genes and are also the result of collective breeding, it concluded that benefits should be shared on one hand, but not be linked to direct access to genes. The working group also regarded BCPs as a useful tool for communities to establish breeds as their "prior art" and as a means of claiming ownership over AnGR and raising awareness about a community' contribution to breed development.

The working group also discussed that small-scale livestock keepers provide a collective service by maintaining breeds and stewarding eco-systems. These services can be rewarded monetarily at national level through payments for environmental services, such as carbon sequestration and biodiversity conservation. Furthermore, they can be rewarded through the provision of an enabling environment that supports them to continue their livelihood and breed conservation activities (livestock keepers rights, grazing rights, services). It recommended establishment of a benefit sharing fund/pool at international level to support communities which maintain and use local breeds.

Conditions for receipt of funds would be that the beneficiaries have a BCP in place. Furthermore, communities should have direct access to the Benefit-sharing fund (no obligatory government involvement).

All in all, BCPs are an approach to save not just a breed, but an entire production system, including the livelihoods of livestock keepers. In fact, the breed may change, as is illustrated by the example of the nomadic shepherds from Rajasthan who several decades ago kept the Boti sheep breed, but have since experimented with new breeds that they have come across during their migrations. The important issue from the perspective of food security is that their production system is upheld and that they have the appropriate genetic resources for that purpose, rather than sticking to a particular breed.

2. LIVESTOCK BREED SOCIETIES IN INDIA: STATUS AND A VISION

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Introduction

The act of breed characterisation and conservation has successfully been brought into the public arena by the strong institutional support system, especially during the last two decades. There is an increase in the general awareness on the importance of indigenous breeds in terms of their local adaptations, local livelihoods and local nutritional support, and the attempts at saving the breeds with vibrant joint support from NGOs and civil society has started showing results. It is time the thus far attained 'local awareness' is transformed into 'local forces' to attend to the local breeds before any further dilution of the locally defined robust populations. In view of the important role of the breed societies, it is expected that establishing more Breed Associations/Societies in the country will bring in the local support to save the breeds, and also to nurture these for strengthening local livelihoods in a sustainable manner.

A Breed Society

A Breed Society is an officially recognised association of people with common interest in respect of managing the breed. Aims and objectives of a breed society generally include: improvement of the breed, maintenance of purity of the breed, supporting the breed as well as the livestock keepers maintaining the breed, arranging breed-shows to highlight importance/ uniqueness and relevance of the breed to the local/regional milieu. The two terms 'Breed Association' and 'Breed Society' are often used interchangeably; the former is more used in Americas while the latter is more common in Europe.

It is the common interest of improvement or development of a breed which draws people together so that the benefits from the breed can be enhanced or the breed is made more sustainable for long term contributions to the local society. As one consequence, increased utilisation of the breed leads to its conservation. Many-a-time conservation itself is the main aim of the society - either explicit or implied.

Breed Societies in the country

India can not boast of many Breed Societies like in Europe, or Breed Associations like in Americas. Touching the figure of one dozen in the country, there are still fewer Societies that are functional and communicative. Some Societies like for Horses and for Banni Buffaloes make exemplary cases. Their initiation, evolvement and working can auger establishment of newer breed societies in the country. This presentation draws from the few established Societies and attempts to explore 'how to initiate a new Breed Society'.

History of Breed Societies in India

Before the era of establishing breed societies, India has had stable systems around local livestock which acted like an association and met the objectives, even though these were not named or registered as an association or a society. In the earlier times, several kings are known to have acted as patrons of the local breeds. For example, Amritmahal breed in Karnataka was developed by the patronage of the kings. Similarly, the Parlakhemundi buffalo of Odisha also received patronage of the king.

In some cases of relatively recent times, villagers or the breeders maintaining a breed are associated to maintain a breed and have functioned as a loose Association. For example, Spiti horse (ponies) is managed by a few villages in Himachal Pradesh for the last several decades in the form of an open association and effectively acting like a society without bothering for registration as a breed society. A set of 15 villages in the breeding area of Spiti horse (Pin Valley) is the core area where Spiti horses are produced. The stakeholders in the valley are carrying out breeding of Spiti horses since ages. The breeders in this area sell the surplus stock as a source of livelihood. On a pre-decided day all the available stallions are paraded before a selection committee comprising of elderly and experienced people of the area. Selection criteria as acceptable to all is followed. The selected stallion is used for natural service within the few villages which share common pastureland. All other eligible male stallions in the villages are castrated. The owners of mares are required to pay a nominal fee (in cash or kind) on account of getting their brood-mares served by the selected stallion. This amount is utilised by the owner for the upkeep of the stallion.

At present, there are very few breed societies in India. Ongole society named as "The Ongole Cattle Breeders' Association" in Andhra Pradesh has the reputation of being one of the first breed societies in the country. It was started by one Mr Narendra Nath in erstwhile AP state, but detailed account of this society has not been documented and scarcely printed. After working for several years, it appears the society was not active until recently.

In Odisha, a Buffalo Breed Society named as "Chilika Buffalo Promoters' Society" was established during 2004 in Bhubaneshwar. It was during the formation of this society that the norms for establishing a livestock breed society in India were written and subsequently also used for establishing more breed societies, notably the 'Banni Buffalo Breed Society' named as 'Banni Pashu Uchherak Maldhari Sangathan' with the help of Sahjeevan NGO, and 'Gaolao Cattle Breed Society' in Nagpur, Maharashtra. A camel breed association is also planned by 'Sahjeevan' in Bhuj, Gujarat.

There are some Breed Societies on horses as well. Indigenous Horse Society has been established in Rajasthan [http://horseindian.com] which maintains standards of the Marwari, Kathiawari, Manipuri, Zanskari and Spiti breeds. In Maharashtra, a 'Deoni Breed Society' was reported to have been established. The same is not functional as of now. Other Societies are: Marwar Horse Society Jodhpur; Indigenous Horse Society of India, Jaipur; The Chetak Horse Society of India, Udaipur; Umbalacherry Breeders Association; Katchakatti Sheep Breeders Association; Vembur Sheep Breeders Association; Malai Madu Cattle Breeders Association

Major support to establishing breed societies in the country is noted in Tamil Nadu (mainly by SEVA, a Madurai based NGO), Gujarat (mainly by Sahjeevan, an NGO), Kerala and Rajasthan. In Kerala, there are four Breed societies viz. Vechur Conservation Trust (VCT), Kerala Local cattle Breeder's Society (KELOBS), Kasaragod Dwarf Conservation Society (KDCS) and Vadakara Cow Conservation Trust (VCCT).

Further, some initial activity for establishing breed society has been made by some thinkers as detailed in Annexure-2.

Formation of a Breed Society

Formation of a breed society needs social acumen, dedication on the part of the stakeholders and a team approach. Breeders maintaining the local breed, local sympathisers, researchers and conservators need to work together to form a breed society. This article presents the format for getting a society registered and delineates how to establish a breed society under the Indian conditions based on the examples of Chilika and Banni buffaloes.

There are two basic steps to forming a Breed Society.

(A) Getting together of the stakeholders of the breed

Once it is established that a society is to be formed for the breed at hand, a small group from the main stakeholders i.e. breeders, livestock keepers, farmers along with other promoters viz. scientists, interested scholars, animal husbandry and other officials join together and work for registration of the Breed Society. The breed undertaken at this stage may be a 'loose' breed, but the stakeholder group should be convinced that the animals make significant contributions, it should be maintained pure and the need is felt to develop it in a sustainable manner. It is very likely that a core group of stakeholders takes interest and makes arrangements for meetings to strengthen the cause of the breed development and also strengthen the communication within this group. The group would use the case studies of other breed societies in the country, draw analogies and establish communication with other breed societies in the country as well. It is necessary that the group works to establish the traits of the breed and also gather relevant information on the production, reproduction traits, adaptation level, capacities and the contributions of the breed. So much as possible, all norms of the breed and its environment need to be recorded. 'Environment' should include the local climatic conditions, feed-fodder regime, traditional knowledge, activities of the keepers and interactions with local agriculture.

(B) Registration of the Breed Society

A Breed Society is to be registered under the 'Society Registration Act' in the nearest Registration Office. Chilika Society was registered at Bhubaneshwar while the Banni Society was registered at Bhuj.

For registration, a document needs to be prepared giving details of the breed, objectives, rules/regulations etc. A sample document on Chilika Buffalo is available from the author by Email. First page is reproduced as Annexure-1.

Role of a Breed Society

Main objective of a Breed Society are: general welfare, improvement and overall development of the breed and the system surrounding the breed i.e. breed keepers and the facilitating environment including feed fodder resources, water-availability, value addition and utilisation of the products and by-products obtained from the breed. A breed society often has a cultural attachment with the breed as well. It can be argued that this cultural affinity is the outcome of special utility of the breed to the local people. The local breeds utilise the meagre resources in the vicinity which have little alternative value and also provide benefits to the local population in terms of nutrition and/or the much needed draft power.

Major membership of the society being the breeders and breed-keepers, there is increased local driving force in maintaining purity of the breed. It is well known that a breed in its own local area in combination with the local environment leads to a system of highest efficiency i.e. best input-output ratio. A breed society attempts to remove hurdles [including the use of external breeds] in the safe perpetuation of the breed.

A Breed Society can play different roles; it can arrange breed shows, and periodic events to highlight importance of the breed and the biodiversity. Chilika Buffalo Promoters' Society has participated in national events to highlight the uniqueness of the breed and its products. One notable product is curd prepared from Chilika milk which has a shelf life of a week at room temperature. Banni Breed Society is presently in its fifth year of existence and arranged 5th Pashu Mela in the breed tract in Gujarat. The society earlier reported an increase of 27% in the income of Banni buffalo keepers by way of sale of Banni buffaloes during the Banni Pashu Mela, since the Banni buffaloes are purchased from its tract in Bhuj to other parts of Gujarat and even up to Andhra Pradesh. Such benefits to the livestock keepers ultimately help in conservation of the breed.

Epilogue

Breed societies have made significant contributions to development of livestock breeds. In certain cases in the world, it has been the breed society that has conserved the local breed which otherwise might have gone extinct. Formation of a Breed Society is a positive step to supporting the development of the breed. An association or a society is seen as an embodiment of dedicated sympathisers of the breed who are convinced the breed is useful in the given area (often its breeding tract) and needs protection from further dilution or extinction. The society will find local ways and means to further developing and conserving the breed. There is a dire need to establish breed societies for all the local livestock breeds and strains in India.

- Annexure 1-

BYE LAWS OF THE CHILIKA BUFFALO PROMOTERS' SOCIETY BHUBANESWAR, ORISSA

1. Name, Address and Area of Operation

(i) THE CHILIKA BUFFALO PROMOTERS SOCIETY

(ii) Dr.R.Pradhan, M.V.Sc, Ph.D.(Vety.Med),Ph.D.(Alt.Med)D.Sc(IOUCM)

(iii) 4/4, IPDP Campus, Laxmisagar, Bhubaneswar, Orissa, India (Telephone No. 0674-2570726)

(iiii) The area of operation shall be extended to the entire State/Nation/ World as regards embership is concerned but the working jurisdiction will be places where CHILIKA BUFFALOES are habitant.

(v) It may be referred in this Bylaws briefly as SOCIETY.

(vi) Chilika Buffaloes may be referred as Chilika Buffalo Population or Chilika Population or Chilika Breed or Chilika Strain or simply as Chilika.

(vii) In the event of any change of address of the society notice of such change shall be sent in writing to the Register, Co-Operative Society, Orissa and to the Financing Bank and other funding Agencies within 15 (Fifteen) days of such change provided that any proposed change of address of the CHILIKA BUFFALO PROMOTERS SOCIETY can be effected only after permission in writing have been obtained from the Registrar

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- Annexure 2 -

List of workers who thought of or accepted to establish a Breed Society [this list is as per communications in regard with establishing a new breed Society, and is not purported to be an exhaustive list]

1. Dr R. Pradhan of AH Dept Odisha supported the idea during the Chilika Buffalo Project of NBAGR during 2001 which resulted into "Chilika Buffalo Promoters' Society". Norms for establishing a Breed Society were developed here. These norms were provided to subsequent cases #2 to #7, mentioned below, as a guideline to develop details for their breed.
2. Dr. K. Pradhan of AH Dept, Odisha (Retd) had accepted to establish Sambhalpuri Buffalo Society in Odisha during 2002.
3. Dr Sabyasachi Das of Sahjeevan (NGO) accepted to establish Banni Breeders' Society during September, 2007 which resulted into "Banni Pashu Uchherak Maldhari Sangathan".
4. Dr. K R Tajane of Sardar Krushinagar Dantiwada Agricultural University (Gujarat) desired to establish a Breed Society for Mehsana and for Kankrej during Nov., 2007.
5. Dr. Ranvir Singh of IVRI desired to establish a Sahiwal Society during 2012.
6. Dr. Hekha Mao of AH Dept Nagaland had desired to establish a Society for Pigs [EMail of28 Feb, 2011].
7. Shahaji Arvindrao Nalge at Kandhar distt Nanded and Dr B M Thombre, Parbhani, Maharashtra showed keen interest to establish Society for Red Kandhari cattle during 2014.

3. STRENGTHENING THE ROLE OF TRADITIONAL LIVESTOCK KEEPING COMMUNITIES TOWARDS CONSERVATION AND DEVELOPMENT OF BREEDS, PRACTICES AND RIGHTS

P. Vivekanandan, SEVA*, D.K. Sadana, NBAGR, Anil Gupta, IIMA and P.K. Singh, NBAGR
NBAGR & Ilse Köhler-Rollefson, LPPS

Introduction

Indigenous breeds habituated in different agro climatic zone of India have evolved over several generations of natural selection and domestication and are well adapted to their habitat and environment and are often a livelihood bastion for poor households because they are easier to keep than exotic breeds. They are capable of withstanding harsh climatic conditions, diseases and scarcity of feed, fodder and drinking water. In a world threatened by climate change, breeds that are resistant to drought, extreme climatic conditions or diseases are of major potential importance for the livelihood of rural poor.

Traditional pastoral communities in India such as *raikas, maldharis, gaddis, gujjars, yadavas, gawlis, todas, konars* etc., play important role in the society by keeping variety of livestock through nomadic or semi nomadic way of life. They conserve local livestock breeds which provide draught power, manure and valuable animal products such as meat, milk, wool to the society and contribute to the economy of our nations. Over the last 1½ decade the pastoral communities have been deprived off their grazing rights and they are marginalized leading to loss of local knowledge, breeds and livelihoods. In order to protect their lifestyle and animal production system there is need for policy level intervention.

India has rich repository of animal genetic resources with 144 registered breeds along with several population not yet recognized which needs characterization and recognition. Government policy for intensive agriculture, commercial livestock keeping discourages keeping native livestock breeds and it is therefore replaced with high yielding dairy animals or fast growing exotic species in order to maximize profit through production of meat, dairy products, eggs, fiber etc. Closing of forests / traditional grazing lands under the policy of “ protected areas / sanctuaries/ national parks ” poses major threats for customary practices of village poor /nomadic pastoralists who depend upon them for grazing their animals for their livelihoods.

Getting Government’s attention and creating awareness among those who actually conserve local breeds and attempting capacity building of such communities and livestock keepers will be the starting point in stopping decline of livestock genetic diversity. Improving knowledge of breeds and their production environments and developing suitable policies that support community level conservation for native breeds is very important. SEVA a NGO registered in 1992 has initiated much focused activities by working with livestock keepers and share their accumulated experience working at grassroots over the past two decade.

Breeders Association

SEVA has promoted pastoralists / herders/ tribals (todas – Nilgiris) groups / associations of livestock keepers to conserve Umbalacherry cattle, Toda buffalo, Kachakatti black sheep, Pulikulam cattle, Malaimadu cattle and Vembur sheep breeds and “*Korangadu*” pasture land in Nagapattinam, Ooty, Madurai, Virudhunagar, Sivagangai, Thoothukudi and Thiruppur districts of Tamil Nadu. SEVA facilitated local Panchayats to renovate common property resources (viz. animal drinking water ponds, tanks, bore wells in 14 places in Nagapattinam, Thoothukudi districts), arranged animal health camps, supplied breeding bulls and prepared action plan for conservation of 10 native animal breeds by involving all the stakeholders. In several cases, notably for *Umbalachery* cattle in Nagapattinam district, there has been a significant increase in population of the breed as an outcome.

The members of the association are breed keepers and they have been inculcated regular savings program. The association convene regular meetings and few workshops by collaboration with Government for addressing their local issues viz. animal grazing land, drinking water problem, animal disease, supply of bulls and construction of animal shed. SEVA has provided small revolving capital to extend micro credit program to the members.

Herbal treatment for animals

SEVA has organized farmers training programme (2-3 days) to popularize low cost herbal treatment for animals in Tamil Nadu (55 villages), Karnataka (2 villages), Kerala (3 villages) and more than 5,000 farmers / livestock keepers were benefitted. SEVA has trained 120 youth in herbal treatment for animals through 4 weeks training module and now they are becoming the expert community animal healers in villages. Recently the outbreak of Foot and Mouth Disease devastated and more than 10,000 cattle and small ruminants in Tamil Nadu died and the herbal treatment (based on traditional knowledge) saved more than 500 animals through low cost herbal treatment which any farmer can prepare by himself.

Articulating Livestock Keepers Rights

LIFE Network Network members have developed the concept of Livestock Keepers Rights and it is being articulated in many national and international fora and it is to be implemented by governments in order to realize the benefits for those who conserve native breeds of animals. It includes 3 principles and 6 rights.

Principle 1: Livestock keepers are creators of breeds and they are the practical custodians of animal genetic resources for food and agriculture to the society.

Principle 2: Livestock keepers and the sustainable use of traditional breeds and their products are dependent on the conservation of their respective ecosystems and their continued access to such natural resources .

Principle 3: Traditional breeds represent collective property, products of social culture or indigenous knowledge and innovation and practices developed by livestock keepers.

Based on these principles articulated and implicit in existing legal instruments and international agreements, livestock keepers from traditional livestock keeping communities and /or adhering to ecological principles of animal production, shall be given the following livestock keepers' rights:

1. Livestock keepers have the right to make breeding decisions and breed the breeds they maintain including keeping bulls of local breed for natural mating.
2. Livestock keepers shall have the right to participate in any policy formulation and implementation processes (on animal genetic resources for food and agriculture / joint forest management / forest working plan etc) which affect their life style, customary practices, pasture land and breeds they maintain .
3. Livestock keepers shall have the right to graze their animals in traditional grazing lands including forests or protected areas as per Forest Rights Act 2006 / National Policy for Farmers (2007), their migratory routes recognized and accessible to veterinary services during migration.
4. Livestock keepers shall have the right to appropriate training and capacity building and equal access to relevant services enabling and supporting them to raise livestock and to better process, market their products and to enable their status and income .
5. Livestock keepers shall have the right to be rewarded for their efforts in keeping the local breeds as provider of services to the society and compensated if their animals / animal materials are taken for breed multiplication or commercialization purpose with their prior informed consent.

6. Livestock keepers shall have the right to participate in the identification of research needs and research design with respect to their genetic resources and access information on issues related to their local breeds and livestock diversity.

Traditional pastoral communities in our country are known for keeping indigenous livestock breeds. These breeds are maintained in herds under migratory or semi-nomadic trans-human system. During rainy season the customary practice of pastoralists grazing their livestock in forests has been officially permitted from pre-independence times. However once the Joint Forest Management programme was implemented during 1996, grazing in the forest areas has been withdrawn and the pastoralists are excluded in participatory planning. In association with LIFE Network NGOs and volunteers SEVA lobbied for their grazing rights in forests and it has been successfully incorporated in "The Scheduled Tribes and other Traditional Forest Dwellers (Recognition of Forest Rights) Act, 2006" (refer Section 3(1)(d)). In this regard he made case studies / community protocols of *Vangujjar* pastoralists in Himalayan forests, *Lingayats* communities in Bargur forests (Erode), *Malaimadu* cattle pastoralists in western ghats and working for their animal grazing rights in forests. SEVA has filed a petition with Central Empowered Committee of Supreme Court of India for restoring grazing rights of Raika camel pastoralists and Malaimadu cattle herders during 2009. National Policy for Famers 2007 has incorporated pastoralists rights under section 6 of special categories of farmers.

Breed Saviour Awards for Conservation of Livestock Breeds

Recognition of ground-level efforts leading to conservation of indigenous breeds is a moral boosting approach for the livestock keepers. Recognition through cash & kind awards also carries a positive message amongst the keepers and other stakeholders for accepting the importance of the local breeds and for developing renewed perspectives on the relevance of the local breeds in the local milieu. The concept of such Awards was developed during 2008 by members of the LIFE Network and Honey Bee network (a loose network of NGOs and individuals working on animal genetic resources and grassroots knowledge and innovations in the country). The issue was further discussed in a LIFE Network meeting at NBAGR, Karnal on the 2nd September, 2008. SEVA, an NGO working on Animal Genetic Resources liaised with National Biodiversity Authority (NBA), Chennai to arrange necessary funds. Financial support was also provided by LPPS (Lokhit Pashu-Palak Sansthan, http://www.lpps.org/), an NGO. Necessary performa were developed and the modus of gathering cases and details on conservation at the field level from different parts of the country was finalized during 2008 by the members of LIFE Network. The first Breed Saviour Awards were given in 2009 in the presence of the NBA chairman and have since been continued annually with the financial support from the NBA. Thus far given to a total of 104 breed saviours during the last five years, the awards have covered 52 recognized breeds and also the following defined populations: Gangatiri cattle, Belahi cattle, Kasargod cattle, Zo-Bawng cattle, Himalayan cattle, Mizo cattle, Binjharpuri cattle Nattumadu cattle, Malimadu cattle, Gojiri buffalo, Rairakhol buffalo, Ari-Adu sheep, Chevvadu sheep, Bhagli sheep, Boti sheep, Katchakatty Black sheep, Nattu Karuppadu goat, Alwari goat, Kharai camel, Ankamali pig, Hanseel poultry, Hajra Poultry, Indian Runner duck, and Kuji duck. The Awards recognised the presence of these defined populations which warrant further attention of different agencies as some of them are strong candidates for registration and further efforts at conservation at the official level. The award functions have highlighted the presence of such populations in different parts of the country, and it is encouraging to note that some of the defined populations that had been recognized by the Awards were subsequently accepted and registered at the national level, e.g. Banni and Chilika buffalo, Pulikulam and Malnad Gidda cattle. This is unique effort deserving of more attention and support.

Annexure - I

Karnal Declaration for Conservation and Augmentation of Indigenous Livestock Breeds

The participants of **National Workshop on Livestock Keeper's Rights & Breed Saviour Award Ceremony At NBAGR, Karnal during July 8-11, 2014** have passed on the following resolution to adopt Karnal declaration on 9 July 2014.

1. Breeder's Associations should be established for each of the livestock and poultry breed in the respective breeding tract. These associations should be linked registered with National level authority /Foundation or through a federation of animal breeders association and should meet at least once in a year to exchange the experience and views in different aspects of management of animal genetic resources.
2. National authority on animal genetic resources may be established to register, conserve and augment indigenous animal breeds. Such authority should be established under umbrella of an Act of Indian constitution. It shall promote capacity building of livestock keepers conserving native breeds through incentives and enable them access to grazing land, drinking water, shelter, health and bull services, credit and marketing their products and for industrial utility.
3. The conservation of livestock and poultry breeds can be successful in true sense only under in-situ mode along with conservation of respective eco-systems. Therefore, conservation of pasture land and associated water and eco-systems are essential so as to conserve livestock and poultry diversity.
4. Computer applications should be developed on tablet or mobiles for pedigree and performance data recording of the livestock and poultry breeds on different aspects of management, habitat and climate adaptive potential. For this purpose training of livestock keepers and their children may be taken up at large scale.
5. Every member of parliament and legislative assembly should be persuaded for the expenditure of 5% of their funds on conservation of local breeds
6. Veterinary science UG/PG students should study and document animal breeder communities and their way of managing animal genetic resources during internship program for at least one month period with their stay in the villages.
7. Women's knowledge about livestock breeds behavior, psychology, peculiar habits, management needs etc. should be recorded and documented. Special training should be given to the women for empowering them with respect to management of animal genetic resources.
8. National awards should be given to the livestock keepers, communities for their contribution in conservation of livestock diversity as well as eco-system especially pasture land.
9. Identification of markers and other indicators to enable children of breeders to maintain purity of breeds. A special scholarship scheme for encouraging youth to conserve breeds and as fixated knowledge systems.
10. Document outstanding practices / innovations of breed conservators and link with National Register of grassroots innovations and traditional knowledge of National Innovation Foundation for dissemination / recognition / rewards.

4. ROLE OF RAINFED LIVESTOCK NETWORK IN CONSERVATION AND IMPROVEMENT OF LIVESTOCK BREEDS IN INDIA

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The Rainfed Livestock Network (RLN) came into existence about five years ago when various NGOs working with livestock keepers in different parts of the country felt a need to unitedly work in more networked manner and in a joint action mode to be more effective. RLN is anchored by the Foundation for Ecological Security (FESbased at Anand, Gujarat.

RLN is a consortium of organizations that work in the livestock and natural resource management (NRM) sectors. Thebase membership consists of WOTR(Watershed organization trust based in Pune,Maharastra working in seven states),ANTHRA (Pune, Maharashtra),SAHJEEVAN(Bhuj,Gujarat), LPPS (LokhitpashupalaksanghatSadri and Jaisalmer in Rajasthan) and FES(Foundation for ecological security based in Anand, Gujaratworking in ten States)

Objectives

The network's core objective is to strengthen the knowledge, information and analytical base of livestock rearing, with specific reference to arid and semi-arid regions.

This is envisioned as pivotal for effective planning and policy making which in turn should help in increased public investments towards livestock development in these regions.

Approach

The network's approach emphasizes more on the need to address the issues pertaining to livestock rearers in a holistic manner.This would notjust be economic profitability, but has to be economically and ecologically sustainable policy initiatives.RLN aims at building an action-learning cycle, which facilitates knowledge sharing and effective outcomes.Further, the network works to increase the spiral of influence and learning by building multi-stakeholder and sectorial partnerships.

Action Learning Cycle Approach envisaged as

- **REFLECTION**
- **LEARNING**
- **PLANNING**
- **ACTION**

The priority areas

RLN has identified five priority areasthat not only can strengthen livestock rearingin the arid and semi-arid regions of India but also can have a potentially significant impact on the lives of the communities involved.RLN envisages building up momentum through its activities and influencing policies and actions on the ground, that focus on the issues and the concerns of the poor with special focus on the location-specific natureof the issues.

The five priority areas are

- Better Access to Markets
- Breed Conservation through development and emphasis on livestock keepers' rights through the Biocutural protocols

- Livestock and Commons
- Healthcare through community and state interaction
- Backyard Poultry
- Each of the five partner NGOS of the RLN network are nodal leads for each of the themes based on their work experience.

RLN Collaborations

The Rainfed Livestock Network collaborates withthe following NGOs located in various States across India for action pilots in their locations and shares good practices and strategies, by providing technical support and designing pilot interventions.

- MARAG in Ahemdabad
- SEVA and SKRF in Tamil Nadu
- Wassan inHyderabad
- Future greens samste at Bhagalcot and Janastu at Bangalore in Karnataka
- LPPS in Jammu
- KJS in Belgaum
- Honeybee network node inBhuvneshwar
- SevaMandir in Udaipur
- SPS in Madhya Pradesh

The very first moves of RLN, after defining the critical themes/priority areas, was towards organizing workshops around these themes. A workshop on 'breed conservation' was organized by LPPS at Sadri in February 2011. Speakers/participants were invited from all ICAR institutes, various agricultural /animal husbandry universities,NDDB,other NGOs working with livestock, besides representatives of livestock keepers.The workshop resulted in underlining the present status of livestock breeds, work happening in various parts of the country and the organizations involved. It helped in drawing a roadmap for the network on what needs to be done and what are the priority areas for action.

Sahjeevanhas beenchosento lead the 'breedconservation and development' theme.

This organization has been chosen as the thematic lead for its efforts towards getting the Banni breed of Buffalo recognized and has resulted in effective outcomes for the livestock keepers namely the maldharis.

The organization has worked closely with livestock community, the state government departments, the State University and the NBAGR in the process and in last few years Sahjeevanhas been working intensively towards getting registered a new camel breed namely the Kharai camel in Kutch following the same *modus operandi.*

Following the organization'sinteraction with the State animal husbandry department with regard to breed conservation and registration,the Gujarat Government has allotted it a task of identifying and getting registered all the lesser known breedspertaining to all the domestic livestock species within the State.Special funds have also been allotted for the same.

The process is being adopted and replicated in other states like Karnataka and Madhya Pradesh.In Karnataka, Sahjeevanis guiding an NGO named Future Greens Samastein getting registered a local buffalo breed located along the Krishna river in Bhagalcote. Alongside, inMadhya Pradesh,Sahjeevan is guiding a local NGO named AKRSP in evaluating a cowbreed located in Khandwa. Besides this, SPS, anNGO located at about 150 km away from Indore is working towards getting recognized a buffalo breed. In all these processes local Veterinary/ Animal husbandry departmentsare being involved so that the State Governments can carry forward the process for other lesser known/undocumented breeds.

An important aspect of breed conservation has been identified as ‘livestock keepers rights and the BioculturalProtocols(BCP)’ and this is being guided by the LokhitPashuPalakSangh (LPPS).

LPPS developed the first BCP for the Raikacommunity in the Pali district of Rajasthan with the help of South Africa based lawyersNGO working for farmers/community rights. The protocols are developed by the community and documented by the supporting NGO.

The BCP records the history of development of their livestockas well asthat of the community.It also records the topography/ mapping of their working areaalong with thethe flora/ fauna of the area. Besides this, traditional practicesand local knowledge are also documented. All in all, a comprehensive document is prepared. This is then supported by locatingthe documentary evidence from archival records and already existing documents. The relevant elements of theBCP are being recorded in the local biodiversity registers.

At present, present thereabout five BCPs and NGOs in Gujarat,Rajasthan,Maharashtra, Karnataka,Orrisa,Tamil Nadu and Jammu & Kashmir, working towards developing new BCPS.

5. COMMUNITY CONSERVATION OF AnGR AND IT'S ROLE IN THE RURAL LIVELIHOOD SECURITY OF KERALA

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Kerala, popularly known as God's own country, is believed to have a less favorable atmosphere for dairying owing to the high population density, small land holdings and a large number of small and marginal farmers in the dairy sector when compared to any other Indian State. Animal wealth contributes significantly to about 40 % of rural livelihood in the State and hence plays an important role in the State economy. Animal Husbandry contributes to about 26%o to GDP. According to the Livestock Census (2012), 14% farmers keep bovines, 23% has poultry and 10% has goats. Out of those rearing cows, 55% rear 2-3 cow units and 32% single cow units. Therefore though not congenial for commercial dairying, Kerala can be considered as a hotspot of biodiversity in livestock species contributing to the sustainable growth of the rural livelihood security of the region.

The small holder and landless farming system of Kerala scattered across the State from Kasaragod to Thiruvananthapuram is characterized by 1242282 cattle of which 75292 are indigenous. Mixed crop-livestock farming is more prevalent and over 80% of the rural households keep livestock of one species or the other and earn income out of them. Out of these, around 9% are conserving native breeds or lesser known varieties and some 0.5 % of them are registered members of the community conservation initiatives of the State. Many of the AnGr reared by these conservationists in Kerala have not so far been brought to their full performing potential except the Vechur breed of cattle and Malabari breed of goats. Hence, immense scope has been identified with the conservation of the lesser known varieties of Kerala and the concept of Community Conservation has been launched from the year 2000 with the same vision.

The Domestic Animal Diversity of Kerala

The local animals of Kerala are predominantly of dwarf types and are well adapted to the hot and humid coastal or high range climate of the region. They are a genetic insurance for future with their excellent ability to withstand adverse changes in climate under global warming and the consequent abiotic stresses and emergence of new diseases and infestations.

Vechur cattle: Vechur is the only cattle genetic resource of Kerala with national and international recognition finding place in the breed calendars of NBAGR and FAO. Ever since the starting of conservation efforts by Kerala Agricultural university way back in 1989, the Vechur cattle have been conserved under the farms of Breed Associations, Conservation Trusts and Kerala Veterinary & Animal Sciences University. Around 1296 number of small and marginal farmers of Kerala are engaged in the conservation of this priced genetic resource in the districts of Kottayam, Ernakulam, Alappuzha, Thrissur and Palakkad. The milk yield of the cows is low (2-3 Kg per day) but sufficient enough for household nutritional security and this nevertheless hinder the passion of the breed-keepers to rear the cows. More so, this breed of cows requiring a less sophisticated management and low feeding levels, fit into the scattered habitation pattern of Kerala homesteads with small land holdings. It has emerged as the most popular 'family cow' of Malayalees contributing to food baskets with an A2 milk rich in healthy proteins to combat diabetes, cardio-vascular ailments and Sudden Infant Death Syndrome (SIDS). A Germplasm Centre for faster multiplication of the breed has been set up in the home tract with the technical support of Vechur Conservation Trust and Kerala Local cattle Breeder's Society (KELOBS).

Kasaragod Dwarf cattle: The local cattle found in Kasaragod district of Kerala are also of dwarf type, predominantly black with high heat tolerance, disease resistance and hard hooves to survive in the laterite rocky terrains of the district. They also have good adaptability to the hot and humid coastal climate of the region. The cows yield 1-2 litres of milk daily but famous for their high reproductive potential popularly known as '*Aandukanni*' meaning 'a calf a year'. The rearing of these cows is an excellent example of a zero-input animal husbandry wherein the cows are let loose in the morning and in the evening they come back on their own to feed on the kitchen waste. Kasaragod dwarf cattle have a prominent place in the agriculture-based rural economy of Kasaragod thriving heavily on plantation crops like arecanut. The manure of the cows is left to get mixed with leaves and organic waste and allowed to accumulate over a month's time. This is popularly termed as *'Gobboro'* by the local farming community and this organic fertilizer is found to be the back-bone of the arecanut plantations of Malabar region of Kerala. With fewer numbers remaining on advent of intensive crossbreeding, the conservation efforts for the variety were initiated by Kerala Agricultural University way back in the 1990's and now the baton is safe in the hands of some of the dedicated breed associations like Kasaragod Dwarf Conservation Society (KCDS).

Kuttampuzha Kullan: Kuttampuzha Kullan (dwarf) cattle are mostly seen on the banks of Periyar river, bordering the districts of Kottayam and Ernakulum districts. Traditionally, they were kept by Muthuva tribes who lived in the Neriyamangalam-Kothamangalam forest stretch of Kerala extending upto Tamil Nadu. The early settlers of these high-land regions with diverse flora and fauna characteristic of Western Ghats were mostly Christians who got these cows from the tribesmen and kept them homestead. The cows generally go for grazing in the nearby forest lands at the break of dawn and return by evening on their own. They move in small herds comprising of bulls. The cows are found to be very good milk yielders of daily production upto 4.5 litres with a lactation length of 200 days. This trait is impressive when compared with the other dwarf breeds of cattle. They are fed with roughage from forests, rice gruel, household edible waste or rice bran. The concentrate feeding is abysmal and need not attract mention in most cases. The bulls move about in the herds and reproduction happens naturally with very high calving rates in the herds. The high reproductive potential and the decent milk yield make these cows a natural choice for the rural households. The average height is 105 cm, the color mostly single in red, white and their shades with patches. The cows are docile and have good mothering ability. Management practices like post-partum disinfection of umbilicus of calves and vulva region of cows are not exercised and no complications are observed in this regard. Noting their survivability and resistance to FMD outbreak in 2013, the cattle have gained extreme local importance. The indiscriminate killing of Kuttampuzha bulls for meat in the recent years together with shrinkage of their grazing lands due to an upcoming hydroelectric project in the area have led to a declining trend in their population. Conservation by way of demarcation of the breeding tract, ensuring zero movement of cattle and conservation *in situ* with support of LSGs and government departments with breed-keeper and his community at the core is the need of the hour.
Other lesser known cattle varieties: Some of the other lesser known dwarf cattle varieties found in different parts of the State are *Cheruvally* dwarf, *Elappully* dwarf, *Wayanadan* dwarf, *Vilwadri* dwarf, *Thenmala* dwarf and *Ananganmala* dwarf spread across the various agro-climatic zones of the State.

Malabari goats: Being the first recognized breed of livestock in Kerala hailing from Calicut, Kannur and Malappuram districts, Malabari goats are found to be more economic with regard to milk, meat and prolificacy when compared with other Indian breeds and Boer crosses under local conditions. The contemptuous false propaganda about the superiority of other breeds is constantly kept at check and State level community conservation initiatives are continued to protect the breed from dilution. The breed has a significant presence all over the state, thanks to the breeding support of Kerala Livestock Development Board.

Attappady black goats: The rural livelihood and economy of the major tribal communities of Irulas, Mudukas and Kurumbas of the Attappady hills of Western Ghats located in the Palakkad district of Kerala are heavily dependent on the rearing of Attappady black goats. This is a local goat variety solely evolved and developed by the tribal families as their livelihood option often making them the '*black gold* 'useful as a ready cash crop to be sold at the time of financial crunch. The goats are medium – sized, lean bodied and jet black in colour. Though poor milk producers, they are mainly reared by women and old people for meat and manure. The uncontrolled natural breeding by bucks of other breeds during grazing has led to the dilution of the breed at a faster rate. The total population in the home tract is as low as 90,000 leading to its enumeration in the insecure category of domestic animal diversity listed by FAO.

Ankamali pigs: The black pigs of Kerala locally known as *'Kutta'* were once upon a time the exquisite source of pork for the Christian communities of Central Travancore region of Kerala comprising of Kottayam, Ernakulam and Thrissur districts. These pigs were part of the culinary feasts associated with the family get-togethers arranged at the time of the local church festivals. The main attractions of this breed are their small body size of 20 kg, ability to survive on local feed and kitchen waste and hence a low input cost, the prolificacy (7-12 in a litter) and a good mothering ability. The introduction and popularity of exotic white pigs has led to their near extinction in the recent decade and concerted efforts are essential for multiplication of the breed.

Kuttanad buffaloes: The river-type buffaloes found in the low-lying paddy fields of upper Kuttanad are found to be a neglected lot but are an excellent genetic resource with a decent milk yield and high SNF content. The water-logged ecosystem of the breeding tract is very conducive to satisfy the wallowing habits of these buffaloes and hence if concerted efforts are undertaken, the dwarf buffaloes of Kuttanad also can turn out to contribute to the global food basket.

Kuttanad ducks: Kerala has vast expands of wetlands, ideal for duck rearing. The area is broadly called Kuttanad, popularly known as 'the rice bowl of Kerala' encompassing parts of Alappuzha, Kottayam and Ernakulam districts lying 1m below MSL and suitable for paddy cultivation. Paddy cultivation and duck farming co-exist here as a year round activity and almost 50% of Kerala's duck population thrive here making it a prospective venture among the local people. The desi ducks occur in two varieties viz., C*hara* and C*hemballi*, and they are reared in the backwaters, rivers, rivulets and marshy lands peculiar to the wetland of Kuttanadu to add to the beauty of the tourist destinations in Alappuzha and Kottayam. Instead of an intensive / factory system of rearing, an extensive management style of providing only a night shelter to the birds and daytime free range management on paddy fields just after harvest, is commonly followed. *Chara* means 'ash' in Malayalam. Chara drakes have dark orange beak, black and brown feathers intermingled body and the neck may show a white ring with characteristic glistening green color. Chara ducks are generally bigger than Chempalli and they lay eggs which are off white color. *Chempu* means 'copper' and these ducks have copper color. Males have yellow beak, copper color or blackish plumage, the head dark green color and are very beautiful. Females lay pure white eggs. Feeding and breeding show similarity between the varieties and Kuttanad ducks in general lay 180-200 eggs per year. The ecosystem of these birds is to be protected and sufficient research need to be conducted on the common beliefs about the medicinal value of their eggs and meat as a part of the community conservation efforts initiated by the various NGOs in the recent years. The department of Animal Husbandry, has a Duck breeding Station at Niranam where conservation activities are actively undertaken. is especially suited to their survival. Prophylaxis protocols against duck plague and pasteurella are in place with the network of AHD which provides vaccines and services, free of cost. Of late, the incidence of bird flu has adversely affected the prospects of the enterprise.

The Kerala model of Community Conservation of AnGR

The above mentioned reports on the status of animal genetic resources clearly indicate the diversity available in the State, the contributions of such diversity and the threats to them in the near future. The *desi* cattle, buffalo, goat and fowl varieties of Kerala have become an integral part of the cultivation of spices, plantation crops like rubber and arecanut, paddy, vegetable and ornamental flower farming all over the State. In this regard, the seminal work currently being undertaken in Kerala by the Breed Societies and Trusts is laudable in recognizing the animal breed diversity and promoting and recognizing the breed-keepers and professionals supporting such efforts. Kerala has emerged as probably the only State in India with four of such recognized Breed Societies functioning for the conservation of these prized genetic resources. Vechur Conservation Trust (VCT), Kerala Local cattle Breeder's Society (KELOBS), Kasaragod Dwarf Conservation Society (KDCS) and Vadakara cow Conservation Trust (VCCT) have been registered in the State to conserve these breeds/ varieties. Through the concerted efforts since 1989, the policy makers and the stake holders have realized that a scientific planned conservation and multiplication of these genetic resources with people's participation is the social need of the hour for ensuring a safe and healthy future of food security and rural livelihood in the State.

The breeder's societies function with the mandates of documenting the unique varieties, maintain them as pure stock and register them to prevent misappropriation. Many educated youth from various walks of life have taken up the noble cause of conservation of domestic animal diversity of the State and the networking services find an important place in sustaining their motivation towards a cow-based agriculture and 'zero-budget family farming' with these native varieties. The National Biodiversity Authority, State Biodiversity Board and NABARD are a few other prominent organizations spearheading the initiatives with their financial assistance and technical guidance. The Government of the Kerala has been keen in distributing suitable incentives to the registered breed-keepers and supporting the community conservation efforts through frequent conduct of breeder's meets. Kerala Livestock Development Board (KLDB), the nodal agency of the State for the formulation and distribution of breeding inputs in the animal husbandry sector also has joined the community conservation movement by introducing the frozen semen of Vechur, Kasaragod and Vatakara dwarf to the registered breeders. Kerala Veterinary and Animal Sciences University, Pookode is offering immense support to the movement with their regular capacity building programmes for breed-keepers of native cattle breeds and varieties on the various sustainable bio-dynamic models of conservation based on value addition of dung, urine and organic farming. The University also has been taking a lead role in conducting advanced biotechnological research in these valuable breeds very frequently, paving way to many a findings on the merits of these genetic resources and their products followed by a dissemination of knowledge among the masses.

It is observed that farmer's preference to native cattle has increased substantially during the past decade due to many factors. The single most important reason to be cited is awareness on its role to keep the soil in good health and the production of safe organic food. With higher literacy and greater emphasis on pro-health lifestyles, the demand for pesticide free rice, fruits and vegetables grown without chemical fertilizers has grown manifold. Panchagavya, Jeevamrutha, Khana Jeevamrutha have become very popular and therefore keeping a native cow becomes a natural choice. In a nut-shell, there is a paradigm shift on thinking from COW=MILK to COW=SOIL. Further, indigenous cow milk or ghee has earned the status of a fitness/ wellness product or even a medicine from a mere FOOD item. This fast growing trend is fetching good price for the *desi* livestock keeper for all the native livestock products even among the urban elite.

Conclusion

Conservation of AnGr has a definite role in supporting the rural livelihood security of Kerala. In the case of recognized breeds, utility indirectly drives conservation; but the many more lesser known unlisted varieties should immediately be conserved to protect the "diversity" so that we are taken one step closer towards food safety and food security.

6. BIO-CULTURAL PROTOCOL (BCP) OF GOLLA COMMUNITY IN ODISHA: MAPPING THE BIO-CULTURAL ASSETS OF LIVESTOCK KEEPERS

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Introduction

Convention on Biological Diversity (CBD) and Indigenous and Local Communities (ILCs) and Nongovernmental Organizations (NGOs) stress upon the fact to adequately respect and promote communities' ways of life that have contributed to the conservation and sustainable use of biodiversity.

At the same time the indigenous local communities sincerely feel to call upon the state, national and international authorities for their rights and actions in regards to grazing rights, animal genetic resources and associated traditional knowledge under Indian law. These communities have the rights to set out bio-cultural values to empower themselves to continue their livelihood in the natural environment where they live and graze their animals. Hence the development of bio-cultural community protocols (BCPs) by local community, that can empower themselves, while there is local implementation of international and national environmental laws.

A BCP is a protocol that is developed after a community undertakes a consultative process to outline their core ecological, cultural and spiritual values and customary laws relating to their traditional knowledge and resources, based on which they provide clear terms and conditions to regulate access to their knowledge and resources. The process of developing a BCP involves mapping of the community biocultural assets and also making them aware about the legal empowerment so that community members can better understand legal regimes that regulate various aspects of their lives, such as ABS (Access and benefit sharing etc, (Kabir Bavikate etal.2009).

In this study, the bio-cultural assets of the Golla community are mapped with the help of consultation with community members at different times and places.

Methods

For developing the BCP ,The consultative process is undertaken with the help of an innovative institution called "Pathe Pathshala"- A Peoples' University on move, where scouting, documentation and consultation takes place at peoples' place, in peoples' time and with peoples' language. These pathshalas are conducted in different parts of Odisha.

Golla, the semi-nomadic pastoralists of Odisha

Golla, the semi-nomadic pastoralists of Odisha, is one of the ancient nomadic pastoralists of southeastern part of India. In the state of Odisha, *Golla* are found in districts of Ganjam, Gajapati Rayagada and to some extent in Nayagrah district. In Ganjam and Gajapati, the *Golla* are mostly present in different villages, locally called as "*Golla Gaon*" means *Golla* village. There are about 2500 families of Golla who keep Ganjam breed of goat and sheep. The population of Ganjam breed of goats is 2, 35,969 and 1, 43,515 numbers of sheep.

The *Gollas* rear Ganjam/Dalua breed of goats and sheep by practicing migration through natural grass, forests and pasturelands. The people of *Golla* community are generally illiterate, hard working, enduring, brave and efficient traditional healers of small ruminants. The practice of migration, not only help in biodiversity conservation of local sheep and goat breeds but also help in propagation of seeds, grains, herbs and significantly contribute to social unity and land fertility. Now, the Golla youth are literate and educated.

According to Kornel Das et al (1976) linguistically Golla in Odisha are divided into two groups such as Odia and Telugu Golla. But all the Golla can speak and understand Odia and Telugu language well.

Golla Life Style

Most of the *Golla* people live in *Golla* villages called '*Golla Gaon*'.

Each *Golla Gaon* is situated near a forest and/or near a hill.

Each *Golla* male starting from the young age of 16 to 70 years old, remain outside the village with the flock of sheep and goats locally called "*Mandaa*".

They go on migrating from place to place through the traditional pasturelands in valleys and mountains. *Gollas* move near about 20-30km a day while grazing the animals. A '*Mandaa*' of goats and sheep may contain 3000-5000goats and sheep. Generally a number of 7-8 *Golla* pastoralists move with one *Mandaa* of livestock along with 4-5 pet dogs.

In the evening, before the dark falls, the animals are grouped on lands on the invitation of the landowners. The landowner in turn gives Rs200-250 per '*Mandaa*' per night stay and offers rice to the *Golla* pastoralists for food in the night. Near the flock; the *Golla* people cook their 'Rice' and 'Dal' for supper. There are three to four watchdogs accompanying the flock stay in position near the flock. *Golla* pastoralists cook food, sing songs and mostly discuss the health problems of any of the animals and eat food by 12 in the mid night. They go to sleep in batches while others watch the animals in rotation.

1. By early in the morning one of the *Golla* checks the animals and kids, if there are any sick animals.
2. Landowners come and examine, his/her land for droppings/urine.
3. There is exchange of better seed stocks of animals between the near by villagers and the *Golla*.
4. There is also exchange of best local agricultural commodities, seeds with those brought by the *Golla*.

The migration

1. Before the flocks move, the sheep and goats are separated. This facilitates sheep in practicing grazing and goats in browsing the fodder.
2. Kids and new born are kept together. The *Golla* physically carries the most sick and newborn kids.

The Noon

1. One of the *Golla* moves in advance and cooks food for the lunch for other *Golla.* While *Golla* takes the lunch, the animals group together and take rest.

The Night stay

1. The night stay is repeated on the same way described earlier.

Golla Sociology

1. *Golla* tribes are mostly illiterate, simple, honest, brave, hard working, God fearing but eccentric people.
2. They are very much friendly to their animals. Even, they share the rice with their loved animals from a same bowl.
3. They never take goat or sheep meat except on the occasion of the death of a family member.
4. Brides often bring goats and sheep as gifts for the groom from her mother's house.
5. *Golla* women, old and young remain in village, while the men migrate for 6-7 months in a year.
6. The evening starts with prayer to Lord Krishna, the Hindu God for inviting welfare of their animals.

7. The mother goats (Daalua or Ganjam breeds) even feed the *Golla* children by putting own teat into the mouth of the baby.
8. No woman is allowed to visit a *'Mandaa'* of goats when she is under menstruation cycle. With smell of the menstruated lady, the *Golla* believes, there will be no crossing between Buck and Doe.
9. Whistling is an important art of the *Golla* tribe. The adult *Golla* whistles in different way than a young *Golla*. The whistling is used to send message to other *Golla*. Even the animals are commanded through whistling. The intensity of whistling sound varies as per the context of the message. Whistling to send sad news is different from that for happy news.
10. Polygamy and homosexuality is absent in *Golla* community.

Traditional knowledge and belief of Golla

1. Dropping of goat is mixed with goat milk and warmed a little. Then a paste is prepared and smeared on the site of a bone fracture and immobilized the bone with a bamboo splint. This heals the fracture wonderfully within 20 days
2. Heating an iron rod in the fire and cauterizing the head and neck treats paralysis. The fire is prepared from the dry goat dropping. This method of activating nervous system is very effective.
3. While migrating, sick animals (Daalua breed of goats) identify the herbs in their own and eat them as auto treatment and also for autodeworming.
4. In rains, most of the animals move to graze on mountains.
5. The young kids are not allowed to drink water from outside. Only milks are fed to kids up to 3 months age.
6. They allow eating of Neem (*Azadyrachta indica*) leave to young kids for deworming. It tremendously works as deworming agent and also as prevention against goat and sheep pox.
7. In the night, the teats of the mother does are sealed by locally prepared caps to prevent over eating by kids.
8. There is better conception rate in Does, after crossing, if the head *Golla* will not leave the '*Mandaa*" and return to his home.
9. For better conception, the head *Golla* do not wash his head for 10 days.

'Golla' - The Biodiversity conserver

The *Golla* community while practicing migratory pastoralism contributes immensely to biodiversity conservation.

1. *Golla* are the best traditional animal breeders. People in villages, wait for the *Golla* to come to their village. People get best breeding stocks of sheep and goat from *Golla* and in turn they exchange their best animal breeding stock. This is like an informal animal fair on move
2. The night stays are sometimes longer, that lasts 2-3days in one village, by which the land on which they keep their flock get fertilized.
3. The *Golla* brings seeds, grains from their own village and take back seeds from the farmer's enroute, thereby conserving biodiversity. .
4. The *Golla* plants herbs, grass enroute to ensure fodder availability during future migration.
5. The *Golas* are traditional animal healers who utilize local plants and herbs during treatment. Thereby they train localites how to utilize the local biodiversity products and best nurture the biodiversity.

Golla and the livestock economics

Golla are the traditional small animal (Goat and sheep) keepers who breed, rear and market goats and sheep. Although middlemen control the bulk of mutton and chevon trade in Odisha, *Golla* contributes significantly to the fair-trading and ensures availability of ruminants during high demand time of Durga Puja, Eid, New Year parties and marriage celebrations. The dynamics of the small animal trading is still in fluid state, causing loss against the *Golla.*

No doubt, the *Golla* system of rearing and trading the livestock is a perfect example of low external input based sustainable livestock rearing system. The migration and sustenance of life together makes the system a perfect endogenous development.

Threats and challenges to Golla life style

1. The young generation is unwilling to live the life of traditional *Golla.* They prefer to go to urban areas and earn livelihood as laborers/taxi drivers than grazing sheep and goats.
2. While migrating with livestock, they are often robbed by thieves, thugs. These cases are increasing day by day.
3. Now a day, in some parts, people of forest Dept are restricting their entry to certain areas of fodder and forests.
4. Large-scale plantation of cashew nut causes no growth of fodder grass in plain as well as in hills. So difficulties in grazing of goats and sheep
5. Traditional grasslands and pasturelands are decreasing day by day.
6. In the areas of Golla settlement, mining /quarries are not yet been a big problem, but can be future problem in some parts of Rayagada district.

Conclusion

While developing the BCP for Golla Community in Odisha with help of consultative process , the members of Golla community articulate strongly about their right on grazing in forest area, their role as custodian of the native livestock breed, rights to the associated traditional knowledge , their positive role in biodiversity conservation and local ecosystem and safeguard of their traditional lifestyle.

This BCP would not only set out the bio-cultural values of the grazing community but also to safeguard themselves in view of the changing national and international laws vis-à-vis climate change and biodiversity conservation

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7. ANIMAL GENETIC RESOURCES OF ZAMBIA AND THEIR IMPROVEMENT, ITS CONTRIBUTIONTO LIVELIHOOD SECURITY IN RURAL FARMERS

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Introduction

Human societies worldwide depend upon animals and animal genetic resources for a wide range of services ranging from livelihoods and welfare to social and cultural needs. Globally, consumption of meat and milk has been increasing over the past thirty years. The total meat and milk consumption in the developing world grew from approximately at 4% to 6% per year during the same period (FAO 2011). However, current population demographic data from the United Nations Food and Agriculture Organization (FAO) strongly indicates that world demand for livestock and livestock products is likely to continue increasing into the near future as the human population is projected to rise to 9.2 billion in 2050 (UN Population Division 2007; FAO 2011).

Zambia is a landlocked country of 752,630 square kilometres with a population of about14.5 million people and an annual growth rate of 3.9%. The agriculture sector contributes about 11-16% of the GDP. The livestock sectorcontributes 35% to the agricultural GDP excluding the benefits from use of animal draftpower and manure. The sector comprises of about 85% small-scale farmers who utilize about 75% of the cultivated land and 15 %commercial farmers who utilize 25% of the land.

The diversity of Animal Genetic Resources (AnGR) in Zambia comprise of about 3.1million cattle, 1.2 million goats, 0.5 million pigs, 80,000 sheep, over 20 million poultry,few donkeys, rabbits, turkeys, guinea fowls, ostriches and quails. Apart from ostrichesand quails that are reared exclusively by commercial farmers, the traditional sector ownsthe majority of Zambian animal genetic resources (83% cattle, 97% goats, 64% sheep and90% pigs) as indigenous animals or crosses with exotics.

Livestock, especially cattle, play multi-purpose roles worldwide.in Zambia livestock sector livestock has value in investments, savings and supply of high quality dietary foods (such asmeat, milk, eggs), provide hides and skins for leather industry, manure and draught power for agricultural systems;generate employment opportunities and income among rural people. The socioeconomicimportance of these animals cannot be over-emphasized. Through animal draftpower and manure, cattle contribute directly to increased crop production. Studies have shown that a pair of oxen can produce crops valued between $3500- $4500 per year in Zambia.Failure toaccess cattle manure in the sandy flood plains of Western Province is synonymous withcrop failure as animal manure in these sands is essential for crop growth. Crop productionin Southern province over the last 12 years has drastically reduced due to inadequate draftanimal power. High mortalities of cattle due to tick borne diseases (especially corridordisease) have left many families in Southern Province without draft animals and unableto cultivate adequate areas of land with consequent acute food insecurity.

Animals are banks on the hoof for rural people. They are converted to cash in times ofemergencies especially now with introduction of Liberalization Policy in 1992 that removed free educational and free health services among other things. The last 15 yearshave been years of repeated droughts due to changing weather patterns. Sale of cattle,goats, pigs and chickens generate income to buy grain and sometimes these animals areexchanged for grain thereby alleviating food insecurity. Farm animals are an integral partof sustainable development of rural Zambian people.Non-Economic Value of Cattle in Traditional Cultures of livestock cannot be over emphasised. cattle are important as an agency of bridging the social gap between the wealthy and the poor. This occurs when the cattle herd size increases to the point that extra animals are leased out to less fortunate people through a processing called 'herding out'and a number of cattle are paid in the dowery (Lobola) transaction that usually creates a strong bond between participating families. Most traditional ceremonies in Zambia involve cattle, such as Shimunenga ceremony in Namwala districts and Ncwala ceremony in Eastern Province of Zambia.

One of the indicators of acute food insecurity and poverty in a Zambian village by acasual visitor is the absence of chickens and other livestock around the village. Chickensare the first choice of animals to be sold in times of food hunger. Households that do notown any animals are usually considered the poorest in the rural communities and thosewith large numbers of animals are rich members of the community. Lack of animals isassociated with abject poverty and food insecurity. When food and prosperity returns tothe village, presence of village scavenging chickens and other livestock are evident.

Animals are also an important focus of innovation in science and technology across a wide range of sectors from agriculture to pharmaceuticals, biotechnology and emerging areas of science and technology such as synthetic biology and technologies to address climate change.

The global plan of action for the World Animal Genetic Resourcesof theFood and Agriculture Organisation (FAO 2007) is aimed at ensuring the characterisation, utilisation and conservation of animal genetic diversity worldwide. However, most unique characteristics in livestockare found in developing countries including Sub-Sahara Africa. The study conducted on Zambian cattle revealed that cattle farmers believe cattle survival is amongst the most important traits. This Inevitability, with the ever-escalating changes in the environments and predicted increase in human population growth, cattle must firstly survive for them to improve in size, grow faster, provide other functions (e.g traction), and reproduce. Otherwise, they may face extinction in near future. During the past 50 years, the Zambian government has established several livestock breeding schemes across the country. These breeding centres failed because cattle from these centres could not survive in grazing land that are characterised by a high number of ticks, endemic diseases and erratic water supply and feed. Furthermore, the schemes could not work well because the type of cattle distributed was new to local farmers and local farmers did not have the opportunity to indicate their preference for the type of cattle.

The identification of the preferences of livestock traits byruralfarmers can aid the livestock improvement/ breeding programs that are still run by government departments. If preferences traits are known,tared improvement/ breeding programs are more likely to provide genetically improved cattle, to pastoral rural communities. In addition, government must deliver training in the management of livestock to small-scale livestock farmers in Zambia as well. Genetic improvement of indigenous livestock breeds is key in improving the livelihood of most livestock farmers by increasing animal production.monitoring the genetic resources and conserving the most unique characteristics of the breeds is very important. Fortunately, the local herds have wide range of genetic diversity and have proven to be well-adaptable to local environments. Therefore, the local indigenous breeds are potentially an important source of animals for breeding programs and conservation of genetic resources.

Genetic improvement programs that involve opening up nucleus breeding schemes by involving local farmers who are willing to join the schemes is very important. However, the farmers highlighted numerous caveats during the study, such as inadequate veterinary services, poor infrastructure and little knowledge of livestock management practices. These problems need to be addressed at the inception of designing the livestock breeding programs for each specific region. Other limitations that were found are common among developing countries, like Kenya, and included the lack of proper guidelines on land property rights, poor and lack of access to clean water throughout the year and uncontrolled breeding. Disease prevention and control also significantly contributes to livestock loss throughout the regions as observed by others.

Pockets of farmers showed unwillingness to share out their best animals with other livestock farmers. Consequently, the potential of working with such farmers in setting up a nucleus herd for replacement stocks from their herds may be limited, especially if such an individual farm unit is considered. Therefore, it is important to involve several farmers as co-operatives (Smith 1988) or as a group in individual nucleus farm units with a considerable number of animals from which replacements can be obtained. Implementing breeding programs for pastoralists which involve local farmers as an integral part of the production system from the inception are more likely to be successful.

From our study, it is clear that there is the need to develop a different program framework for livestock production in the three regions to benefit all rural populations in Zambia. In the Namwala areas, in which the pastoral communities practice transhumance based on Brahman and Angoni cattle, farmers are dependent on adapted breeds of large size with an increase in the demand for such type of cattle is likely for the foreseeable future, In the Lundazi and Chipata regions, it may be possible to select foundation stock from within their cattle populations for distribution to local farmers through artificial insemination

Numerous organisations involved in livestock production reported to the Zambian Parliamentary Committee on Agriculture that there is a need for genetic improvement in livestock for them to profit from such programs (ZNA 2013). However, appropriate roles need to be clearly defined, in order to circumvent misinterpretation in the process of implementation of the breeding programs. It will be important to learn lessons from the experience of successful breeding schemes in in Kenya and in Côte d'Ivoire.Our study provides an insight on the level of genetic diversity in the Zambian indigenous livestock both among and within livestock populations. The results indicated that the three breeds studied share some common genotypes and can be placed into two main populations, although there is some overlap. The overlaps observed could have been due to crossbreeding that occurred during the livestock dispensation from east Africa to central Africa. However, limited sample size might also contribute to the observed results.

Genetic selection depends on the different hereditary characteristics of breeds. From an historical perspective, livestock have adapted to different environments through natural selection. Despite this selection, the results indicate that Zambian indigenous livestock have a large amount of genetic diversity that can be exploited in breeding programs without the need to introduce other genetic material from elsewhere.

Using various genetic improvements approaches and technologies to maximise the rate of genetic gain occasionally promotes inbreeding that is unfavourable in breeding programs. The results showed a very low level of inbreeding in the indigenous cattle populations. Therefore, the majority of Zambian cattle that possess desirable characteristics (such as a reduced susceptibility to East Coast Fever and the ability to survive and reproduce in hash environmental conditions with little veterinary attentioncan be used for breeding. Studies have shown that if inbreeding is avoided, then local cattle can be used in such breeding programs. For instance, the Nandi Zebu is tolerant to most external parasites (such as ticks, biting flies) and resistant to tick-borne diseases, yet can be bred for increased milk production. In Gambia, a successful breeding program that involved local cattle farmers has been implemented, resulting in genetic gain for body weight and milk yield in N'Dama cattle.

In order to predict the rate of genetic gain in the Zambia indigenous cattle, genetic parameters for weaning weights were estimated. Measuring genetic parameters is important in beef cattle selection programs. The results show that selecting for weaning weight is feasible in Zebu cattle in Africa and other countries worldwide. Therefore, efforts that focus on developing sustainable genetic improvement programs for local and well-adaptable breeds taking into account these production and adaption traits will be beneficial to farmers and help implement sound conservation of genetic diversity by the government agencies.

Conclusion

Using cattle that have proven to grow, reproduce and provided multiple purpose functions with unique genetic diversity, Zambia can achieve its objective of reducing poverty and grow its economy. This depends on developing a flexible and operational breeding program that suits local farmers. Demand for meat is increasing in Africa and South Asia. Elsewhere the demand is for meat without the use of growth promotants and antibiotics. .

In Zambia, the indigenous cattle breeds, will continue to be raised under traditional management systems without feed supplementation and minimal use of drugs. However, access to these global markets will only be possible if farmers are provided with opportunities to improve their local well adapted cattle.There was no significant difference in the traits that are most preferred by small cattle farmers across major cattle producing regions of Zambia. However, farmers with large herds of cattle preferred cattle of larger size and those who fewer cattle per herd slightly preferred cattle that are highly fertile to increase in the numbers. Interestingly, size and fertility were found to be slightly negatively correlated and farmers were aware of this fact even without a formal education. This implies that information gather from people who have raised cattle for a long time is important.

Amongst the cattle breeds investigated, the Angoni cattle revealed the highest level of genetic diversity presumably because of a large gene pool in a region does not defined borders. Although the Zambian indigenous cattle breeds did notexhibit high or unique purity, these breeds offer a valuablegenetic resource relevant to breed conservation. Therewas evidence of some gene flow between the threepopulations and inbreeding was largely insignificant. Theresults suggest existing divergent and multi-loci geneticadmixtures between and within breeds.The most striking feature is the close relationship betweenthe Angoni and Bartose breeds. However, the populationstructure clustering indicates there is a distinct separationfrom the Angoni breed. The clustering patterns can beexplained by the coexistence of breeds in some regions of Zambia

In most developing countries, record keeping and measurements of growth traits is not been undertaken. Therefore, it was important to use data from commercial farms that keep traditional cattle breeds and good records to estimate genetic parameters for traitsand also encourage most farmers to keep on taking records on performance data. Among the growth traits, weaning weight is easily measurable at low cost. Using weaning weight for Angoni and Boran cattle, the direct and maternal heritability were found to be comparable to other Zebu cattle in Africa and other countries in world. However, separating the genetic effects and residual, the Angoni had higher direct and maternal heritability than Boran. This indicates that improving the local Angoni breed will be possible as has been done in the Boran for a long time.

8. NEED TO CREATE STATE LEVEL GENETIC DISEASE TESTING FACILITIES FOR IMROVEMENT OF FARM ANIMAL GENETIC RESOURCES

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In India reproductive inefficiency is one of the most costly problems facing dairy industry and even for improvement of farm animal genetic resources , today. Hence, for improving the same under present context investments for bringing livestock improvement in India through AI is the basic and the only practicable tool in field conditions needs to be much more strengthened with respect of quality status of the semen especially genetic quality. As we are aware of the purpose of artificial insemination i.e to use genetically best or superior males to bring fast change / improvement in livestock especially cattle and buffalo population within a short span which is otherwise not possible with natural service. This is leading to indiscriminate use of even genetically defective quality bulls through AI or NS due to lack of genetic testing facilities and skilled hands even in the academic / research institutes and lack of awareness of it's need even in field veterinarians affecting the base required for bringing any improvement. It reflects even from CMU norms of minimum standards for FS lab/ semen stations that more attention is still been given in India to semen parameters than the genetic quality of sperms being inseminated, when it is simple to understand that if semen is genetically defective it's parameters viz. motility , live and dead sperm count has no value for expecting any improvements in next generation through AI, instead this is becoming an important factor for our failure in tackling reduced breeding efficiency, fertility due to chromosomal mutations/aberrations spreading fast through AI leading to early embryonic death responsible for more incidences of repeat breeding . In short semen meant for bringing improvement fast through AI causing fast reduction in fertility due to it's large scale use through AI or will lead to slow reduction in fertility with that of NS , if it possessed genetically defective sperms. As per literature the Indian dairy cattle population is showing presence of carriers of major genetical disorders affecting fertility/productivity even in reputed herds.

Genetic diseases caused by the vertical transmission of defective genes can lead to significant economic losses. The technological advances that have taken place in the fields of molecular genetics and bioinformatics during the last decade have enabled the identification in dairy cattle of the genes responsible for a number of important genetic diseases with a monogenic origin. In most cases, the defective allele carries a mutation that results in the synthesis of a non-functional protein variant leading to, development of metabolic disorders. When this allele is recessive, heterozygotic (carrier) animals have a normal phenotype but can pass the genetic defects to their offspring. Carrier individuals within the bovine livestock, therefore, imply the silent transmission of genetic diseases and hence increase the chances of appearance of genetic defects among calves, with its associated economic implications (Uffao and Acosta, 2009).

According to the world health organization, over 10,000 of human diseases are known to be monogenic and about 3000 diseases were unknown . In animals smaller numbers of genetic diseases are also identified (Vijaykumar et al., 2010) with fewer than two hundred genetic diseases in cattle (Houston, 1993). Currently 40 disorders and traits in cattle have been characterized in which the causative mutation has been identified at the DNA level (Online Mendelian inheritance in animals; http://omia.angis.org.au). The known inherited disorders in cattle are mostly caused by autosomal recessive genes. The autosomal recessive genetic diseases are mostly breed-specific .The characteristic feature of autosomal recessive genes is that they are only expressed as a diseased phenotype if both alleles are present. Therefore, unrecognized dissemination of such defective genes is possible and autosomal recessive disorders are of greater concern in cattle breeding. The disorders with dominant inheritance or recessive X-linked inheritance as these are easily recognized , hence are of lesser concern. Inherited genetic disorders affect all kinds of farm animals. Functional and physiological defects arising from inherited disorders have negative impact on health and productivity of farm animals and lead to economic loss in the dairy cattle industry. This has made the screening a mandatory practice for autosomal recessive disorders in farm-born HF and its crossbreds prior to their introduction into the breeding programs. Even though the initial incidence of these disorders is low, number of carriers could be substantially higher in coming days if the animals are not randomly checked routinely for same. Spread of undesirable genetic disorder is hastened by the artificial insemination programme. Therefore, vigilance is required to diminish the risk of dissemination of recessive disorders resulting from increased selection pressure within the dairy industry, which is presently dominated by HF breed worldwide.

Carriers when left in the population keep passing the defective gene onto the population through breeding and create more carriers. This is amplified when artificial insemination is practiced, since, the transmission of genetic material by this route is much faster and rapid. Hence it may be summarized that if regular check on genetic status of breeding bulls or blind screening of animals in population is not done and carriers for economically important genetic diseases / chromosomal disorders are allowed to breed, the entire herd / population will be saturated with carriers, which will then lead to devastating effect. Since, the cattle and buffalo population in India is high, it will take time for this event to occur. This is possibly the reason why the visible effect of retaining carrier animals in breeding population appears at a much later stage, is irreversible and a huge risk in the long term. However , routine analysis of only a few monogenic recessive disorders ,have entered breeding programmes so far and in some instances mandatory for animals that are used for breeding particularly bulls used for AI. At present, there are identification records for several inherited bovine disorders e.g. bovine leukocyte adhesion deficiency (BLAD), deficiency of uridine monophosphate synthase (DUMPS), complex vertebral malformation (CVM), bovine citrullinaemia (BC), and factor XI deficiency (FXID) reported in HF and its crosses. These disorders in cattle may occur at very low frequency and therefore, carriers are usually not detected in breeding programmes. The incidences of recessively inherited genetic disorders resulted in attempts to select animals using molecular markers worldwide. Routine and obligatory screening of HF animals have controlled the rapid spread of these disorders in several countries. Restricted breeding and long-term investigations have enabled a great reduction of this threat to the population.

Worldwide reports about the economic losses due to molecular genetic disorders

1. BLAD (Bovine Leukocyte Adhesion Deficiency) As per NDDB, Anand, Biotechnology laboratory information broacher, in USA 80 per cent of the ten million dairy cows are Holstein. It was estimated that 16,000 calves were born with BLAD each year. Hence, the average economic loss per calf was roughly 300 US dollors. Thus BLAD alone cost US dairy industry consumers and producers about five million US dollors annually, placing this genetic disorder among the most economically significant one.
2. Prevalence of BLAD in Indian HF crossbred cattle population is an alarming situation due to consistent reports from 1999 to 2013.
3. Factor XI deficiency (FXID) is responsible for repeat breeding in carriers leading to the financial losses . In Turkey (Akyuz et al., 2012) reported an extra $ 324 financial loss compared with a normally fertile cow due to this syndrome. This disorder is different to other disorders like BLAD and DUMPS (Deficiency of Uridine Monophosphate Synthase) as it affects fertility.
4. CVM (Complex Vertebral Malformation) carriers in India and worldwide much more higher than other four disorders i.e. BLAD, DUMPS, Citrullinemia and Factor XI
5. In 2012 in New Zealand Livestock Improvement Corporation (LIC) , a farmer cooperative that sells bull semen was been warned for supplying defective semen to farmers who produced 1500 defective calves with genetic defect leading to excessive hairiness and intolerance to heat ultimately reducing milk producing ability (Smith, 2012)

In India, since past few years, the carriers of monogenic disorders responsible for death of young ones at early ages are reported more frequently.

1. *Bovine Leukocyte Adhesion Deficiency (BLAD)* : (i) At NDRI, Karnal in Karan Fries two carriers and one affected (Yathish et al.,2010) ; 21.82 per cent carriers (Kumar, 2009) and 7.31 per cent carriers (Mahadi et al., 2010) (ii) Two carriers HF bulls (Muraleedharan *et al*.,1999) (iii) 13 HF carriers and 10 HF cross carriers (Patel,2007a) (iv) Two carrier HF /HF cross in Gujarat (Patel et al., 2011) (v) Two HF bull carriers (Roy et al., 2012) (vi) At DCK,Mumbai semen station one HF cross bull carrier under use through AI (Sawane et al., 2013)
2. *Complex Vertebral Malformation (CVM)* : (i) At NDRI in Karan Fries bull calves 76.36 Per cent (Kumar 2009) and 20 .35 Per cent (Mahadi ,2010), one carrier (Kotikalapudi *et al*., 2013)
3. *Citrullinaemia* : (i) At Animal Breeding Center of NDDB in U.P. Raibareili (Muraleedharan *et al*. (1999)- one HF bull carrier (ii) Two HF cross carrier bull (Gaur *et al*., 2012)
4. *Deficiency of Uridine Monophosphate Synthase (DUMPS)* : In Haryana at Holstein bull station one carrier (Gaur et al., 2013)
5. *Factor XI deficiency* : Two HF carriers (Patel et al., 2007b)

With the discovery of the major chromosomal defects like Robertsonian translocations or Centric Fusion Translocation (CFT)in Swedish Red cattle in 1964 (Gustavsson, 1969) when the deleterious effects on the fertility of carriers were demonstrated the cytogenetics was routinely applied to the domestic animals.

The losses due to spread of Robertsonian translocation in cattle from various countries have been reported by many workers Gustavsson,1969 ; Popescu,1974 ; Queinnec et al.,1974 ; Refsdal, 1976 ; Blazak and Eldridge,1977; Zahner, 1977 ; Zahner et al., 1979 ;Langhammer and Schwerin 1985 ; Yakovlev et al.,1986 . In Sweden the lower fertility demonstrated was estimated to be causing a loss of two million Swedish Kroners per year. In India the crossbred cattle carriers of Robertsonian translocation might result economic losses more than 1.5 crores per year per defective crossbred bull tentatively due to reduced fertility of his daughters by considering 5-15 percent reduction in fertility in carrier cows

In India since 2005 the genetic testing has been made essential as per CMU norms set by GOI for grading the FS labs / semen station etc. However, efficiency and accuracy of test reports is hampered due to availability of less number of labs and manpower, land lack of awareness , leading to fast spread of defects through NS or AI. The use of molecular cytogenetic approaches for effective diagnosis of chromosomal disorders is a new trend. The use of G-, R- and C-banding patterns, combined with the FISH technique by using molecular markers and some human chromosome painting probes/ spectral karyotyping, allowed the precise identification of chromosomes involved in the chromosomal abnormalities. The chromosomal disorders noted in India are;

1. 1;29 CFT in Jersey cross cow in Chennai (Thiagarajan *et al*., 1990)
2. 1;29 CFT in Jersey cross bull in MS used through AI for 9 years (Chauhan *et al*.,
3. 2009)
4. 7;16 CFT in HF cross bull under use through AI in KDC Mumbai (NDDB Biotech lab report 1999- 2000)
5. 7;16 CFT in HF cross bull before use through AI in MS (Patel,1999)
6. 1;9 CFTs in Gir bull in Gujarat State (Paderi et al., 2011b)
7. 16;20 CFT in Deoni bull calf in 16;20 in Karanataka State (Paderi et al., 2011a)
8. 8;29 CFT in one Gaolao Bull and it's 12 progeny in MS (Umrikar et al., 2013)

Less number of reports of Robertsonion Translocations / Centric Fusion Translocations (CFTs) in India is due to weak testing facility and awareness and not due to less prevalence of CFTs in Indian cattle population unlike wide distribution of the defect worldwide. Few reports on CFTs in India are sufficient to guess the probable fast spread the defect in dairy cattle population through AI as happened in Hungery, where one bull imported from Italy has transmitted 1;29 transloaction in many herds of Hungery (Kovacs , 1989). This is an alarming situation for livestock development programme of India , because all our future investments on applying progeny testing programme and biotechnological tools on such genetically unclean population so also spending on their maintenance, feeding, treatment will go in vain unless we identify and prevent such defective breeding livestock especially cattle and buffalo.

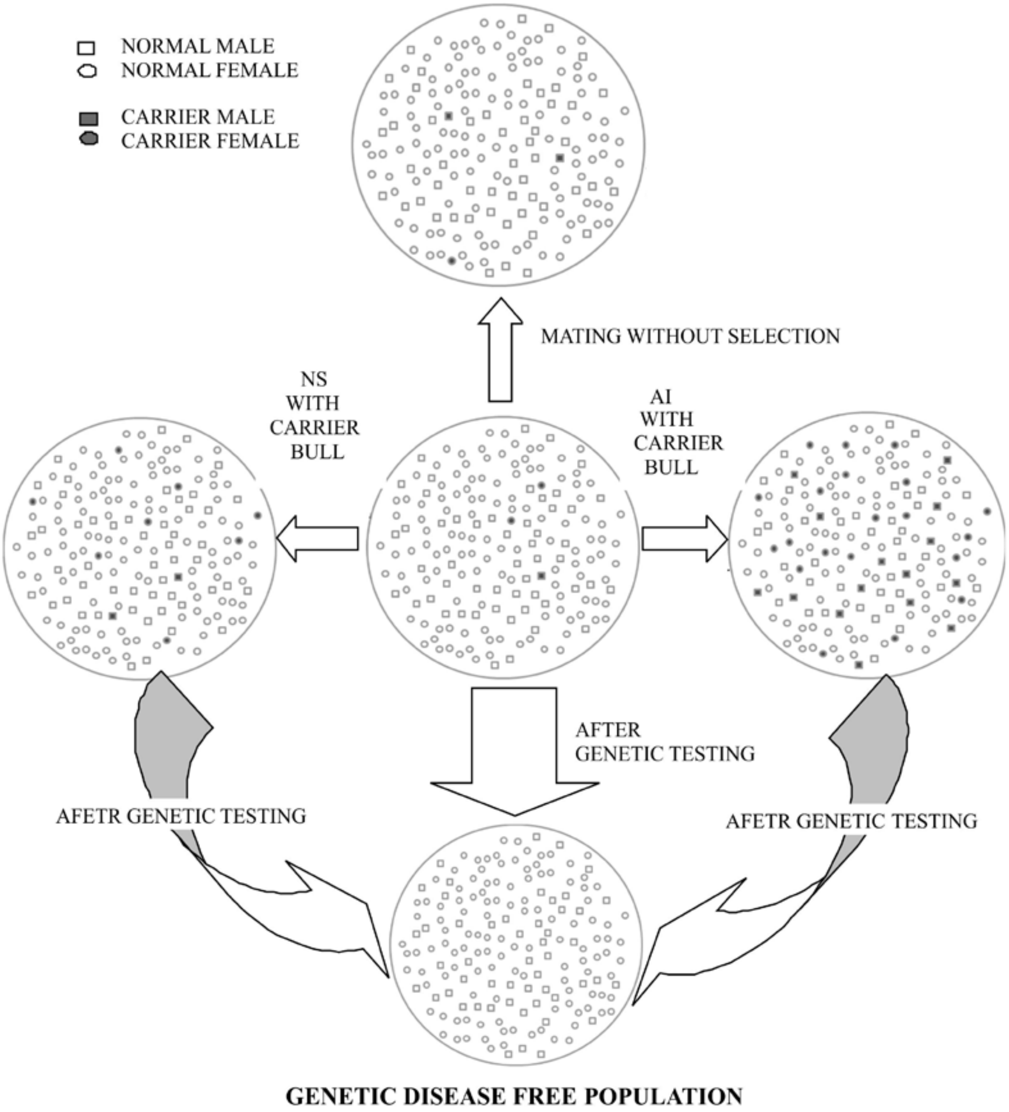
In Maharashtra State there are past incidences of spread the cytogenetic disorders in crossbred HF and Jersey breeding bulls used through Artificial Insemination and in Gaolao cattle through natural service . Maharashtra state has five cattle breeds, three buffalo breeds. Cattle breeds of Maharashtra are of draft and dual purpose and play important role in rural agriculture. Hence, it is prudent to more thoroughly investigate chromosomal abnormalities in breeding stock of cattle and buffalo in each state of the country for strengthening the conservation / improvement programme of various breeds and monogenic disorders in HF/HF crosses. Such defects were already known to affect badly the national economy worldwide and India can not escape from that unless strict measures been followed to create well equipped animal genetic investigation labs nationwide by provision of specialized manpower and infrastructure, for probing bulls with genetic defects. A Genetic Investigation Laboratory has been established in Maharashtra Animal and Fishery Sciences University at Bombay Veterinary College, Mumbai with support from Government of India under Rashtriya Krishi Vikas Yojana . Since 2012 peripheral blood samples of various cattle and buffalo breeds of Maharashtra and Punjab State viz. HF , HF crosses, Jersey , Jersey crosses , Sahiwal , Dangi, Khillar, Deoni, Gaolao, Red Kandhari cattle and Murrah, Nili Ravi and Pandharpuri buffalo after establishment of the laboratory. The said laboratory could strengthen the Gaolao Cattle Conservation Programme in MS by detecting a herd with large number of carriers developed from common source bull Also a HF crossbred bull under use in AI have been detected as carrier of genetic disorder BLAD and eliminated.Thus this laboratory has a great potential to prevent economic losses in future to the Animal Husbandry sector depending upon future support received as presently the laboratory has acute shortage of skilled manpower. The MS state AH department is taking serious concern on this aspect and the possibilities are being explored .

Considerable investments are happening in India for genomic selection research to increase the selection efficacy in future. However, investments on improving selection efficacy with presently available tools of elimination of carriers of genetic diseases at field level as per national breeding policy are still desired.

Reccommendations

There is an urgent need to create statewise genetic disease testing laboratory network in India with few regional labs and a core laboratory for successful livestock improvement particularly breed improvement / conservation programme.

DISSEMINATION OF GENETIC DISEASES IN THE POPULATION AFFECTING IMPROVEMENT STRATEGIES



ABSTRACTS

TS-III-01

SUSTAINABLE MANAGEMENT OF NATIVE CATTLE VARIETIES THROUGH VALUE ADDITION OF CATTLE WASTE

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The economics of rearing heat-tolerant and disease resistant indigenous cattle breeds that provide healthy A2 milk should not be one-dimensional and restricted to their low milk yield instead shall also encompass their other cost-effective outputs like livestock waste and draft potential. There is hence an urgent need to standardize the conservation and management practices of native cattle breeds and varieties towards a more sustainable approach based on the value addition of livestock waste, in addition to milk. The present study was therefore undertaken to explore the various value addition strategies of dung and urine of native cattle maintained at the Vechur cattle conservation unit of Instructional Farm, Pookode. A specific formulation of *Panchagavya*, a bio-fertilizer made from the combination of five livestock products was prepared and standardized. Field trials were conducted on fodder and orchid plants in horticultural nurseries to assess the utility of *Panchagavy*a in agricultural operations. The studies revealed that the flowering rate, flower size, germination rates, drought hardiness and pest resistance of the plants improved by around 30% after the application of *Panchagavya*. A more sophisticated approach was formulated for the collection of fresh urine and successful marketing linkages were established with some of the leading Ayurvedic R & D centers of Kerala. The distillation of Vechur cow urine for the production of *Arka*, already proved to have immuno-modulant, anti-oxidant and bio-enhancing properties in bacterial, fungal and cancerous conditions, was also explored and a sophisticated mechanized approach was introduced for the same. A wide range of several other value added products from cattle dung and urine also have been successfully formulated. From the initiatives, it can be concluded that introduction of value addition strategies for livestock waste of indigenous animal genetic resources can ensure their sustainable conservation and management for improving the livelihood security in developing countries.

TS-III-02

LIVESTOCK OR LIABILITY: THE CHALLENGE SIDE TRACKED

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The 19th Livestock Census (2012) reflected that there are about 512 m livestock in India, of which about 96 and 4 % are located in rural and urban habitations respectively. All of these livestock population is not equally favoured by their keepers to maintain and care due to priority differences in their utility. These ignored ones could be called as burdening. Including those roaming as 'STRAY' and those highly uneconomic with their keepers, the number of the total burdening livestock becomes quite enormous i.e. 22.33 m (7.5%), significant and alarming for livestock keepers of India as a whole as well as for policy makers and implementers. These include 16.4 m cattle and 5.9 m buffaloes. A judicious and rationale placement approach of these burdening stocks would not only economically benefit their keepers but would also help improve their miserable life. It has been seen that without any practical and legally approved culling policy, these burdening stock have found themselves in miserable conditions for

survival. There is a lot of scope to find out solution to this grave problem, provided it is genuinely thought over by all concerned agencies and parties. By sincere placement of these burdening stocks at better sites would also help our indigenous and crossbred animals to express their potential, which otherwise seemed difficult, and thus extend their sustainability period. The paper discusses possible options to this grave problem.

TS-III-03

IMPACT OF INDIGENOUS TECHNOLOGICAL KNOWLEDGE IN CONSERVATION AND SUSTAINABLE MANAGEMENT OF AnGR FOR RURAL LIVELIHOOD IN NORTHERN INDIA

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The concept of sustainable animal husbandry in Indian agricultural scenario has aroused interest in Indigenous Technical Knowledge which are based on experiences which gathered momentum through generations and are being developed and improved through informal experimentations. The indigenous practices have not been recognized and documented in a scientific manner though livestock breeders and farmers have well recognized old aged parental practices and widely used for sustainable production and their livelihood. Indigenous technical knowledge in animal husbandry production management is in vogue throughout rural India and is hardly or little documented and there is danger of extinction of these knowledge. It is very important to document ITK's, its assessment and validation. The ITK's are being used in almost all the category of farm animals by the farmers / breeders for health, reproduction, breeding, feeding, housing and routine management practices of cattle, buffalo, sheep, goat, pigs and poultry. The study was carried out purposively in eight districts namely Sasaram & Kaimur in Bihar, Yamunanagar & Ambala in Haryana, Ludhiana & Gurdaspur in Punjab and Srinagar & Bandipora in J&K. Twenty practicing farmers (ITK users) / Key informants were selected randomly from each districts. A Semi-structured Interview Schedule and Participatory Rural Appraisal (PRA) were used for collection of data and Quantification on Indigenous Knowledge (QuIK) technique was applied for validation of ITK's. Some important ITK's were documented and validated in cattle, buffaloes, sheep, goats, pigs and poultry. The results in cattle and buffalo group for different ITKs were observed in (I) thatched housing (100%), (II) storage of dry grasses / bhusa on roof of dwelling houses / tree trunk (95%), (III) crossbreeding of cattle x yak (60%), (IV) milk protection during grazing of cows with calf at foot (80%), (V) perforated bottle for showering of dairy animals (60%), (VI) control of ecto-parasite using BYP (75%), bloat (80%), clinical mastitis (85%) and tail rotting in buffaloes (75%). The results of management in sheep and goat group were observed in (I) identification / marking of animals with pucca colour / paint (90%), (II) milk protection bags in goats (95%), (III) ear-cutting in goats (95%), (IV) curtain in breeding buck (100%), (V) hair cutting of tail and hind legs in goats (70%). In pigs the most common ITKs observed in Haryana and Punjab was (I) jiggery maili (only) feeding (65%) and (II) mange control with diesel + 10% phenyl spray (90%) and in poultry the common ITK practices observed were (I) carrying birds in net / basket for marketing (62%), (II) thatched / wooden Darba / bamboo basket (95%), (III) grazing + kitchen waste (100%), (IV) local egg-nests (90%), (V) locally improved feeder / waterer (55%) and (VI) pecking in chicks (70%). In most of the cases, indigenous breeds were maintained by the farmers under study except in cattle. Based on study it may be concluded that if we have to document and conserve our AnGR of India, it is also very important to document, validate and conserve indigenous technical knowledge of livestock husbandry practices which is on the verge of extinction, because the livestock and ITKs are dependent on each other for sustainable management, production and rural livelihood at large.

TS-III-04

ROLE OF TELEVISION IN DISSEMINATION OF ANIMAL CONSERVATION AND LIVESTOCK DEVELOPMENTAL PROGRAMMES

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Telecommunication is a communication at a distance by technological means, particularly through electrical signals or electromagnetic waves. Television plays a major role in communication of information regarding animal husbandry and intern in the conservation of animal germplasm. In this regard research work was taken up to assess the response of the farmers towards telecommunication and its role in germplasm conservation and other Animal Husbandry activities with 120 sample of televiewers from three mandals of Chittoor district, Andhra Pradesh by administering a structured schedule to the respondents and the results were analysed with standared statistical tools. Majority of the televiewers had medium level of televiewing behaviour (78.3 %) and opined that the duration of telecast (100%), time of telecast (91.66%), repetition of the programmes (79.16%), local information coverage (31.67%) and regularity of the programmes (29.16%) should be increased to attract the views of farmers towards television. Majority of the respondents suggested that the time (100%) and duration (96.67%) of telecast programmes should be changed, schedule of the telecast programmes may be intimated well in advance (95.83%) and some preferred for a separate television channel (96.67%) to make the telecommunication a better media in the conservation and development of valuable animal germplasm by adopting the improved scientific technological information telecasted through television.

TS-III-05

TANUVAS EXPERT SYSTEM ON GOAT HUSBANDRY – A TOOL FOR ANIMAL GENETIC RESOURCE MANAGEMENT AT FIELD LEVEL

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Agriculture and livestock sector plays a significant role in the livelihood of rural population in India. Livestock is essential to millions of poor households across the country, as a source of income. Among various animal husbandry practices, goat farming plays a pivotal role as a source of livelihood for the rural poor since it provides sustainable income. The application of information communication technology provides new tools for improving access to information and disseminates knowledge widely at low cost. An expert system "*TANUVAS – GoatES*" was developed on goat farming and an experimental study was planned with the objective to test the effectiveness of the developed expert system on symbolic adoption behaviour. The study was conducted in Dharmapuri, Salem and Thiruvannamalai districts of Tamilnadu. From among the total number of goat farmers owning intensive system of goat farming, a total of 20 goat farmers and 10 goat farmers were selected randomly from each district totalling to a sample size of 60 for treatment group and 30 for control group. It is concluded that 65.00 per cent of the respondents were medium extent category followed by 35.00 per cent in low extent before pre-exposure on goat husbandry practices. Exposure of the developed computer based goat expert system led a remarkable increase so that 83.33 per cent of the respondents had higher symbolic adoption followed by 16.67 per cent for medium categories, signifying better conviction among them to adopt goat husbandry practices. Hence, it was concluded that the extension delivery system should not depend too much on conventional extension methods, instead they have to adopt the new methods like expert systems for disseminating the needed information to the farming community.

TS-III-06

INDIGENOUS TRADITIONAL KNOWLEDGE USED FOR PRODUCTION AND MANAGEMENT OF BANNI BUFFALOES

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Banni buffalo has unique qualities associated with the ability to survive and produce under the hardships of hostile climate and limited feed resources in Banni area. Buffaloes are reared under traditional extensive production system through night grazing. In Banni, Maldharis adopted animal husbandry exclusive livelihood approach; they have invented locally adapted extensive production system and probably the most economic buffalo production system in the world. Buffaloes are trained to typical grazing on Banni grassland during night and come to the villages in the morning for giving milk. Maldharis have social and cultural bonds and affinities with Banni buffaloes. This has resulted as being part of day to day life and confers on their status symbol in community. Maldharis of Banni, have evolved number of Indigenous Traditional Knowledge (ITK) related to rain water harvesting and traditional extensive production system of Banni buffaloes, based on experience in dealing with the climatic conditions and available natural resources in Banni area. The ITKs are the part of considerable heritage of Maldharis and day to day management system under vulnerable climatic situations. The information on ITK were collected and compiled during survey work carried out for characterization, evaluation and conservation of Banni buffaloes (2004 to 2012). Maldharis of Banni area has developed a "Well in Pond" system for harvesting, conservation and utilization of rain water for their animals and domestic use, called VIRDA. The traditional extensive Banni buffalo production system through night grazing adapted by Maldharis and more specifically buffaloes trained under this unique system clearly reflected their ITK used for homoeothermic measures to overcome the heat stress problems and also better feed conversion efficiency. The '*Talu*" means lock of wooden device used for avoiding calf suckling during night grazing, traditional method of concentrate feeding to animals without any wastage of concentrate and management of buffaloes during night grazing with the help of bell in the neck are the important traditional knowledge system contributed by Maldharis for management of buffaloes under extensive production system.

TS-III-07

KNOWLEDGE LEVEL AND CONSTRAINTS FACED BY THE FARMERS IN DAIRY CATTLE BREEDING

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An attempt was made to measure the knowledge of livestock owners regarding breeding and feeding of mineral mixture and the constraints faced by them in these two activities. The present study was conducted at Hyderpuram village of Vellore District in Tamilnadu. Random sampling was adopted to find out 50 dairy farmers in the selected village. A tailor made, pre-tested tool was applied to collect the data and analysed statistically. The study revealed that the knowledge level of the farmers regarding the major domain – importance of heat signs was 68.75 per cent followed by the knowledge about artificial insemination (AI) (53.80 per cent) and knowledge about pregnancy diagnosis (48.33 per cent). Under the domain – importance of heat signs, majority (97.33 per cent) of the respondents possessed the knowledge about the heat signs followed by the knowledge on nature of discharge

(72.66 per cent), change in milk yield (65.33 per cent), estrus interval (48.75 per cent) and metestral bleeding (13.33 per cent). In the domain of AI, majority of the farmers (77.33 per cent) knew the advantage of AI over natural service followed by the knowledge on time of breeding / insemination (56.00 per cent) and post-calving insemination (40.00 per cent). With regard to pregnancy diagnosis, it was found that 82.67 per cent of the farmers knew about the importance of timely pregnancy diagnosis and only 15.35 per cent of the farmers had the knowledge about the gestational heat. Regarding the knowledge about the scientific feeding and its importance on the reproduction, majority (84.33 per cent) of the farmers were unaware of the importance of mineral mixture feeding. Only 32.33 per cent of the respondents had the knowledge about the wholesome concentrate feeding and 45.00 per cent of the respondents knew about the feeding of pulses and legumes as green fodder for better reproduction in their animals. As far as the constraints in breeding, most (86.50 per cent) of the farmers reported unavailability of timely AI service as the major constraint. With regard to feeding, majority (73.50 per cent) reported that unavailability of mineral mixture in their village itself as the major constraint followed by high cost of mineral mixture (65.33 per cent), non-availability of fodder seeds and slips (58.75 per cent) and lack of water for irrigating the fodder plots (43.25 per cent).

TS-III-08

SUSTAINABLE FEEDING AND MANAGEMENT PRACTICES BY CATTLE'S KEEPERS IN WESTERN UTTAR PRADESH

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The study was undertaken in Shamli district of Western Utter Pradesh. Nine villages from the three blocks were selected. Ten dairy cattle owners randomly selected from each of the village were interviewed randomly. Thus, the entire sample consisted of 90 respondents from selected villages. The adoption level of cattle husbandry practices varied from farmer to farmer. To measure the intensity of constraint in the adoption of recommended cattle feeding practices, three point continuum scales was used. The recorded responses were counted and accorded ranks. The adoption level regarding feeding practices of cow rearing by providing the clean and fresh drinking water was ranked 1st with a score of 180; and grazing was ranked last with a score of 17. Out of eight practices included in adoption of calf rearing management practices, feeding of colostrums to new-born calves within two hours after the birth had the highest score (1st rank). The 2nd and 3rd ranks were occupied by attending new-born calf and proper cleaning of mucous from mouth and nostrils (139 score) and trimming of hooves (94 score), respectively. Lighting, disinfection of naval cord, regular deworming of calves, right time and method of dehorning and right time castration were ranked 6th, 5th, 4th, 7th and 8th respectively. However, such types of practices are followed for sustainable livestock husbandry in this area since long time.

TECHNICAL SESSION – IV

AnGR information management system and breeding strategies for improvement of livestock and poultry

INVITED PAPERS

1. STATUS OF SHEEP AND GOATS IN DEVELOPED COUNTRIES AND THEIR CONTRIBUTIONS TO LIVELIHOOD SECURITY OF RURAL FARMERS IN DEVELOPING COUNTRIES

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Introduction

Role of Sheep and Goatsin Global Agriculture

World human population is growing at a fasterrate and presently has passed theseven billionhead countbut the rate of food production is moving at a slower pace. Almost 40% of the people are living in countries with economies growing at 6% annual rate that could create a large middle class population with higher purchasing powerthatwill lead to moredemand for animal proteins.Classification of countries asdeveloped and developing is based on a few economic and social indictors, "Developed countries" are in highly industrialized regionsand"Developing countries" are in other regions of Africa, South and Southeast Asia, Western Asia, Latin America and the Caribbean.

Among livestock species, ruminants are well known as the most efficient converters ofan abundant biomass into valuable animal products such as milk, meat and fiber. Economic contributions of sheep and goatshave been well recognized in animal-agriculture and goats have an inherent ability touse coarse fibrous feeds much more efficiently than sheep (Lu, 1988; Devendra, 2007; Liang and Devendra, 2014).The preference for rearing sheep and goatsby rural farmers is mainly due to their small size, low initial capitaland input costand animal's adoptabilityto harsh dry climatic conditions. Further,these animalshave been playing a significant role by providing high quality nutritional products and food security to rural farmers in developing countries. Beside food security,they are also important assets for millions of farmers during unexpected economic crisis or uncertainties to maintain theirlivelihood and socialstatus (Devendra andChantalakhana, 2002; Devendra, 2010; 2013). Goats and sheepalso have been usedto keep unnecessary weeds under control in plantations, orchard crops and in range lands. Additionally, animals will add their dung and urine to improve the fertility of soil to maintainoverall productivity of the land.

Current levels of meat and milk per capita consumption in the developing world is only about one-fifth of that in the developed world, and increasing the productivity of sheep and goats may provide anadequate supply of low cost meat and milk that are very much desired foods by humans due to their high quality protein source, taste and other nutritional aspects.

Sheep and Goat Population Growth Trend in the World

Latest statistics (FAO, 2013) shows that during the period of 1993-2013, total worldwidesheepand goat population have increased from 1.7 billion to almost 2.3 billion head. Though, the sheep population had a slight downward trend during the first half (1993-2002) of the presented decade,but thereafter the population steadilyincreased to 1.2 billion headbyyear 2013.Almost 65.2% of the world sheep population is confined to Asia and Africaand therest are in Europe, Oceania and Americas. The highest numbers of sheep werefound in China, Australia, India and the Islamic Republic of Iran (Table 1).On the other hand, during 1993-2013 periods, the goat population increased from 600 millionto one billion headacross the globe of which 93%(~930 million) of goats werelocated in Asia (60.6%) and Africa (32.4%), respectively and China,India, Pakistanand Nigeriaarecountries with highest number of goats (Table 2).

World Milk Production from Goat and Sheep

Dairy goat has been considered asthe "poor man's cow" in developing counties. Milk from dairy goats has several beneficial attributes and fresh milk is consumed by children, pregnant mothers and elders especially in developing countries. Sheep and goat milk are used predominantly for cheese production in developed countries

According to recent FAO (2013) statistics (Table 3),world sheep milk production in 2012 reached to 10.1 million tonnes that is an increase of about 2.3 million tonnes (a 29% increase) from the 1992 production level of 7.8 million tonnes. Highest sheep milk producing countries were China, Turkey, Greece, Italy and France and mostsheep milk goes into specialty cheese production. The world cheese production from sheep milk was 614.9 thousand tonnes in 1992 and that amount increased to 684.4 thousand tonnes in 2012. Highest cheese producing countries were Greece, China, and Italy, and Syrian Arab region.

World goat milk productionin 2012 reached17.8 million tonnesfrom the 1992 production level of 10.5 millionthat is an increase of 7.3 million tonnes (~ 3.5% annual rate of increase) (Table 4). Highest goat milk producing countries were India, Bangladesh, Sudan, Pakistan and France.The world cheese production from goat milk was 338.7 thousand tonnes in 1992 and it increased to 457.4 thousand tonnes in 2012; highest goat cheese producing countries werenamely, Sudan, France, Iran, Greece andSpain.

World Meat Production from Sheep and Goat

Meat production from sheep and goatshas increased steadily over the past 20 years. Nutritive analyses indicate that goat meat is lower in fat, lower in cholesterol, higher in protein and iron content than beef, pork, lamb and poultry (USDA, 1989).

World mutton production from sheep during the 20yrs period (1992-2012) increased from 7.2 million tonnes to 8.5 million tonnes (Table 5), of which 61% was from Asia and Africa combined and the balance 39% were produced in Europe (17.7%), Oceania (15.8%) and Americas (5.5%), respectively. The top lamb/mutton producing countries were China, Australia, New Zealand and United Kingdom.During the same period, world goat meat production increased from 2.9 million tonnes to 5.2 million tonnes (FAO, 2013) where 93.2% of meat production were from Asia (68.7%) and Africa (24.5%), respectively. The top goat meat producing countries were China, India, Pakistan and Nigeria that had a combined output of ~ 3.5 million tonnes (Table 6).The future demand forlamb and goat meat may continue to grow at a higher rateespecially in Asia and Africa and it appears that for millions of farm families in the above regions, raising sheep and goat would provide a good source of income, livelihood and food security.

World Fiber Productionfrom Sheep and Goats (Wool and Mohair)

Wool production is declining across the world in spite of the rapidly growing human population.This decrease may be due to large portion of population increaseis in warmer regions where demand for wool is low. In the temperate zone there is a demand for wool but the farm price of wool has not been sufficiently high to stimulate increased production. Furthermore, the main substitute for wool is synthetic-fibersthat are sold for low prices and are competing with products made out of wool. According to FAO (2013) statistics, world wool production has declined from highest production level of 2.9 million tonnes recorded in 1992 to the level of about 2.1 million tonnes in 2012. Combined wool production of 57.1% was reported from the regions of Oceania, Europe and Americas and the top producing countries were Australia, China, New Zealand and Argentina, respectively.

Mohair is considered a high quality specialty fiber for producing attractive, expensive textile products. Details of mohair production are not available from FAO statistics. Before mid-1970s US Government had a program of subsidy for wool/fiber production and there were large numbers of Angora goats in Texas producing mohair but with the elimination of wool/mohairsubsidy program, production of mohair declined.

Status of Sheep and Goat Industries in Developed Countries

Unlike inthe developing countries where mixed crop-livestock farming is a common practice, livestock production (dairy, beef, lamb and pork etc.) in developed counties is generally a specialized mono-operation. Thoughthe total number of sheep and goatsin developed countries is less than 25% of the total world population, the average animal performanceis generally much higher than the average performance of animals in the developing countries. It is because in developed countries, animals generally receive ahigher level of nutrition, better management and use ofsuperior genetics and selective breeding of high performing stockscombined with application of various technologies.

Interestingly, in the developed nations there has been an increase in animal numbers and product output, during the past decades, due to the effect of large scale industrialization, "Factory farming" of livestock has led to economics of "scale" which played a major role to move livestock producers to "get big" or "get out" of business that has resulted in decline of farm numbers in rural communities and it'sespecially so with dairy cattle and sheep enterprises. There is a strong belief and a negative image that intensive animal production may have contributed to land degradation, pollution of water resources,emissionof greenhouse gases, and erosion of biodiversityacross developed nations.

Sheep Industry (Meat, Milk and Wool)

Historically, Australia, New Zealand and United Kingdom are the leading lamb and wool producing countries among developed nations. The sheep and wool industry remains one of Australia's most important agricultural commodities, contributing around 18% of the gross value of farm production and over $5.2 billion in export income (Ashton, 2003). Over the past decade, Australian lamb industry has been on a downward trend in total sheep number and the export market for live-sheep stays good. The popular meat sheep breed is the Australian Merino.

In some EU counties, for example France, Greece and Italy beside production of meat and fiber, milking sheep are used to produce substantial quantity of milk for specialty cheese production. Milking sheep in France produce on average about 2.8 times more milk as they did in the '60s because of the improved management and genetics through selective breeding of superior animals and providing with better nutrition and management of ewes (Lindsay and Skerritt (2003).

GoatIndustry (Milk, Meat and Fiber)

In developed counties, goat farming is typically for milk production and European countries are the main producers of goat milk with Francetaking the lead. Goat meat production has not been a popular enterprise in developed countries. Angora goats are used for mohair production. In fact before 1990s, there weren't any specific "meat goat" breeds availablein the developed world. A few dual purpose dairy-meat breeds, such as the Nubian and LaMancha, and any other goats (ex: Spanish goats)were considered as goats for meat production. Goat meat is rarely sold in any large grocery chain stores except in a few specialty ethnic food stores or directly from small processors. Further, theSpanish goats that were essentiallyused to control noxious weeds in range and native grass lands by ranchers and owners of orchards/tree cropswereproducing additional meat for local markets.However, over thepast decade, that trend has changeddue to growing demand for fresh goat meat that is being created by the influx of a large number of immigrantsfrom Asia, Africa, the Middle East, Latin America and Caribbean regions moving into USA, Canada and EU countries, and traditionally these people have a strong preference for goat meat over other red meats due to their religious faith.

Except in Australia and New Zealand, in general, the supply and demand for goat meat situationin most developed countries with large immigrant populations may be similar to that in the USA. Current supply of goat meat produced in U.S. farms is not enough to meet the demandand more than 18 million pounds of goat meat (i.e. approximately 500,000 whole goat carcasses) were imported into USA from Australia and New Zealand. It appears that meat goat production is one of the fastest growing enterprises in USA, particularly in small farms (Solaiman 2006; Nadarajah 2010) and that has led to the importationof a few meat goat breeds during the mid-90s intoNorth America, particularly the "Boer" breed of South African origin and the "Kiko" breed from New Zealand. Both of these breeds have distinct characteristics and are most suitable for meat production (Casey and Van Niekerk, 1988; Newman and Paterson, 1997; Lu, 2002; Browning et al., 2004). Prolificacy in Boer goat is high and twin births are common and have been reported that approximately 50-60% of does produce twins and another 10 to 15% does produce triplets (Campbell, 1984).Presently, these breeds have gained global recognition as the premier meat goat breeds due to their excellent body conformation, fast growth rate and good carcass quality. In addition, these breeds have been used for crossbreeding with and other goats to boost goat meat production (Blackburn, 1995; Waldron et al., 1997;Ward et al., 1998; Ball et al., 2001;Browning et al., 2004; 2009; and Getz 2010).The interests in these breeds have led to registry of herd books and formation of the respective breed associations namely,the International Boer Goat Association, the American Boer Goat and the American Kiko Goat Associations.

Factors Contributed to Higher Performance of Sheep and Goatsin Developed Countries

Availability of high level of nutrition and management

In most developed countries, sheep and goat producers have well-developed pasture/forage resources and high quality hay/silage to feed their animalsduring summer and winter monthsalong with access to adequate minerals. Often lactating/fattening animals receive small amounts of supplemental grain or by-products of grain sources. Additionally, animals are well managed or cared to improve health, reproduction and overall productivity by providingprotective shelter and clean water.

Developmentof breeding objectives and infrastructure for genetic improvement programs

Breeding objectives for genetic improvement of sheep and goats have been aimed to improve a variety of economic traits depending on the products for which animals are bred for but all are focused on overall improvement of the efficiency of production.The genetic progress achieved over the past decades in other livestock species like the dairy and beef cattle through organized selective breeding programs in the developed countries are remarkable.Performance recording of individual animals and subsequent evaluations for genetic merit has been long recognized as a prerequisite for genetic improvement of livestock for desirable traits (Owen, 1971;Ponzoni, 1988;Uljee and Rennie, 1990; Galal,1998). Although sheep and goat numbers in developed countries are relativelysmall, thesuccessful experience of genetic improvement programs in other livestockspecies have motivated the sheep and goat industries for adopting technologies such as artificial insemination, individual performance and progeny testing to select the best genetics (Moioli and Pilla, 1994; Shrestha and Fahmy, 2005; 2007a) .

Recording pedigreesof individual animals and their performance

Identification of all animals and adopting a record keeping system with full pedigree and performance of animalsin breedingflocks/herds have allowed for performance/progeny testing and the use of BLUP analysis to obtain estimated breeding values (EBVs)of individual animals to rank them for genetic merit.

Dairy goat and sheep industries have taken the lead to setup programs for adoption on-farm record keeping systems. Electronic record keeping is an efficient tool for monitoring performance of individual animals to examine the herd productivity and for generating necessary data for regional and national genetic evaluations. An individual animal's performance is a combination of genetics and environment (example: sex, birth types, age of dam, herd/flock management etc.) and such environmental factors could make an animal look good or bad and must be corrected by applying analytics to identify true genetic component to rank individuals for genetic merit. Meat goat industry is slowly adopting of on-farm electronic recordkeeping systems(Waldron et al., 1997; Nadarajahet al., 2008; 2009).

Identification and characterization of economically important traits

For dairy sheep and goats, common selection criteria are milk volume, content and concentration of milk fat and protein. Other factors considered by industry are milk characteristics (total solids and somatic cell count), and length of lactation, ease of milking, udder shape as well as udderhealth, reproduction, conformation and managementcharacteristics (feet, worm resistance, temperamentand fertility etc.). For lamb and goat meat production, important economic traits include growth, reproduction, and carcass merit, resistance to parasites and diseases. However, for meat goats, being a small size industry, currently there isminimal infrastructure and support available to improve genetics and enhance production. The meat goat industry needs to organize with stakeholders to establish performance and progeny testing programs for selecting superior animals for economically important traits.

Ranking of individual animalsfor genetic merit to increase production efficiency

Among developed counties, Australia has taken the lead on genetic evaluation of sheep through their flagship genetic evaluation program "LAMBPLAN" and recently extended to genetic improvement of meat goats through their "KIDPLAN" (Ball, et al., 2001). These evaluations are used to make accurate selection to increase genetic progress over other conventional selection procedures. Well established national/regional genetic improvement programs are available to support lamb and wool production using analytical models that are applicable to respective industries in collaboration with large number of producers participating in such breeding schemes.

Similarly, France has taken the lead to provide the best organized progeny testing program for genetic improvement of dairy goats. Other EU countries are adopting similar technologies and their program is still in the growing phase. They do have established organizational structures for goat and sheep breeding and selection programs managed through farmer's cooperatives for progeny testing of young males and to make sires available for AI (artificial insemination) and natural mating while maintaining nucleus herds with superior genetics for overall improvement of dairy goats and milking sheep.In USA, genetic evaluations for dairy goats are computed annually by USDA from records made available through Dairy Herd Improvementprograms of the American Dairy Goat Association. For evaluation, a multi-trait statistical model similar to that used for dairy cattle is applied but lactationrecords are editedappropriately for dairy goats. Evaluations are computed for milk, fat, and protein yields and component percentages and conformation traits; an economic index based on genetic merit for milk, fat, and protein yields is calculated based on economic values for dairy(Wiggans and Hubbard, 2001).

Genetic evaluation for sheep in the USA is limited to a few breeds using the LAMBPLAN, and beside that to support sheep and meat goat producers a few ram/buck performance testing centers are in place for evaluating bucks for growth, rate of gain, structural soundness, body condition, and overall ranking for genetic merit based on phenotypic test records. Evaluating and ranking young rams/bucks from participating farmer's herds under a common environment for growth, average daily gain, body condition and resistance to internal parasites is a step in the correct direction in the absence of progeny testing. Interested producers have an opportunity to participate in theram/bucks performance testing program and end-of-test sales at test stations are an excellent place to purchase rams and bucks for breeding.

Evaluationof appropriate breed resources and crossbreedingto increase production

Compared to the developing countries, number of sheep and goats breeds available in developed countries is a very small percentage (FAO, 2013) ,and through research and evaluation over time, only a few breeds have gained recognition as suitable for their production of milk, meat or fiber. Most of the research was aimed on evaluating them for economically important traits as purebreds and as crossbreeds with other breeds to take advantage of the hybrid vigor and complementarity among crosses (Waldron et al., 1997 and Browning et al., 2006; 2009; Shrestha and Fahmy 2007b).

A potential exists to increase sheep and goat productivity and efficiency by increasing reproductive rate, largely through exploitation of genetic variation among breeds. Use of high prolificacy breeds, applying crossbreeding systems, improved reproduction and accelerated lambing/kidding to produce more than once per year could increase the overall productivity of sheep and goats.

Breeding sheep and goats for resistanceto parasites and diseases to maintain a healthy herd/flock

Infestation of gastro-intestinal parasites is one of theproblems facing sheep and goatindustries across the world including in the developed nations (Krawczyk and Slota, 2009; Mandonnet et al., 2014). Loss of production, costs of anthelmintic drugs, and animal death are some of the major concerns associated with widespread infection of internal parasites, particularly, the blood sucking pole worm (Haemonchuscontortus). Chemical control of parasites has been successful to some extent but continueduse of them has led to the parasites become resistant to many drugs (Mortensen et al., 2003). There is evidencethat selection for resistance tointestinal parasites is feasible in sheep (Bishop, 1997; Bishop and Stear, 2003). Beside the fecal eggs count, another technique for estimating intestinal parasitic infestation iscalled FAMACHA© which is designed to provide sheep and goat producers as a tool for improving their management of Haemonchuscontortus infestation (Kaplan et al., 2004). The FAMACHA© system is designed to assess animals with clinical anemia by scoring the eye color due to Haemonchuscontortus infestation and widely used in buck performance testing centers to screen animals for worm infestation and rank bucks for resistance to parasite (Nadarajah et al., 2013).

Application of other technologies

In developed countries, seed stock producers have been successfully using several technologies to improve the sheep and goat production such as the AI, Estrus synchronization, super ovulation and embryo transfer (Greylingand van der Nest, 2000). There is room for expansion of such technologies, particularly wide use of AI using semen from superior ram/bucks for overall improvement of sheep and goats. Also, application of othermodern technologies to include introgression of major genes (QTLs)and genomics selection by identify potential genes that control economic traits could further improve milk, meat and wool production of sheep and goats..

Improved marketing for meat, milk and live animals

Since meat andmilk productsarewidely consumed by humans, the production systems, processing and marketing these products with good hygiene is utmost importance. Modern day consumers are becoming more concerned with the quality and safety of the food they eat. As major lamb producers,Australia and New Zealand have well-organized marketing systems to meet local and export market forlamb and goat meat as well as live animals. Similarly, Europe has alsoestablished marketchannels to sell their cheese and meat both locally and internationally. Wool trading is usually done through open bidding/public auctions.Live sheep export trade is mainly to the Middle Eastern countries and are sourced primarily from Australia and New Zealand.

In USA, live sheep and goats for meat are mostly sold through local livestock auction barns by weight or per head to interested buyers, often with some sort of gradingdone by federal marketingagents. Farmers have access to up-to-date market information published by the federal market agency at regular intervals. Some goat producers also sell live goats directly to consumers at the farm-gate and this practice allows goat producers a chance to interact with consumers and understand consumer's needs.

Improvement ofSheep and Goat Production in Developing Countries

Role of Sheep and Goats in the Livelihood of Rural farmers in Developing Countries

Traditionally, sheep and goat farming is an integral part of the livelihood and survival of millions of small farmers across many parts of the developing countries. Mixed crop-animal systems are very common in developing regions of Asia and Africa and often farmers raise mixed flocks of sheep and goats together for sustainability and productivity to maintain their livelihood and food security. It's estimated that about 200 million smallholder farmer families are living in the regions of Asia, Africa and Latin America and their livelihoods depends on livestock farmingand beingtheir main source of income (McDermott et al., 2010; Devendra, 2013). Although goats and sheep are producing significant quantity of milk and meat in developing countries, individual animal performance is far below than the animals in developed nations and has a great potential for improvement.

Goat population in India is ~ 124.6 million which is about 15% of the world's goat population and are predominantly handled by women living mostly in rural areas spread over 600,000 villages across India (Singh et al., 2008) and Indiaranks second in goatsand third in sheep across the world. Thus, India has a tremendous potential to diversify, expand these industries to meet the growing demand for meat and milkproducts, if provided with research, education and extension support to increase production through improved nutrition, reproduction, genetics, health, product quality and marketing.

What can the sheep and goat producers in developing countries learn from developed nations?

A misconception is that innovation is just for the more advanced developed countries and with limited understanding of technologies, and what it means to producers in developing countries. Production of products, processing methods, marketing and distribution are often new to them although not to the developed world. However, it is becoming increasingly important as global competition increases in markets for livestock products and with the available information and communication technologies.

Sheep and meat goat producers are small producers from rural villages with minimal access to any type of institutional support for education, technical training and access to quality breeding stock to improve the productivity of their herds.

Evaluation of appropriate breed resources, identificationand characterizationof important economic traits

High producing breed types imported from the developed regions may not necessarily be the best breeds suited for the local environmental and managementconditions in developing countries. Indigenous breeds that are more adopted local conditions have to be evaluated for expansion, upgrading and crossbreeding with other promising breeds.To a limited extent, with support from central governments, the dairy cattle industryhas adopted performance recording and genetic evaluation programs in some developing countries but little has been practiced for sheep and meat goats.

Lately, there are signs for adaptation of new technologies to improve sheep and goats in developing countries and a good example is the work at a non-governmental organization, Nimbkar Agricultural Research Institute(NARI) near Pune in Maharashtra State.The Animal Husbandry Division of NARI is involved in breeding and genetic improvement oflocal sheep and goatsand has introduced the Booroola gene (FecB gene) discovered in Australia for increasing fecundity into the Garole breed of sheep that led to the development of NARI Suwarna and NARI Composite breeds, respectively. The sheep flock with FecB geneat NARI hasresulted inmore than 60% ewes having twininstead of single lambs.Both the NARI Suwarna and Composites reported to have 50% higher lamb production than the local Deccani sheep that have only single lambs (Nimbkar et al., 2002).The NARI is also responsible for introducing the popular meat goat, the Boer, breed into India through importationof Boer embryos from Australia to establish a nucleus herd and promote crossbreeding of local goats with the Boerby offering frozen semen and Boer bucks to producers.

Establishinggenetic improvement programs

High quality genetics contribute to production, efficiency and increase profit. Development of the necessary infrastructure and support for national/regional genetic evaluation programs in developing countries will be very expensive. Initially, it would be easy to establish a few regional performance test centers to evaluate rams and bucks for growth, rate of gain, feed efficiency, conformation and resistant to parasites and ranking young males for genetic merit would be feasible and less expensive. Such programs could provide an opportunity forproducers to purchase performance-tested siresfor breeding and owners of sires that ranked as top genetics should be recognized and rewarded to motivate other producers to participate in the testing program. Using performance tested superior males selected for economically important traits should benefit substantially to the producers of sheep and goats in developing countries.

Improved feeding and management of animals

Providing high quality pasture and forage to sheep and goats is very important to increase the productivity of flocks/herds. Individual animal performance can be improved through better management and care to enhance the health, reproduction and overall productivity of animals while allowing them tohave access to clean water and minerals, along with supplemental feeding of grain or by products of crop residues during shortage of pasture or forage source.

Provide necessary research, education and extension/ outreach support

There is a need to improve sheep and goat production in developing countries for the benefit all farmers. To shift from the subsistence production to a more market-oriented opportunity, it is necessary to provide theinfrastructure and supported by an objective official policy, institutional commitment and increased resources to improve the livelihoods of the ruralfarmers through application of new and appropriate technologies to improve overall productivity of sheep and goats in rural communities.

Producer training/workshops, that teach about animal genetics, goat management and handling, feed sources and nutritional values of feed, record-keeping, production of high quality meat and milk, and the Hazard Analysis and Critical Control Points (HACCP) system, should be included into the educational programs. The ultimate goal should be aimed to empower and motivate farmers especially the women and the vulnerable by improving their skills and capacities to enhance the sustainability of their livelihoodthrough financing productive demand-driven investment projects.Additional support such as access to agro-inputs and credits, adequate storage capacity, access to formal markets, and up-to-date market information, extension services and formulating cooperative forms of organizations should be continued until the sheep and goat industries become a self-supporting enterprise.

Conclusion

There is a real need to increase the production and supply of food from animal-agricultureto meet the increasing demanddue to population growth, but also due to such factors as income growth, urbanization and changing consumer preferences towards favoring of high quality proteins from milk and meat products. More food must be produced sustainably, through the spread and implementation of existing knowledge and by investment in technology to improve quantity and quality, food safety, environment friendly production and processing.

Sheep and goats are well positioned as preferred animals for meat and milk production among small farmers in many parts of the world, particularlyin developing countries. Increasing the production of sheep and goats could reduce malnutrition, improve food security and enhance livelihoods, and perhaps the most significant effect would be elimination of extreme poverty, particularly in rural communities that involved in farming these livestock.

Genetic improvement of sheep and goats can contribute to production, efficiency and profit. There is an urgent need for the sheep and goat industries to develop suitable genetics with significant potential for higher production and resistance to internal parasitic infestation. Farmers should be encouraged and motivated to keep useful records for individual animals in their farms.Wide propagation of genetically elite rams/bucks will result in producing healthy, stronger, improved future progeny with near full expression of their productive and reproductive performance. Farmers need the necessary infrastructure and support to take advantage of the opportunity for a profitable and sustainable production system. The challenge is therefore to identify appropriate technologies and adopt policies to develop a sustainable livestock production system to meet the increasing demand for livestock products.Sheep and goat producers need necessary researchand extension support as well as the motivation, education to understandall aspects of the sheep and goat production systems.

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Table 1 World sheep population (in million heads) and their distribution

Heads by region Average 1993-2013	1993	2013	Based on numbers - Top five producing countries
World Total - in million heads	1120	1200	
Asia - 41.0%	459.2	492.0	China & China Mainland
Africa - 24.2%	271.0	290.4	Australia
Europe - 13.4%	150.1	160.8	India
Oceania - 12.9%	144.5	154.8	Iran (Islamic Republic of)
Americas - 8.4%	94.1	100.8	
Info from FAO, 2013Livestock Statistics: http://faostat3.fao.org/browse/Q/*/E			

Table 2 World goat population (in million heads) and their distribution

Heads by region Average 1993-2013	1993	2013	Based on numbers - Top five producing countries
World Total - in million heads	600	1000	
Asia - 60.6%	363.6	606	China & China Mainland
Africa - 32.4%	194.4	324	India
Americas - 4.4%	26.4	44	Pakistan
Europe - 2.2%	13.2	22	Nigeria
Oceania - 0.4%	2.4	4	
Info from FAO, 2013Livestock Statistics: http://faostat3.fao.org/browse/Q/*/E			

Table 3 World sheep milk production (in million tonnes) and their distribution

Output by region Average 1992-2012	1992	2012	Based on output - Top five producing countries
World Total - in million tonnes	7.8	10.1	
Asia - 44.5%	3.47	4.49	China and China mainland
Europe - 34.1%	2.66	3.44	Turkey
Africa - 20.9%	1.63	2.11	Greece
Americas - 0.4%	0.031	0.040	Italy
Oceania - 0.1%	0.008	0.010	
Info from FAO, 2013Livestock Statistics: http://faostat3.fao.org/browse/Q/*/E			

Table 4 World goat milk production (in million tonnes) and their distribution⚜

Output by regionAverage 1992-2012	1992	2012	Based on output - Top five producing countries
World Total - in million tonnes	10.5	17.8	
Asia - 55.9%	5.87	9.95	India
Africa - 22.4%	2.35	3.99	Bangladesh
Europe - 18.0%	1.89	3.20	Sudan
Americas - 3.7%	0.39	0.66	Pakistan
Oceania - 0.0%	0	0	France
Info from FAO, 2013Livestock Statistics: http://faostat3.fao.org/browse/Q/*/E			

Table 5 World lamb-mutton production (in milliontonnes) and their distribution

Output by region Average 1992-2012	1992	2012	Based on output - Top five producing countries
World Total - in milliontonnes	7.2	8.5	
Asia - 44.3%	3.096	3.765	China & China Mainland
Europe - 17.7%	1.274	1.504	Australia
Africa - 16.7%	1.202	1.419	New Zealand
Oceania - 15.8%	1.138	1.343	United Kingdom
Americas - 5. 5%	0.0396	0.0 468	
Info from FAO, 2013Livestock Statistics: http://faostat3.fao.org/browse/Q/*/E			

Table 6 World goat meat production (in million tonnes) and their distribution✾

Output by region Average 1992-2012	1992	2012	Based on output - Top five producing countries
World Total - in million tonnes	2.9	5.2	
Asia - 68.7%	1.99	3.57	China & China Mainland
Africa - 24.5%	0.71	1.27	India
Europe - 3.2%	0.09	0.167	Pakistan
Americas - 3.0%	0.087	0.156	Nigeria
Oceania - 0. 5%	0.0145	0.0261	
Info from FAO, 2013Livestock Statistics: http://faostat3.fao.org/browse/Q/*/E			

2. ISSUES AND IMPACT OF MODERN IPR REGIME ON MANAGEMENT OF ANIMAL GENETIC RESOURCES IN DEVELOPING COUNTRIES

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The conflict between intensive system of livestock rearing and the sustainable technological innovations generated by livestock keepers based on native livestock genetic resources and traditional knowledge (TK) associated with them will pose important challenge for technology driven productivity enhancement of livestock in developing countries. In the present knowledge based global economy, technology driven growth in livestock sector helped dominant players to corner the benefits at the cost of smallholders in under developed and developing countries particularly in poultry and pig industry which led to many challenges pertaining to control of technologies. Generally the animal breeding and production takes place within the national boundaries as per customary laws and knowledge; whereas the livestock products are marketed at global level. Therefore, national and international as well as regional laws and Intellectual Property Rights (IP) and global commitments are relevant to development of livestock sector. In the present knowledge based global economy protection of intellectual property (IP) is critical for technology development and diffusion in all fields including livestock sector (Ramesha *et al*., 2010). International conventions and treaties together with the rapid developments in biotechnology have led to new conditions for the access of genetic resources and TK. The Convention of Biological Diversity (CBD) and the requirements under WTO/ TRIPS have led to stricter mechanisms for access to benefit sharing and control of genetic resources as well as the new regimes for protection of biological innovations. This new environment has created both threats and opportunities for biodiversity rich developing countries. The future development of livestock sector depends on adoption of new and innovative production and processing technologies, and proper market tie-ups. Diversification and high value produce will add new dimensions to this sector. A paradigm shift is required in livestock sector from production orientation to quality and cost orientation in the WTO era (Ramesha, 2011).

In the recent past livestock farming in developing countries have changed rapidly and become technology intensive, similar to that had taken place in the plant sector during 1980's. The increased exploitation of animal genetic resources from developing countries is also becoming a major concern. The challenge for biodiversity rich countries is to guard against bio-piracy of their indigenous animal genetic resources, and safeguard associated traditional knowledge of livestock keepers and traditional healers. Another concern is the export of genetic material to countries that did not ratify the Convention on Biodiversity.

The proliferation of free trade agreements, both multilateral and bilateral, has led to an unprecedented growth in international trade in livestock products. During last decade cheap livestock products particularly meat and milk powder from developed countries (European Union) flooded the markets of under developed and developing countries resulting in loss of livelihood to livestock-keepers from these countries. Thousands of chicken farmers in the Philippines went bankrupt during the "Broiler Crisis" in 1999–2000, when huge quantities of cheap poultry were imported from the USA (Susane Gura, 2008). Differential subsidies and tax benefits enjoyed by the industrial livestock producers particularly in the developed world and international trade agreements are impacting livestock production in developing countries.

Under Trade Related Intellectual Property Rights (TRIPs) any country ratifying the Global Agreement on Trade and Tariffs (GATT) and becoming a member of the World Trade Organization (WTO) must establish minimum standards for intellectual property rights. Under TRIPS Article 27.3, members must provide various forms of intellectual property, many of which are relevant to livestock sector. Intellectual Property (IP) is a category of property that confers rights over intangible creations of human intellect. IP rights as a collective term which includes a) patents b) trademarks, trade names and service marks c) geographical indications d) trade secrets e) industrial designs f) layout designs (topographies) of integrated circuits g) protection of plant varieties and h) copyright and related rights and trade secrets. With the advent of genetic engineering and novel multilateral IPR agreements a new era of gene hunting has started. This has alarmed and threatened the general public and raised economic, legal and ethical concerns (Rothschild *et al*., 2003).

PATENTING IN LIVESTOCK SECTOR

Patenting of life forms is the most controversial aspect even among WTO members. Patents represent the largest form of Intellectual property (IP) and their development is regulated by laws differing from country to country. These laws and their interpretations are subject to change, especially when new technologies are introduced. Any product or process or design which involves an inventive, novel and non-obvious step capable of industrial application could be patented. A patent represents a legal monopoly granted by a country's government to an inventor, permitting the patent owner to prohibit anyone else from making, using or selling this invention for a specific period of time (presently 20 years).

Mega biodiversity countries provide genetic resources for modern animal breeding and biotechnology industry. The genetic resources have been transferred freely to other countries in the past; under the understanding that these are common heritage of humanity. With the development of modern biotechnology, there is possibility that our breeds/varieties may be genetically altered and the new variety/breed may later be substituted for the original breed/variety from which it was developed. There is a threat of bio-piracy with regard to native livestock breeds and associated traditional knowledge. If proper controls and checks are not included in the system of IP protection relating to AnGR, there is a danger of Multi National Companies (MNCs) becoming owners of breeds/varieties originating from biodiversity rich countries. Patent protection will discourage the natural selection that, at present, takes place at farmers' level.

In the livestock sector, patents have been granted for gene sequences with utility such as genetic markers. A New Zealand company, Agmark, has claimed a patent on the "Booroola" gene, which regulates the ovulation rate in sheep. The Booroola gene can be traced back to Bengal sheep, which were imported from Kolkata and crossed with Merinos (Köhler-Rollefson, 2005). The patent covers animals that are produced in a breeding programme in which the DNA test has been used, but not those animals that carry the gene naturally. The open question is whether the patent also covers the offspring of the animals that have been tested for the presence of the gene. Another notable patent application is one by Monsanto for a series of twelve patents on pig breeding. One of the first conflicts in quantitative animal breeding resulted from a patent entitled "Method of Bovine Herd Management" granted to the Cornell Research Foundation (Cornell University) in the USA in 1994 and Canada in 1998. The invention is for the "test-day model" and includes the gathering of data, mathematical treatment and the use of the data by dairy producers (Rothschild *et al*., 2003; Scholtz and Mamabolo, 2006). The novelty and non-obviousness of the patent has been seriously questioned. The practices of gathering, manipulating and using data by dairy producers have existed for nearly 100 years (Schaeffer, 2002). In South Africa, these principles have been in use since 1917. The patent therefore claims rights to a practice that has been public knowledge for a long time. The novel idea within the patent is the specific mathematical model and procedures that were developed for the analysis of test day yields. In European Union and some other countries patents can also be granted on normal animals, which have merely been subjected to certain techniques like a gene diagnosis, or a process for determining the animal's sex. The European Patent Office granted patent on Dolly the cloned sheep to the Roslin Institute in Edinburgh (patent application EP 849 990) in 2001. The US Company XY Inc. was in 2005 granted patent EP 1257168, which covers a method for selecting sperms by sex for the artificial insemination of mammals. The first European patent on genetically manipulated dairy cows was granted in 2007. Under patent number EP 1330552 "inventors" from Belgium and New Zealand claim processes for breeding cows, which give more milk or milk with altered constituents. The cows are produced either by marker assisted breeding and bred normally, or by having more milk genes additionally incorporated into their genome.

PATENTING OF LIVESTOCK BREEDS

Biotechnology is providing the capability to produce novel genetically modified organisms (plants, microorganisms and animals), which are commercially valuable and industrially useful. Patent protection for these innovations is being sought in many countries. Under TRIPs agreement it is not possible to have a valid patent claim, which claims an essentially biological process. Hungary is one of the few countries that grants patent protection for animal breeds (WIPO, 1995) , as specified in Articles 110 and 111 of the 1995 Hungarian Law on the Protection of Inventions by Patents.The Bulgarian Law for Protection of New Plant Varieties and Animal Breeds has been enforced since 1996. In terms of patentability of higher life forms, such as animals, they are not treated any differently by the Australian Patent Office from the way in which lower life forms are treated. The East African Boran cattle breed has also been patented in Australia (Scholtz and Mamabolo, 2006). The practice in New Zealand is similar to that of the Australian Patent Office. In general patents to animals are also allowable in Japan. In contrast to these countries, animals (whether transgenic or otherwise) are not patentable in countries such as Argentina, Brazil and China (Blattman *et al*., 2002) and India (Ramesha *et al*., 2010 a, b). Animals and animal varieties *per se* are not patentable in South Africa.

TRADEMARKS

Trademarks are signs or symbols registered by a manufacturer/producer or merchant to identify goods and services. Genetic material *per se* cannot be protected or covered by a trademark. A trademark could be a useful tool in biotechnology sector as a means of value addition tool.

GEOGRAPHICAL INDICATIONS

Geographical Indications (GIs) are signs or expressions used to indicate that a product or service originates in a country/region or specific place. Both Trademarks and GIs are used to identify the products. A Trademark puts emphasis on the producer or a manufacturer of a product whereas a GI highlights the geographical origin of a product and the characteristics derived from it. GI does not protect the breed or genetic material *per se* but adds commercial value to the animals of breed reared in a particular region. They may be used as a value addition mechanism. Origin-based marketing in which control over production processes remains with the livestock keepers can empower livestock keepers versus corporate interests and provide greater earning power. Geographical indications prevent others, except the producers of goods from the original region from using that particular geographical indication incorrectly as a trademark for other products than those from the area. Trademarks and geographical indications could be used for value addition and thus aid to protect registered breeds. In France Bresse breed of chicken is produced in the Bresse geographical area only as defined by law under protected designation of origin (Verrier *et al*., 2005) and sold at 50-60 per cent higher price. Roquefort cheese can be made only from the milk of the Lacaune sheep breed. Geographical indications are used to protect interest of livestock keepers in developing countries also like Karoo lamb (South Africa) and Chos Malal goat meat(Argentina).

BIODIVERSITY RICH COUNTRIES AS PROVIDER OF GENETIC RESOURCES

Mega biodiversity countries provide genetic resources for modern animal breeding and biotechnology industry. The genetic resources have been transferred freely to other countries in the past; under the understanding that these are common heritage of humanity. With the development of modern biotechnology, there is possibility that our breeds/varieties may be genetically altered and the new variety/breed may later be substituted for the original breed/variety from which it was developed particularly in poultry and pigs. If proper controls and checks are not included in the system of IP protection relating to AnGR, there is a danger of Multi National Companies (MNCs) becoming owners of breeds/varieties originating from biodiversity rich countries. Though plant varieties are protected through a *sui generis system* in many countries since 1920s, no such system is available for AnGR. Biotechnology firms are interested in patenting processes and genes used in animal breeding as such. The recognition of patents on AnGR would result in banning of breeding protected variety/breed. Patent protection will discourage the natural selection that, at present, takes place at farmers' level. The patenting of broad traits like increased milk yield or broad claims on genes/animals may lead to monoculture and monopoly which would result in suffering to the pastoralists, small and marginal livestock keepers.

Biodiversity rich countries like India should promote bio-prospecting to upgrade local capabilities and to prevent bio-piracy. Indian Biodiversity Act (2002) gives emphasis on protecting traditional knowledge associated with genetic resources (Ramesha *et al.,* 2010a). In India patent applications have to disclose the source of genetic material and associated Traditional Knowledge (TK) in relevant cases (Ramesha *et al.,* 2008, 2010b). In the modern biotechnology era, there is danger of animal genetic material from biodiversity rich countries being exploited by others including large international companies.

NEED FOR A *SUI GENERIS* SYSTEM

In spite of significant contribution of animals to the food security and nutrition, laws and policies including intellectual property protection on genetic resources so far focused only at plant genetic resources. In the modern biotechnology era, there is danger of animal genetic material from biodiversity rich countries being exploited by others including large international companies. The development of legally binding "International Framework on Animal Genetic Resources" is therefore becoming a matter of urgency. During the First International Technical Conference on Animal Genetic Resources held at Interlaken, Switzerland delegates from 109 countries including India on 11th September 2007, have adopted a Global Plan of Action for Animal Genetic Resources, the first internationally agreed framework to halt the erosion of livestock diversity and support the sustainable use, development and conservation of animal genetic resources. (http://dad.fao.org). There is a need for legally binding internationally accepted system for access and sharing of benefits from the use of AnGR and associated traditional knowledge. Biodiversity along with the associated local expertise is a valuable asset as a raw material for biotechnology research and is an insurance against environmental change (Ramesha *et al.,* 2007, 2008). The proponents of IP protection are of the view that patent based approach is essential to provide incentive for innovation and to increase flow of funds to R & D in animal agriculture. They claim that possible negative balance will be outweighed by benefits likely to be derived in terms of new varieties/breeds.

Harmonization of IP regimes, access to technologies required for biotechnological research and development through easy licensing and/or patent exemptions especially for public benefit oriented research would pave way for making private investments and private-public participation attractive.

Epilogue

Protection of native livestock breeds and associated traditional knowledge through appropriate *sui-generis system* is essential for conservation and their sustainable use in the modern IPR regime. Identification of genes for unique characteristics in native livestock breeds will go long way not only in the advancement of science and livestock production, but also pave way for patenting of gene sequences for these traits. If proper internationally accepted legal system is developed with respect to use of livestock biodiversity, patenting of novel genes will bring about economic benefit to the livestock keepers in the modern IPR regime through benefit sharing and help in conservation and sustainable use of native livestock breeds.

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3. SIGNIFICANCE OF MICROCHIPPING IN CONSERVATION OF VECHUR CATTLE

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Introduction

Saving of Vechur cattle from the brink of extinction was an almost impossible task. This could be achieved under the leadership of the author with the cooperation of some environmentally conscious students and farmers. Financial help was received from Indian Council of agricultural research since the second year and all other support was from Kerala Agricultural University. The historic beginning of the project was in 1989 as a Kerala Agricultural University project in the College of Veterinary and Animal sciences, Mannuthy. The details are given in reference 1and 2.

Government were promoting crossbreeding and only cross breeding. The native bulls were getting castrated as a part of the Government Livestock improvement policy Act 1961. Hundred percent transformation to crossbreds was aimed at. But grading up with exotic bulls was happening. All the native cattle were to be wiped off. Conservation of Native cattle was totally against Government policy in Kerala. This was different in other States. Kerala cattle were ND cattle- Non descript- and bulls were scrub bulls Farmers were moving along with the current as they were looking for high producing animals and the advantage of heterosis was there. But as generations passed ,the milk production was below the expected level and diseases were emerging. The periodical foot and mouth outbreak in Kerala inspite of the vaccinations was resulting in setbacks to dairying. The efforts were to industrialise dairying. Integration of Agriculture and Animal husbandry was falling apart. During the green revolution, the short paddy varieties introduced, reduced the roughage to the animals. Agriculture started deviating from using organic manure to chemicals and pesticides. In 80s this trend reached the peak.

It was at this juncture the conservation project started. This was much earlier to the Earth summit which advocated Biodiversity Conservation. Mainly four arguments or beliefs were put forward (Ref.3) (leaflet prepared and circulated in Malayalam in 1989) to convince the public and to join the cause. The arguments for conservation of Vechur cattle were to:

1. Conserve Biodiversity of the nature
2. Preserve the heritage based on Kerala's history and geography
3. Keep the raw material for research in the present and also in future when more modern equipments and technologies would be available
4. As an insurance for the future in the advancing climate change and new emerging diseases.
5. For a small farmer who cannot afford the sophisticated management required by the crossbred cow and at the same time needs milk just for home consumption and not for sale

Now looking back it is felt that the objectives were very apt and feasible..Probably the results came truer and more need based than expected 26 years back.

The conservation project underwent different stages as planned in the beginning. First was just a multiplication to increase the number .this was for the first 10 years. There were calves not phenotypically Vechur. A few had spots here and there as of Holsteins. They were mostly from the cows collected from field and which came to the centre pregnant. The bull details were not known, but most probably they were from crossbred semen. Such calves were sold away. This culling resulted in a good selection and from the next generation calves selection of bulls for breeding could be morerigorous.

Figure 1

Once the animals were given to farmers the problem was pure breeding. Bulls/Semen were not available in far off places. Many travelled long distances to get semen from the University.Semen was not available anywhere else Many cows got crossbred. The purification process started reversing in some cases. So the Vechur Conservation Trust started a germplasm centre in the home tract and chilled semen supply started from there.

As time passed, farmers realised more and more, the importance of Vechur and other native cattle .Demand for Vechur was there from the beginning from farmers. As the news of conservation reached far and wide the demand from other States also increased. In 2002 The University sold 2 cows and a bull to Madhya Pradesh (Deendayal Upadhyaya Institute) and it is understood they multiply there and the number has increased. Many people from other States bought cows from farmers of Kerala at exorbitant rates.

At this juncture Kerala Government became interested in conservation of native cattle. The Government were concentrating on Gir and other breeds of cattle in their farms and supplying semen from these breeds. But there, the problem was that Government's effort was directed to conserve native animals of other states .The zero budget farming propagation gave a boost to using native cattle. The farmers also got the impression that the dung and urine for zero budget farming could be from any Indian cow. But along with the Governmental efforts on other native cattle, this also gave an impression that any Indian breed is a native breed. Actually Native cattle in Kerala means traditional varieties of Kerala. The performance of cattle from other states was not good as expected. The climate and feed availability for the larger animals from other States were not congenial to them in Kerala. So the smaller animals received more attention and demand was higher. The Government realised the importance of Vechur cattle and other native cattle and included native cattle conservation in the policy in line with the national policy.

Once it was thought that the major problems in conservation are over the second phase started.

Pure breeding is the key to conservation

The medicinal value and certain other qualities proved or attributed started making a hype for Vechur. The market value went up. This led to extensive sales of cows majority from unreliable sources. Other small cows from Kerala and neighbouring Karnataka were sold as Vechur. Fraud practices in sale might look just unethical. But deeper, the whole conservation programme could get upside-down.

Cows with the farmers are genuine in some cases and not so in many cases . These are to be differentiated. The pedigree shown below is of one of the three cows of a farmer. In many other cases the pedigree is not traceable. This pedigree could be traced from records. This was the descendant of a Vechur cow and bull sold to Malanad society from the University by the end of 90s. The sale details were available and monitoring could be done. But in most of the cases this is difficult. The dam may be known, but not the bull details. Some farmers are not keen to obtain the bull details and keep the records. Some agencies supplying the semen or bull are also not giving the details or they do not have it. But the semen supplied from the University as well as the Vechur Conservation Trust records the donor bull and is shown in the cash receipt and hence the pedigree is traceable. This cash receipt from the Trust is carefully kept by the farmer as the trust charges the farmer for pregnancy and not for dose of semen. Some farmers keep all records accurately. The Trust uses the bulls from the University or their descendants .So pedigree from bull side is traceable from the foundation stock and such bulls are selected.

The University though supplies bulls or semen with details there is no mechanism to follow up. The limitation of the Trust is man power and funding. The Trust is able to trace the animals in limited area .But the Vechur cows though few in number are spread out in all the districts of Kerala and other States. The cows taken far off places in most of the cases are not bred true also.

Probably conservation has reached a stage where more careful strategies are to be implemented. Milk recording started as early as 1900 in Europe .This was the basis of selection. Individuals are evaluated in any improvement process. Bull evaluation for sex limited traits are done based on indirect ways though not on its own performance. It is known that 95% improvement comes from bull side.

How can a bull be selected if its ancestors from maternal and paternal side are not known? How can we make evaluations if individual performance is not known? The very initial step is to identify the animals all males and females of the population Identification of animals.

Animals in the Conservation unit of the University were carefully identified and recorded since beginning. Ear tags were used for identification. All calves born were tagged. So naturally animals sold also had the tags. Whenever tags were lost the animals were renumbered in the farm. This was difficult for the farmers' animals. Many animals with tags from other sources as in insurance and not belonging to Vechur breed are sold as Vechur. Fraud certificates are also available to catalyse this kind of sale, the complication starts here.

At this juncture the Vechur Conservation trust has started a project for permanent identification of Vechur and other native animals of Kerala. Agencies like NABARD and Kerala state Biodiversity Board and GEF are now collaborating with the Trust in conservation and community partnership. Steps are now taken to identify and register farmers' cows. Two breed associations have been started. One is for Vechur and the other for Kasargod under the guidance of the Trust.

Recently the Trust started microchipping. Microchips, Applicators and Electronic reader were purchased using funding from NABARD project. There was some small fund earmarked as incentive to the farmers. It was at the rate of Rs. 500 per animal which could be given in cash or kind to the farmer. There could not be a better incentive than identifying the genuine animal in a permanent way. Microchipping is planned for Vechur and other native cows under the project .

Microchip is a permanent method of electronic identification. Technology in this is passive Radio Frequency Identification (RFID). The chip is very small and is of a grain of rice in length and thinner than a black pepper seed. This is implanted under the skin. The site chosen in this project is upper back of the ear.

Microchip with a pepper seed

Chip implantation

A Microchip Applicator is used for implantation.A veterinarian or any trained person can do the implantation in a few minutes, but it lasts a lifetime. As this microchip is not visible from outside and requires an electronic reader, a numbered plastic ear tag is put on the ear. These two are entered in the record of the individual. The electronic reader is used during visits from the Trust. A pedigree chart is planned for each animal identified with microchip. The Trust is giving different grades to the animals depending on the details of pedigree. A cow whose pedigree is shown in fig.6 is given grade A.

RFID Ear Tagsare used in many countries for identification of individuals and improving managemental techniques .They are Ear tags with RFID microchips .

Uses of microchip

Microchip implantation helps in Accurate selection of Animals for Breeding, Pure breeding & Conservation, Avoiding inbreeding i.e. mating between Relatives, Prevent Fraud Practices in Sale,Tracing lost animals

Microchips are generally used by kennels in India and other places. They are found useful in registries, rescue shelters humane societies, clinics, farms and stables. animal clubs and associations, researchers, and pet stores for identification.

Conclusion

Conservation of native animals is inevitable. The animals from hot or hot humid conditions as in Kerala and other places would be an insurance for the future. In the eventuality of global warming the animals adapted to the cold climate may not thrive and the tropical animals would be needed. Conservation includes proper breeding.

Animal identification is absolutely essential for breeding and also management. Proper identity with permanent method would reduce fraud practices.

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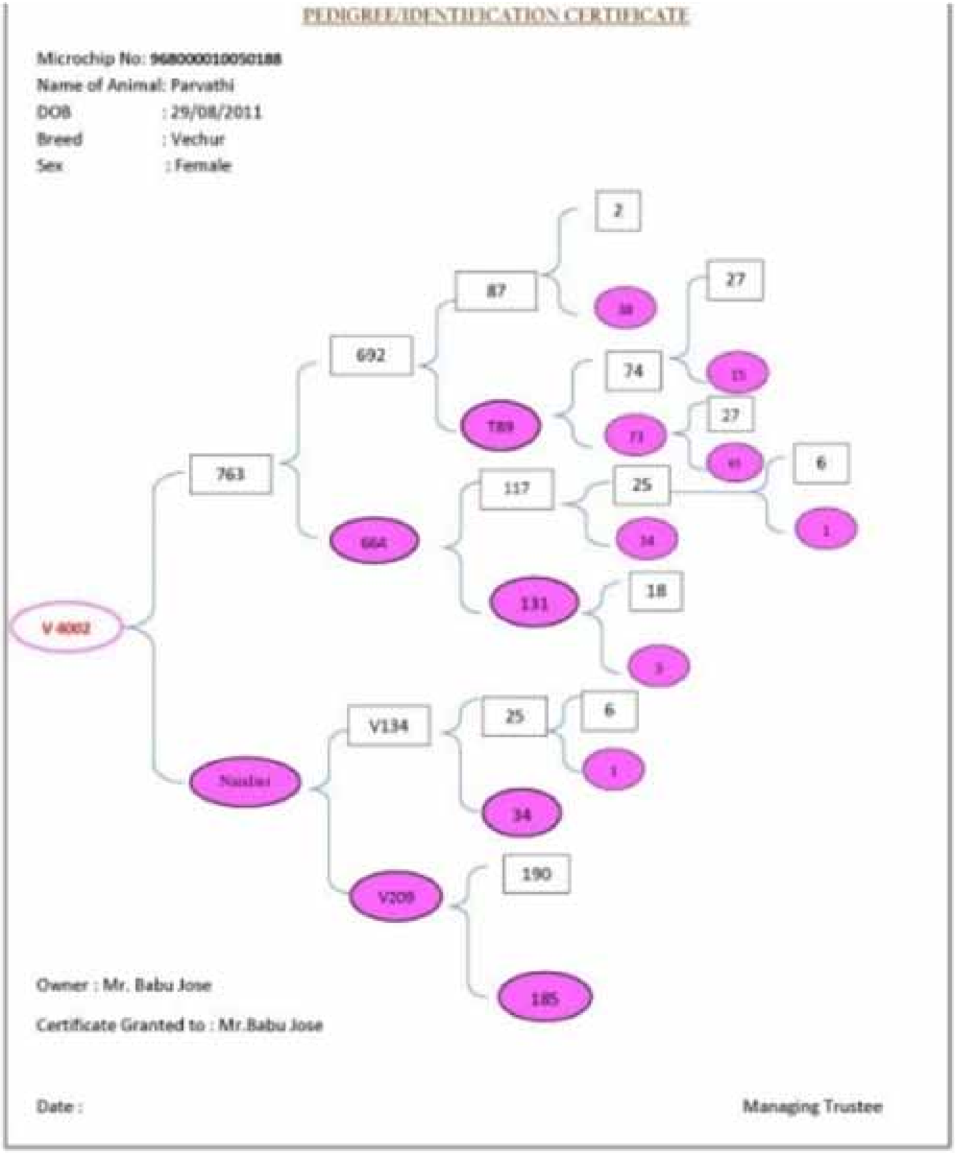

PEDIGREE/IDENTIFICATION CERTIFICATE

Microchip No: 968000010050188
Name of Animal: Parvathi
DOB : 29/08/2011
Breed : Vechur
Sex : Female

Owner : Mr. Babu Jose

Certificate Granted to : Mr.Babu Jose

Date :

Managing Trustee

Pedigree Certificate of cow belonging to Babu Joseph Pala

4. STATUS OF POULTRY GENETICS RESOURCES, CONSERVATION, STRATIGIES AND BREEDING POLICIES FOR THEIR IMPROVEMENT IN INDIA

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Introduction

The Indian sub-continent is considered as one of the most important mega-biodiversity center in the world. It is gifted with a rich reservoir of livestock and poultry genetic resources. The Indian Poultry industry is one of the fastest growing segments of agricultural sector. The agriculture sector has been rising at the rate of 1.5-2.5% per annum while the production of eggs and broiler has been increasing at the rate of 8-12%; broiler production is faster than egg production. Approximately, 66.7% of the total output from poultry is realized from the poultry meat sector and rest 33.3% from egg production. India has emerged on the world poultry map as the 3rd largest egg (67 billion eggs) and 5th largest poultry meat (3.4 million tons) producer. Organized sector of Indian poultry industry is contributing nearly 70% of the total output and rest 30% by the unorganized sector in the country. The poultry sector in India is transforming from a backyard activity to large scale integrated poultry farming with wide spread adoption of modern technology. The growth of the Poultry Industry in India is marked by an increase in the size of the poultry farm. The broiler industry is well developed in the southern states with nearly 60-70% outcome. The Layer industry once again is represented more in southern state especially Andhra Pradesh, Tamil Nadu, and Maharashtra together producing nearly 70% of the country egg production.

Status of poultry population in India

The total poultry population which was only 73.5 million in 1951 has made tremendous growth during the past fifty years and has reached 729.20 million in 2012 (19th Livestock Census, 2012). The poultry population has shown positive growth of 15.02% in rural area and negative growth of 25.60% in urban areas. India is third largest producer of eggs (only next to China and USA) and fifth largest producer of poultry meat (next to USA, China, Brazil and Mexico) in the world. Out of total egg production in India, 75% is consumed by the 25% population living in urban and semi-urban areas. The per capita availability of egg has increased from 5 eggs per year in 1951 to 55 eggs per year in 2012. The per capita availability of poultry meat is 2.1 kg which is very low compare to the world average of 124 eggs and 5.9 kg meat. The National Committee on Human Nutrition in India has recommended 180 eggs and 10.8 kg of meat per annum. According to Indian Council of Agricultural Research vision 2025, an increase in per capita availability of one egg generates 50,000 jobs.

Increasing population, consumption of convenient foods, awareness about inclusion of animal proteins, increasing purchasing power are some of the contributing factor to the growth of poultry industry. The major key issue in the poultry meat sector in India is the processing status to ensure optimum quality and hygiene levels. Inadequate linkage between R&D organizations and industry is one of the biggest challenges.

Poultry Genetic resource in India

The term poultry is applied to wide variety of birds including chickens, Quails, Turkeys, Guinea fowl, peafowl, geese, emu, ostriches and others. Chicken and ducks are two major domestic avian species in India used for eggs and meat production, both under organized as well as unorganized backyard or extensive system of production. According to 19th livestock census**,** Govt. of India, Chicken (including desi fowl) contributes 95% of the total poultry population in India, followed by 3% ducks. The remaining 2% is comprised of other domesticated poultry species.

Chicken

Poultry keeping in India is as old as its civilization. Red Jungle Fowl (*Gallus gallus*) is widely considered as the progenitor of today's modern chicken *Gallus gallus domesticus*. It is magnificent bird with beautiful plumage, aggressive behavior has curved rounded wings enabling swift flight, distributed widely but now restricted to wildlife reserves, yields around 50-70 eggs per year. Domestication of wild fowl started around 8000 years back in South-East Asia (Romanov and Weigend, 2001). In the pre-domestication era, natural selection was the only force evolving it to be fit the local environment, whereas, in post-domestication period, they were subjected to artificial selection initially for fancy traits like plumage colour, comb pattern and other external appearances and later for production traits such as egg and meat production.

Indian poultry farming system comprises of both unorganized backyard venture, patronized by poor and weaker section of the society in rural and tribal areas under zero input system and commercial poultry production under high-input system. The former plays important role in providing nutritional security and employment in the rural areas and thereby improving their socio-economic conditions of rural people and the later attempts to bridge the gap between availability of eggs/ meat and their minimum annual requirement.

Indigenous chicken breeds

The indigenous breeds of chicken are classified into heavy and light chicken breeds, which are characterized by mosaic plumage colour patterns, low egg production, slower growth rates, and broodiness and are spread throughout the country in scavenging flocks. Native non-descript strains have multicolour plumage, and a mixture of brown, yellow and black colour. These are good foragers and have relatively better resistance to some of the common poultry diseases. In heavy breeds, an adult female weighs between 2.0-3.0 kg, whereas in light breeds, adult body weight ranges from 0.9 to 1.5 kg. Fifteen indigenous chicken breeds have been registered and documented by the National Bureau of Animal Genetic Resources, Karnal (http://www.nbagr.res.in/). The description of some important indigenous chicken breeds is presented below: -

Aseel: It is an Indian Game birds, well known for its majestic gate, high stamina, pugnacity, and dogged fighting qualities (Panda and Mahapatra, 1989) with home tract in the states of Andhra Pradesh and in some areas of Rajasthan, U.P, Chhattisgarh and Madhya Pradesh. Amongst nine popular varieties of Aseel are **Peela** (golden red), **Yakub** (black & red), **Nurie** (white), **Kagar** (black), **Chitta** (black & white spotted), **Jawa** (black), **Sabja** (white and golden or black with yellow or silver), **Teekar** (brown) and **Reza** (light red), Aseel Peela and Aseel Kager (Black) are the most common. It is biggest in size among native breeds and measures about 28 inches from back to toe. They have long uniformly thick but not fleshy neck. Tail is small and drooping. The legs are strong, straight and set well apart. They produce plenty of well flavoured flesh but are not good layers (35- 45 eggs annually). Broodiness is very common. They posses small and firmly set pea comb. Wattles and ear lobes are light red. The beak is short. The face is long and slender and not covered with feathers. The body is round and short with a broad breast, straight back and strong tail root. The general feathering is close, scanty and almost absent on the breast. The average standard body weight varies from 4 to 5 kg for cocks, 3 to 4 kg for hens, 3.5 to 4.5 kg for cockerels and 2.5 to 3.5 kg for pullets.

Kadaknath: This is also called as “Kalamasi”, by its local name meaning the fowl having black flesh. It is one of the important indigenous chicken breeds of the country which is in habitat of Western Madhya Pradesh mainly the Jhabua and Dhar Districts and adjoining areas of Gujarat and Rajasthan. The eggs are light brown. The adult plumage varies from silver and gold- spangled to bluish black without any spangling. The skin, beak, shank, toes and soles of feet are slate in colour. The comb, wattle and tongue are purple. Most of the internal organs also show intense black colouration which is pronounced in trachea, thoracic and abdominal air sacs, gonads and at the base of mesentery. Skeletal muscles, tendons, nerves, meninges, brains etc also show various degree of black colouration. The meat is repulsive to look at but delicious. The blood is darker than normal blood. The black colouration is due to presence of an autosomal, dominant Fibromelenosis gene (Fm) causing deposition of melanin pigment in connective tissue of various parts of body and helps to protect the birds against UV radiation. This breed has evolved through natural selection and is well adapted to the local environment. Kadaknath demonstrates appreciable degree of resistance/tolerance to diseases compared with other exotic breeds of fowl in its natural habitat, in free range. Conversely, this breed is poor in egg production (lays around 105 to 110 eggs annually) in comparison to exotic layer breeds. it is categorized under layer among Indian native breeds. Kadaknath is the only Black Meat chicken (B.M.C.) breed of poultry in India. Though, the flesh of this breed is black, it is considered not only a delicacy of distinctive taste but also of medicinal value. The tribal uses Kadaknath blood in the treatment of chronic disease in human beings and meat as aphrodisiac. Kadaknath has special medicinal value in homeopathy and a particular nervous disorder. Research has shown that this species has lower cholesterol than white chicken and high levels of essential amino acids and hormones. The meat and eggs are reckoned to be a rich source of protein (25.47% in flesh) and iron. There are 3 varieties of Kadaknath viz. **Jet Black** (black in colour), **Pencilled** (black with white feathers in neck) and **Golden** (basically black with golden feathers on head & neck).

Ankleshwar: The name of the breed is derived from the area 'Ankleshwar' of Bharuch district in Gujarat state. Its native tract is in Bharuch and Narmada districts of Gujarat. The breeding area is extended to Jumbusar, Zagadia, Bharuch, Hansot and Valia of Bharuch and Dediapada, Rajpipla, Tilakwada and Nadod of Narmada districts. These birds are being kept mainly by tribes under backyard poultry farming as a source of income for their livelihood. These birds are maintained without vaccination and medication, and have reasonable feed efficiency as they survive on 25-30 g of grains, scavenging and maintain excellent fertility.. The average flock size varied from 5 to 10 birds. The comb is single and rose type. The egg shell varies from cream to brown in colour.

Chittagong: This is also called as "Malay". This is a large bird found mostly in eastern parts of country. It is a dual purpose breed with poor mothering ability. The adult birds are very strong, hardy and quarrelsome. The cocks measured sometimes 75 cm from beak to toe. They have a small pea comb resembling a small lump of tiny warts. The head is long. Beak is long and yellow. The wattles are red and hardly visible in the hen. The ear lobes are small, usually red and at times admixtured with a little white. The ear lobes are prominent and over-hanging. The breast is broad, deep and fleshy; the shoulder is broad with slight narrow loins. The wings project at the shoulders and are carried high. The legs are yellow and featherless. The plumage is close to the body, firm, short and glossy. Standard plumage colour is lacking, but the buff, white, black, dark brown and grey varieties are recognized. Standard weight of cock is 3.5 to 4.5 kg and that of hen is 3 to 4 kg.

Nicobari fowl: Nicobari fowl originated long back in the Nicobar group of Islands. This has been developed by Nicobari tribes under natural conditions. Presently there are 3 varieties of this breed having Brown, Black & White colours (Ahlawat *et al.*, 1999). Brown Nicobari is the original Nicobari breed. Black and White Nicobari fowl were developed by crossing with exotic breed, followed by random mating and selection for several generations. Brown Nicobari fowl are brown coloured hardy birds of medium size with short legs, have compact body conformation and are mostly single combed. Occasionally pea comb birds are also found. Wattles and ear lobes are pink or red in colour. They have short and thick neck, black plumage tipped with brown, the breast bulges in front, with a medium sized tail and long saddle feathers fitting well into the tail. The colour of the skin is pink-white or yellow white. The shank colour is pale pink. These birds are classified as a dwarf breed of fowl. It is the highest egg producer (128-142 eggs per annum under free range condition) among all Indian indigenous chicken breeds, resistant to some of the deadliest diseases of poultry, is very much adaptable to the local conditions of Islands and can fly well to avoid predators. They attain a body weight of 1392 g in 184 days (Ahlawat and Chatterjee., 2002). Nicorock and Nishibari were developed through cross breeding of Black Rock with Black Nicobari and Brown Nicobari with White leghorn respectively. Nishibari produces 160-170 eggs/ year and Nicorock produces 130-140 eggs/ year with an average of 1kg body weight at 12 weeks of age under backyard system (Kundu *et al.*, 2012). Other chicken genetic resources would also be presented and discussed.

Crosses involving Indigenous chicken

Besides, pure indigenous breeds, some crosses involving indigenous chicken breeds have also been developed for backyard/ family poultry. Crosses with exotic breed were developed by crossing of two or more exotic/ broiler breeds for developing medium sized, multi-coloured dual purpose strains for rural poultry production. Coloured crossbreds of recognized Indigenous breeds with exotic females particularly the CARI Red/ RIR have been developed which are suitable for rural areas. Some of the light or layer type crosses are **CARI-Nirbheek, CARI-Shyama, UPCARI, HIT-CARI, Garmapriya, CARl-Sonali, Gramsree and Grarnpriya, etc**. Similarly, meat/ dual purpose crosses include **CARI-Debendra,Vanaraja, Giriraja, Kuroiler, Nandnurn, M-Bro and CHB, etc.** Some of the commercial broiler hybrids are **Caribro Vishal** (White Broiler) **Caribro Dhanraja** (Coloured Broiler).

Duck

Duck occupy an important position next to chicken farming in India. As per animal husbandry statistics of Government of India there were negative trend in duck population, around 30 million ducks in India in the year 2003; 27.6 million in 2007 and 23.million in 2012 of which more than 91% are indigenous breeds. Duck account for 3% of total poultry population of India. Most of the duck species have descended from mallard or wild duck. Duck farming is primarily in the hands of small scale and marginal farmers, seems to be a new enterprise in southern and eastern coastal parts of the country. The states of West Bengal, Assam, Bihar, Manipur, Kerala Andhra Pradesh, Tamil Nadu and Orissa have a sizeable duck population. Ducks are the second largest source of table eggs and there are about 16044 lakhs of duck eggs produced in India. West Bengal has the highest duck population followed by Assam, Kerala, Tripura and Jharkhand.

Indigenous Duck breeds

Approximately, 90-95% of ducks are indigenous or non- descript types *viz* Chara and Chemballi of Kerala, Synthetmete and Nageswari of Eastern region, Aarani ducks of Tamil Nadu, Desi variety of West Bengal, and Pati, Deo, Cinahanh and Raj Hanh varieties of Assam.

Nageswari duck are white breasted. The original home tract is believed to be in Sylhet district in Asom which is now in Bangladesh. The average age of first egg is 188 days, and the annual egg production varied from 140-150 per year. Kuttanad ducks are native to Kerala, Chara and Chemballi are two varieties of Kuttanad ducks. Chara duck is named by farmers based on plumage colour. The typical Chara drakes are usually squat in posture and gait.

Modern commercial duck hybrids

Today the commercial stocks available for egg production are pure lines or strains-crosses of either Indian runner or Khaki Campbell or Pekin. The dual purpose strains nowadays available in the market are Pekin or Campbell breed selectively bred for egg production and growth traits. Pekin and Aylesbury breeds are the favorites for the breeders who are developing meat stocks. Strains of Muscovy as well as species hybrids of Muscovy with Pekin are also available for meat purpose.

Advantage of duck rearing over poultry farming: Ducks lay about 40-50 more and 15-20 grams larger eggs than chicken. Ducks eggs and meats contain more amount of omega-3 fatty acid. Duck eggs fetch more price than chicken. Ducks are quit hardy and resistant to many avian diseases. They do not require elaborate housing and need less attention than chicken. Ducks thrive well in marshy and water logged areas where chicken production is not possible. Ducks can be reared in foraging system with minimal supplementary feed, thus rearing is more economical. Cannibalism and agnostic behavior which is very common in chicken is not usually encountered with ducks. Ducks are suitable for integrated farming systems, such as duck cum rice/ fish farming. They are not so susceptible to disease and parasites in comparison to chickens. The down and small body feathers of the ducks are valuable and used for different industrial purposes. Ducks are good exterminators of potato beetles, grass hoppers, snails and slugs.

Constraints of Duck farming in India: Despite above-mentioned advantages, duck farming in India faces a lot of bottlenecks also. Ducks are water birds and live best on or near water. Duck meat and egg are disliked by a large number people due to the flavour peculiar to them. Dark red colour and high fat content of duck meat also appeal the consumers in some part of the world. High amount of feed wastage in duck raised in indoor is a disadvantage in comparison to other poultry. Ducks are more susceptible to mycotoxins than chicken. Non-availability/ inadequate availability of quality ducklings or hatching facilities or healthcare products etc. and lack of knowledge and scientific rearing, diseases prevention practices and disposal of dead birds are some of the potential constraints in duck farming.

Turkey (*Meleagris gallopavo*)

Turkey is approximately 5% of the total poultry in the world. It is one of the valuable diversified poultry genetic resources in India. Turkey is mainly reared for meat and is one of the choicest meats famous for its leanness and delicacy especially for festival occasions during Christmas and New Year. Turkey meat has tremendous commercial viability because of its low and cholesterol fat contents in comparison to red meat and other poultry meat. It is also quite suitable for upliftment of small and marginal farmers. Turkey can be easily reared in free range or semi-intensive system with minimal investment for housing, equipments and management.

Bronze, White Holland, Bourbon Red, Narangasett, Black, Slate and Beltsville Small White (BSW) are the standard varieties. Among a dozen or more non-standard varieties, Broad Beltsville Large White (BBLW) and Broad Breasted Bronze (BBB) are more popular. The white feathered, turkeys are mutants of the original Bronze birds. White birds are preferred over coloured ones because coloured birds contain a black pigment in their quill feathers. In India Beltsville small white type turkey are being maintained at most of the government or university experimental farms. At few centers, Broad Breasted Bronze and Broad Breasted large White are also being kept. Organized tukey farms are limited to few small units at government or public sector only and practically non-existent in private sector. Presently the Central Avian Research Institute, Izatnagar, India is maintaining two exotic varieties Broad Breasted Large Bronze and Broad Breasted Large White and has developed an improved variety of turkey CARI-Virat, which is most suitable for backyard rearing. It produces choicest white meat with low fat and cholesterol.

Guinea fowl (*Numida meleagris geleata*)

The Guinea fowl is an important poultry species comes under family Numidae under order galliformes. Guinea fowl differs from the fowl not only in their phenotypic appearance but also in behavioral and production characteristics. One very important characteristic of Guinea fowl is its inherited resistance to most of the common chicken diseases, which make guinea fowl an important model for studying the mechanism of disease resistance, excellent herding and foraging instinct and inbuilt hardiness.

Indian guinea fowl population

The indigenous germplasm of Guinea fowl seems well adapted to the diversified agro-climatic conditions of the country prevailing mostly in semi-arid regions. The descriptions of guinea fowl breeds or varieties are essentially based on the plumage colour variations, viz., Pearl, Lavender and White. In India pearl guinea fowl are most common among village stocks and usually referred as the "local" breed. This variety is characterized by uniformly dark grey plumage with regularly sprinkled white spots, giving a pearled appearance. Lavender birds are identified by their light gray of colour plumage uniformly sprinkled with white dots. White breasted guinea fowl is characterized by pearl plumage with white breast feathers. Some other plumage patterns are white and violet, while the white variety is characterized by presence of completely white plumage. Violet variety has grey non-spotted plumage.

Improved Varieties of Guinea Fowl

Some attempts have been made to develop the improved guinea fowl. Such attempts were initiated at Central Avian Research Institute. The pure varieties i.e. Pearl, Lavender and White varieties, were developed through selective breeding for higher body weight at 12 weeks of age. Three improved varieties namely, **Kadambari**, **Chitambari** and **Swetambari** are available at CARI, Izatnagar, with pearl, lavender and white plumage, respectively.

Quail

Japanese quail are migratory game birds (Weatherbee and Jacobs, 1961) and is phylogenetically closely related to the chicken, because of its physiological resemblance to chicken, inexpensive maintenance and rapid multiplication. Japanese quail is the smallest domesticated avian species and suitable for the diversification of chicken dominated poultry industry. Japanese quail has been increasingly used in biomedical research besides being raised commercially for meat and egg production. In most parts of the world, it is also popularly called as "*Drosophila of the avian laboratory*". Japanese quail (Coturnix *japonica*) is the most efficient biological machine for converting feed into animal protein of high biological value having amazing tender taste, game flavor, low calorific value and high dry matter content. It is one of the cheapest sources of animal protein for human diets, which is fit for children and pregnant women. They have been found to be highly resistant to common poultry diseases and hence, do not require vaccines like chicken. They are suitable for commercial exploitation as they require little floor space for rearing and have a high rate of egg production.

Japanese quail known as 'Bater' in India, a domesticated avian species, is a natural habitat of Japanese islands. It was first introduced in the Country during 1974 under UNDP/ICAR collaborative education project at CARI, Izatnagar from the Avian Science Department, University of California, USA. Later in 1978, 2 more quail lines were introduced under UNDP from the Hohenheim University, Stuttgart, West Germany. Presently the Central Avian Research Institute (CARI), which is the nerve centre and nodal agency for quail farming technology in India, is maintaining pure lines of quails, adapted for Indian conditions, namely CARI Uttam, CARI Pearl, CARI Ujjwal, CARI-Sweta, CARI-brown and CARI Sunehri, which are being exploited for production of commercial broiler and layer quails.

Conservation of Indian Poultry Genetic Resources

Conservation covers the continued maintenance of genetic variability, improvement and sustainable utilization by the present generation while maintaining its potential to meet the needs and aspirations of future generations.

Most of the countries of the world are witnessing a fast decrease in the population of many native breeds and varieties of chicken, some of which are in danger of extinction. Late sexual maturity, poor egg production, slow growth, broodiness, smaller egg and body size can also be some disadvantages of native birds as far as intensification is concerned. By analyzing the State of the World's Animal Genetic Resources, FAO found that of 2000 avian breeds for which data were available, 30% were reported at risk, 35% not at risk, and the remainder were of unknown risk status (Hoffmann, 2008). From FAO database, it is estimated that around 25% of chicken breeds are included in conservation programmes, but there is no information about the nature of efficiency of these programmes. According to FAO (2010), only 7.5 percent of developing countries have poultry conservation programmes covering 63 percent of local breeds and 11 percent of national populations of trans-boundary breeds. A global plan of action for animal genetic resources including the conservation of poultry genetic resources has been developed by FAO (Hoffmann, 2008).

The conservation efforts in India were started with the establishment of National Bureau of Animal Genetic Resources (NBAGR), Karnal in 1984 under the control of ICAR, New Delhi. In India, most of the poultry including chicken breeds had no population data. The three main sources of information and conservation in the country are State Agricultural Universities, State Animal Husbandry departments, various research institutes, and State Forest department (wildlife programs, sanctuaries and National Parks). The other stakeholders of conservation program are Central Zoo Authority (CZA), NGOs, Animal Breeders' Associations, farmers and pastoralists, hobbyists, and breeding companies. NBAGR has established data bank and information service on animal genetic resources and dissemination of knowledge on these aspects. The bureau has completed the initial survey on evaluation and characterization of various native breeds of chicken.

Importance of conservation of indigenous poultry genetics resources

There is growing awareness to conserve the endangered breeds for future use. Indigenous poultry breeds have been developed over thousands of years; have better adaptability to harsh climate, tolerance to disease and heat and ability to utilize locally available poor quality feed. These are the gold mines of major genes for tropical adaptability and disease resistance. Native germplasm have great utility for backyard poultry production. Native breeds are integral part of ecosystem and the loss of germplasm has adverse effect on the ecosystem which is hazardous to the existence of mankind. The indigenous breeds need to be conserved to meet future needs. The commercial poultry genetic populations should be considered a component of our existing poultry biodiversity and thus, a conservation system for poultry genetic resources should include opportunities and encouragement for commercial companies to conserve and preserve lines for the future

Method of conservation poultry genetic resource

There are two methods used for conservation, viz., *In situ* and *ex-situ*.

***In Situ* Conservation:** It is the maintenance of live populations of birds in their most adaptive environment. The most important advantage is its requirement for simple technologies and allowing birds to adapt to changing climatic, disease, economic and socio-cultural demands. This is best method for the long term protection of biological diversity is their natural habitat, known as on site preservation.

Ex-situ* conservation:** It means, "off-site conservation". It is the process of protecting an endangered species by removing part of the population from a threatened habitat and placing it in a new location, which may be a wild area or within the care of humans. It is the maintenance of small population at a place away from the main breeding tract of the breed is the *ex-situ* conservation of the live birds. *Ex-situ* conservation can be *in vivo* and *in vitro*. ***In vivo method includes conservation of the live birds in small number at a place away from the main breeding tract such as various research institute, state agriculture university, state or central government poultry farms. This type of conservation has the limitation in terms of population size to avoid the adverse effect of inbreeding. Central Avian Research Institute, Izatnagar initiated the work on conservation of native germ plasm as early as 1976 and currently maintains a variety of avian genetic lines including Red Jungle fowl, Kadaknath, Aseel Peela, Aseel Kagar, Ankaleshwar, Nicobari breeds, Naked neck , Frizzle fowl, Silky fowl and birds having Frizzling (F), Slow feathering (K), Non inhibitor dermal melanin (id), Fibromelanosis (Fm) genes of Indian native chicken. Conservation of Aseel and Kadakanath is also being done by the Animal Husbandry Department of the Madhya Pradesh Government and Nicobari is bring conserved by Central Agricultural Research Institute, Port Blair. ***In vitro*** method is the conservation by storage of living cells for long period of time. It is done by deep freezing of sperms, ova and storage of DNA. Cryopreservation of spermatozoa in poultry has already been achieved, however ova or fertilized eggs con not be preserved in the same way because of their large size and yolk laden structure. Therefore, the only alternative is to cryopreserve germ line cells like blastoderm and PGCs in liquid nitrogen. These germline cells could be used to reconstitute viable offspring via *ex-vivo* embryo culture, germline chimeric and transgenic chickens.

BREEDING POLICIES

Breeding strategies for broiler production in India

Starting with red jungle fowl the modern broiler strain have attained about 10 folds increase in five weeks body weight. The initial selection experiment for developing the suitable broiler germplasm in India started with the objective of evolving broiler having 1.5kg body weight at 10 weeks, which at present reached to the same body weight at 5 weeks. Since the body weight has been highly heritable trait, the individual selection was good enough to achieve the desire genetics gain. The common practice is to increase in production volume and productivity per bird by utilizing pure line breeding schemes for exploitation of genetic variation in existing germplasm and then crossing these lines to achieve maximum hetrosis. Crossing of heavy breeds of chicken like Cornish, Plymouth

Rock, Australorps etc. in order to combine their best characters for developing the synthetic grandparents stocks of modern broiler strains which are then crossed to produce parents (two way crosses) or commercials (three or four way crosses). Presently, the high yielding commercial broiler attain 2 kg body at 35 to 40 days with FCR below 2.0. The breeding strategies these years have been directed towards identifying the traits of economic importance, formulating breeding plans, evaluation of parent lines for their crossbreeding performances, genotypes x environmental interaction etc. application of quantitative genetic and biometrical methods to poultry breeding have resulted unprecedented genetic improvement in production efficiency. About 80-90% of the improvement in growth of broiler has come through genetic selection for body weight.

Breeding strategies for layer production

Since the beginning of the 20th century, there was a significant changes have been observed in breeding of layer type chickens and substantial improvement in the performance of several economic traits in layers. All breeding plans have one major objective in common i.e. to increase the genetic potential of the stock to produce saleable, high quality products at minimum cost in a given production system. Layer breeding companies apply selection to improve over 30 traits, important for commercial egg production. In general, there are no worldwide or country-wise standardized breeding goals set. Differences in economic, social and ecological production environments give rise to different approaches and needs in terms of human welfare and well-being. The important economic traits selected or at least monitored by breeder at present for layer breeding programmed are age at sexual maturity, rate of lay, liveability, egg weight, body weight, feed conversion, shell colour, shell strength, albumen height, egg inclusions (blood and meat spots) and temperament. Part production record selection has been advocated by several authors (Bohren *et al.*, 1970) as a means of shortening generation interval to increase genetic progress. Apart from part-period production, annual production is also taken into account for selection criteria. However, uses of whole production records will double the generation interval. In order to optimize genetic gain per unit of time, multistage selection is followed as it reduces the cost and efforts (by discarding inferior birds at early age) and minimizes the generation interval (Hicks *et al.*, 1998). Chen and Tixier-Boichard (2003) studied the correlated effect to long-term selection for clutch length in response to 16 generations of direct selection for increased average clutch length, other egg production traits such as laying rate and total egg number have been indirectly improved. It was concluded that selection for clutch length was an effective method for increasing the egg production in which the clutch length was more heritable than laying rate and egg number. Incorporation of selection on residual feed consumption improves feed efficiency at a faster rate than selection on egg mass and body weight alone.

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5. STATUS OF BOVINE GENETIC RESOURCES, CONSERVATION, IMPROVEMENT AND BREEDING POLICY OF ANDHRA PRADESH IN LIGHT OF STATE BIFURCATION

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"To think of rural development without livestock development is to think of modern industrialization without power stations" - Late U.N. Dhebar, Freedom fighter and Ghandheyan

Livestock is an important component of agriculture sector and plays vital role in our rural economy with highest priority for alleviating poverty and self-employment of economically weaker sections of the society. Now, livestock are valued more as a source of food and income. Demand for animal food products, driven by sustained economic and income growth and a fast-growing urban population, continues to accelerate (Delgado et al 1999; Kumar and Birthal 2004; Parthasarathy Rao and Birthal 2008). Global demand for animal food products is also growing fast particularly in developing countries (Delgado et al 1999). The expanding market for animal food products is an opportunity for millions of smallholders, who have a sufficient endowment of labor but limited land, to improve their income and employment in the livestock sector. In the last three decades, the share of the non-agricultural sector in GDP has increased substantially, while the share of the agricultural sector has fallen from 37% in 1980-81 to 15% in 2010-11. The agricultural sector has also experienced a structural shift, with an increasing share of livestock in agricultural value of output, from 19% in 1980-81 to 27% in 2010-11. In this period, the livestock sector grew at an annual rate of 4.1%, but at a decelerating rate 5.3% in the 1980s, 3.9% in the 1990s and 3.6% in the 2000s. Despite sluggishness in its momentum, the rate of growth in the livestock sector was 1.6 times the growth in the crop sector and 1.3 times the overall agricultural growth. This indicates the importance of livestock in generating sustainable agricultural growth. The sector contributed 31% to the agricultural growth during the 1990s, which increased to 36% during the 2000s (Birthal and Negi, 2012).

Andhra Pradesh (undivided) experienced a robust growth in the livestock sectors in the last two decades (Birthal and Negi, 2012). During 2000s, livestock sector in Andhra Pradesh grew at an accelerated rate of 6% to 8%. Andhra Pradesh is well known for its bovine population (110.4 Lakhs, 2012 Census and after the state bifurcation), which ranks fifth in buffalo population and fifteenth in cattle population in the country. The total population of cattle and buffaloes as per the 19th livestock census 2012 is 46.06 lakhs and 64.34 lakhs respectively. With respect to total livestock, Andhra Pradesh stands 6th position in the country (Table 1). However, the trend shows that there is decline in the number of cattle and buffalo population in the state. The trends in cattle population show that there is priority for crossbred populations rather than indigenous cattle owing to better milk production of crossbred cattle. One plausible reason for such a decline trend is accelerated rate of urbanization. After the recent division of the state of Andhra Pradesh, the state stands 1st in egg production (1272.69 crore eggs per year), 4th in meat production (4.89 lakh metric tons per year) and 6th in milk production (90.83 lakh metric tons per year). Andhra Pradesh stands one among top 5 states as far as per capita availability of milk meat and eggs.

Table 1. As per latest livestock census 2012 the details of livestock population in Andhra Pradesh (after division of the state) and India

S.No	Species	Number as per Livestock Census 2012	As per Livestock Census, 2007		
			Andhra	India	Position in the Country
1	Crossbred Cattle	19.39	17.47	330.60	7th
2	Indigenous Cattle	26.68	37.26	1661.05	15th
3	Total Cattle	46.06	54.73	1990.75	15th
4	Buffaloes	64.34	82.29	1053.43	5th

Cattle genetic resources in Andhra Pradesh

Majority of the cattle in India are Indigenous type (about 58%) and remaining are crossbred cattle. There are two recognized cattle breeds in Andhra Pradesh viz. Ongole and Punganur.

Ongole is a dual-purpose breed. The Ongole breed, like other breeds of cattle takes its name from the geographical area in which it is produced. The Ongole are large-sized animals with large dewlaps, which are fleshy and hang in folds extending to the navel flap and slightly pendulous sheaths. They have long body and short neck; limbs are long and muscular. The forehead is broad between the eyes and slightly prominent. Eyes are elliptical in shape with black eyelashes and a ring of black skin about 1/4 to 1/2 inch wide around the eyes. Horns are short and stumpy, growing outwards and backwards, thick at the base and firm without cracks. The hump in the males is well developed and erect and filled up on both sides and not concave. The skin is of medium thickness, mellow and elastic and often shows black mottled markings. The popular color is white. The male has dark gray markings on the head, neck and hump and sometimes black points on the knees and on the pasterns of both the fore and hind legs. Ongole cattle are efficiently used in their native home for both work and milk production. The average daily milk yield of this breed in its home tract is 4.25±0.05 Iiters, with a fat % of 3.79 and SNF content of 8.68% (Vinoo et al., 2001). The average age at first calving is 34.37±0.15 and average calving interval is 399.03±1.85. The breed is known for its adaptability to harsh climatic conditions and good draught power (Vinoo et al., 2010) and reasonable milk producer. Brazilians have exploited the breed for meat purpose under the name "Nelore". Since there is change in trend of the agriculture and introduction of mechanization in Agriculture, the existence of the breed gradually started declining. Keeping in view of the importance of the native germplasm, as part of the national policy on improvement of indigenous cattle and conservation of native genetic resources, Indian Council of Agricultural Research has started Ongole cattle conservation program at Livestock Research station, Lam, Andhra Pradesh. This project envisages progeny testing of bulls, their selection on the basis of progeny performance and production of superior germplasm for utilization in cattle development programs in the country. The project produced about 3 lakh doses of semen from elite animals and supplied to the Govt. of Andhra Pradesh. In addition, the project also employed embryo transfer technology for producing elite animals at faster rate.

The Punganur breed is another breed from Andhra Pradesh, which is considered as one of the smallest breed in the world originated from Punganur town in Chittoor district of Andhra Pradesh. This breed is known for its short stature, high milk production efficiency and efficient reproductive characters. The Jamindars of Punganur were erstwhile Diwans in the Princely state of Mysore. They took fancy on this small breed of cattle and improved this breed and got the name as Punganur breed of cattle. These animals were found in the taluks of Palamaner, Madanapalli, Vayalpad, Piler and Chandragiri of Chitoor district, Andhra Pradesh. However the breed is on the verge of extinction due to extensive indiscriminate crossbreeding over a period of time in its breeding tract. The most important physical character is the height of the animal, which is approximately one meter. The animals have a long tail almost touching the ground, a unique feature of this particular breed. It was found that Punganur cattle have a lactation yield of 633.4 ± 21.7 liters over a lactation period of 272.0 ± 8.9 days with an average milk yield of 2.29 ± 0.06 liters. The peak yield was 3.92 ± 0.11 liters reached in 33.5 ± 1.6 days and an average dry period of 188.1 ± 11.54 days (Ekambaram et al., 2014). These animals can be maintained economically and can survive on scarce grazing conditions with minimal care and shelter. One interesting feature of this breed is that the milk contain high fat %. The milk is said to contain 8-9% fat. However, no systematic study has been conducted so far to explore this phenotype. One main limitation for systemic studies on this breed is availability of the number of animals. The breed is under the threat of extinction as the population is alarmingly dwindled to 733 animals. (Livestock Census 2007). Now about 150 animals are available at the Livestock Research station, Palamaner. Keeping in view of this problem, a project on "Conservation on Punganur Germplasm by Semen Preservation" was undertaken during the years 1999 to 2004 with the objective to produce 500 doses of frozen semen from 25 unrelated bulls procured from the field and 5000 doses of semen produced during the project was handed over to the NBAGR, Karnal for future use. At present embryos collected from Punganur cows are being cryopreserved for future purpose.

Apart from these two prominent breeds, a small proportion of indigenous animals called Kapila are maintained by some of the farmers. Kapila cattle are infact a color variant of these breeds. Some progressive farmers, by careful breeding, try to evolve dark colored variants of these breeds. They are considered as sacred and the milk is used for worshiping god rather than for human consumption.

Due to cross breeding programs that are taken up by the Government of Andhra Pradesh as part of their breeding policy to improve milk production, there is about 42% of cross bred cattle. These cattle are basically crosses of Jersey or Holstein Friesian.

Buffalo genetic resources in Andhra Pradesh

Andhra Pradesh as such doesn't possess any native buffalo breeds. Majority of the buffaloes used to be non-descript. However, among the Indian buffalo breeds, Murrah is found to be well adapted to the conditions of Andhra Pradesh. Hence the Govt. of Andhra Pradesh adopted grading up of local non-descript animals with Murrah breed of buffalo. Majority of the buffaloes are concentrated in the river Godavari delta region. From grading up of the local non-descript region, in the Godavari delta region, a new genetic group is formed, which is locally called as Godavari breed of buffalo. Breed status of this genetic group is yet to be reviewed. The animals of this genetic group are medium sized with compact body. They are black in color with a sparse coat of coarse brown hair. The forehead of these animals is convex and they possess prominent bright eyes. The horns are short, flat, curved slightly downward, backward and then forward with a loose ring at the tip. The chest is deep with well-sprung ribs. The animals produce milk with high fat. Average daily milk yield of these animals ranges between 5 to 8 kg and lactation yield is about 1200to 1500 kg. The animals breed regularly and have a short calving interval compared to Murrah. They are hardy and possess good resistance to diseases. These animals contribute significantly to the milk production in the state.

Cattle and Buffalo breeding policies in the state of Andhra Pradesh

Andhra Pradesh is one of the pioneer states which has taken up " Restructuring of breeding operations " by involving farmers organization by establishing state level autonomous body APLDA, which provides animal breeding services at farmers door steps, on cost recovery basis, covering total breedable population.

The breeding policy for Andhra Pradesh is in Line with National Breeding Policy, the main features are

- Upgrading the non - descript as well as graded buffaloes with Murrah breed in entire state
- Promoting use of indigenous breeds like Ongole and Punganur in their breeding tracts.
- Cross breeding of non - descript local cattle with exotic breeds like Jersey in all districts and HF in few districts.
- Inter -se – mating of cross breed cattle with cross bred semen ensuring exotic blood level of about 50%
- The main objective of breeding policy is to improve milk yield in non - descript cattle and buffaloes and draught power in indigenous cattle.
- Artificial insemination is the main tool for implementation of breeding policy however, organized natural services (ONS) is pursued in areas where it is difficult to introduce AI.

Conservation and Improvement Programs

There is prioritized attention of the government in conservation of the native cattle breeds of Andhra Pradesh viz. Ongole and Punganur. The ICAR in collaboration with the state Veterinary University i.e. Sri Venkateswara Veterinary University (SVVU) is running conservation projects for the two breeds, at Livestock research stations, LAM and u respectively. At LRS LAM, the project is working with the objective of improving Ongole germplasm. The strategy followed here is by collecting semen from superior sires and supply them to the farmers in the home tract of the breed. Apart from this, conservation measures of Ongole and Puganur breeds of cattle are also taken up at this farm by embryo transfer technology. At LRS u, conservation program of Punganur is taken up by using natural service in this breed. Also attempts were made to standardize the superovulation techniques to speed up the conservation process (Veerabrahmaiah et al., 2012). In addition, due to the problem of endangerment of native germplasm, the Government of Andhra Pradesh, it was emphasized in its breeding policy that the pure breeds should never be inseminated with exotic semen.

Strategies for future development

In spite of the conservation measures taken up to preserve the native germplasm, the major problem at present is lower number of base population of these native breeds. The Ongole breed to some extent is having considerable number, but there are very few animals left from the Punganur breed. It requires urgent attention to characterize the genetic variation in these animals and use the results in designing breeding plans for conservation of these animals.

Measures should be taken to intensify selection of superior bulls & cows by way of establishing open nucleus breeding system. Since there is no systematic data available on production performance of majority of these animals, it is important to modify the progeny testing procedures in order to identify superior germplasm. Multiple Ovulation and Embryo transfer technology (MOET) strategies should be developed to adopt to field conditions to be able to accelerate the genetic gain.

The breeding policy of cross breeding with exotic germplasm should be critically reviewed and if necessary, the non-descript cattle should be upgraded using indigenous high yielders like Sahiwal, Gir etc. rather than exotic germplasm to be able to reduce the untoward consequences of using exotic germplasm in crossbreeding programs.

Epilogue

Careful usage of bovine genetic resources and conservation of native germplasm in Andhra Pradesh have potential in meeting the local needs for milk and milk products and sustainability of rural livelihood.

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6. KANGAYAM CATTLE PRIDE OF TAMILNADU PAST AND FUTURE STRATEGIES FOR THEIR IMPROVEMENT – A FARMER'S VIEW

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Worldwide, specific agricultural systems and landscapes have been created, shaped and maintained by generation of farmers and herders based on diverse natural resources, using locally adapted management practices. In 2002, the FAO initiated a programme known as Globally Important Agricultural heritage systems (GIAHS) for the conservation and adaptive management of world's agricultural heritage systems. These sites have been chosen based on outstanding characteristics, proven history of sustainability and global significance. Korangadu silvi – pastoral system and associated Kangayam breed of Kongu region in mid west Tamilnadu is a unique semi – arid pastoral system. A study of this unique mutually inseparable breed pastoral system provides a window to the rich biodiversity and cultural heritage handed down the generations. Preserving this for posterity is s serious question requiring concerned and collective effort on the part of the stake holders – elected representatives', the state, large and small holders, scientist's academia and civil society. Such unique systems and breeds, however small, located in any part of the world cannot be ignored since it has global significance. Communities and nations can no more detach or remain insensitive to such heritage issues. In this article let me try to capture the different aspects of this unique system from a historical perspective clubbed with contemporary and future relevance.

Breeds in India and Tamilnadu

Evolution of breeds and varieties are product of complex interplay of nature and culture. The human element is extremely important for the evolution and continuity of a breed. India is one of the richest countries in terms of animal genetic resources. It has 45 breeds of cattle, 4 camels, 19 goats, 39 sheep, 6 horses, 19 chicken, and 11 duck varieties. Indian cattle breeds vary in size, form, symmetry, and features such as horns, hair colour, hump, and capabilities suited to local peculiarities of climate, soil and fodder. The ongole, Kangayam, Amrita Mahal, Halikar, Krishna Valley, Alambadi found in various breeding tracts of southern India, and lesser known Bargur Malai madu (in Erode), Manaparai, Umblacherry, Puliakulam, Have distinct physical features and stand as a testimony to human ingenuity meditated through traditional knowledge.

Kangayam Breed

The Kangayam breed is known by the names Kanganad, Kongu, and Kangayam and derives its name from the taluk of Kangayam, are well known for their excellent draught power qualities and medicinal properties of milk (A2 beta – casein protein). They are elegant, medium sized, horns variously sized and set, colours different, but usually white or grey, chest and hind quarter narrow, docile, quick and strong. Dentition is permanently completed by 6 to 6 ½ years and maximum life of stock is between 20 to 25 years. Select bulls are allowed to cover heifers from the age of 3 years or castrated for rearing as bullocks. The pattakarar family of Palayakottai, located in the present day Tiruppur district, especially the 29 Th pattakarar and his son Thiru. Rao Bahadur Nallathambi Sarkarai Mandradiar were directly responsible for shaping the present day Kangayam through selective breeding, improvement, management and protecting the breed at a time when bullock power was indispensable for agriculture and transport. Many small holders in the region also held the breed, but the purest form always came from the pattakarars. Since 1924, the government of Madras state took steps to improve and popularize the Kangayam breed. It was around this period that the Pattakarar contributed a nucleus herd of pure bred bulls and cows for breeding purposes to the Madras Government, the then Ceylon Government and to the Coimbatore district board, thus opening their doors to their intellectual property.

In 1942, then Imperial Council for Agricultural Research (ICAR) implemented the "Kangayam Cattle Improvement scheme" to assess the milk potential of the breed without deteriorating its draft quality. It was only at this point that the pattakarar family started creating and maintaining 'written' pedigree records. As part of the scheme, Bulls were also distributed to other districts and states to upgrade local cattle to suit agricultural operations. Post independence, the state government introduced Key Village Scheme and Key Village Extension Scheme as part of the Five Year Plans, for the improvement of Kangayam in its breeding tracts and adjoining areas. This continued until 1974, when this scheme was replaced with Intensive Cattle Development Project (ICDP) with emphasis on milk production through exotic breeds.

Bio Cultural Events

Jallikattu & Rekhla

Jallikattu or Erutazhuvathal is an important Tamil sport that takes place in several hundred villages in southern Tamilnadu and parts of Kongu region like Salem, Rasipuram etc, in the month of January during harvest festival pongal. Jallikattu bulls belong to a few specific breeds that descended from Kangayam. And it is still used for breed improvement of Jellikat breed, Puliakulam etc. This sport is traced back to Indus Valley Civilization which is depicted in the seals with scenes of bull baiting. The majestic Kangayam is an important breed involved in this game and considered to be more muscular and ferocious.

The sport of ***Jalli Kattu*** (**Bull vaulting**) part of the annual **Pongal** (harvest festival) of Tamil Nadu is a celebration of livestock, the farmers' main support system. There are a number of indigenous breeds like *Puliakulam, Malai Maadu, Umbalachery, Kangayam, Alambadi* and *Barugur* bulls which are fast disappearing. The bull-vaulters are mostly farmhands, in peak physical condition and with electric swift reflexes. Jalli Kattu is a celebration of such Indian breeds of cattle. Jalli Kattu is symbolic of the intimate bond between cattle and agriculturalists. The fourth day of the Pongal festival is geared towards livestock. The animals are bathed, scrubbed and their horns painted. The sport consists of holding on to the hump of the bull and running along with it for a given distance usually **about 20-30 meters which is covered in barely 10-20 seconds**. During Jalli Kattu, the bulls are not harmed, or tormented. Unlike the Spanish sport, there is NO fighting the bull at all. In fact one of the main rules of Jalli Kattu is that even one drop of the blood of the ox cannot be spilt which is strictly followed by the organizers.

Jalli Kattu is an ancient sport. The seals of the Indus Valley Civilization depict this sport which is proof that this sport was in vogue 5000 years ago. Standard texts on Indus civilization provide this information. Ancient Tamil poetry, known as Sangam literature (2nd BCE – 2nd CE), has many detailed references to this sport. It was called *Eru Thazhuvuthal* (hugging the bull). *See Kalithokai, Sangam Literature*. In an ancient Tamil text called Tirukkural, education is considered to be wealth and the word used for wealth is *Madu*, meaning cattle. So it has a socio-cultural connotation which denotes lives and livestock having co-existed and cultures having coined usages around them.

These are concrete evidences to prove that this has been part of the long Heritage of our country. One strong characteristic of life in India is the persistence of certain social institutions, the origins of which are lost in pre-history. Though the profile of these practices change, they retain their essential features. JalliKattu is one such precious heritage that has been preserved over millennia and our duty is to take this forward. Of course we should have rules and restrictions for the conduct of the event but Jalli Kattu should go on. *(See annexure 1)*

Rekhla

Rekhla race is another prestigious and passionate farmer sport conducted in 15 or more places, attracting more than 10000 participants a year. It is a place where small holders and big landlords meet. Small holders can compete with big owners and provides an edge for individual honor. In Kongu and Theni region, only Kangayam cattle are involved in these events, while other breeds are used in other locations. Individuals spend a lot of money to take part in these events. The winners are honored with shields and gold coins. The animal pairs that win these competitions have a great demand. Sometimes they are sold for prices ranging from Indian rupees 400,000.00 to 7000,000.00 per pair.

Kangayam breed is significant to keep the gene pool of the breeds of Tamilnadu intact. While Piliakulam breed is being used in Jallikattu, the Kangayam is purchased from the Shandies in Kannapuram to breed with the Puliakulam at regular intervals for maintaining the pedigree.

Biological Conventions

According to principles 1, 2 & 3 of the Convention on Biological Diversity (CBD) to which India is a signatory states, Livestock Keepers are creators of breeds and

custodians of animal genetic resources for food and agriculture; Livestock Keepers and the sustainable use of traditional breeds are dependent on the conservation of their respective ecosystems; Traditional breeds represent collective property, products of indigenous knowledge and cultural expression of Livestock Keepers. These conventions clearly protect the biological diversity and the cultures of indigenous and local communities which intertwine their livelihood with the culture and diversity of the regions. *(See Annexure 2)*

Future of the Breed

In this exercise, I wish to recall the wise words of J.A.P.R.Kothavala, the Imperial Dairy Expert, Bangalore who, as early as 1935 has said " the pattakarar, through his foresight, now realizes that with advert of mechanical transport and electricity in rural areas, breeding cattle merely for draught requirements cannot be the best proposition and this work must therefore be associated with dairy farming" what was felt as a compelling need 80 years ago, assumes even greater importance after ushering in of the white revolution. The need therefore is to make Kangayam breed a dual purpose animal in the true sense without, of course sacrificing the purity of the breed and impairing the draught qualities. It is here that the then minister of agriculture and animal husbandry Thiru.M.Bakthavachalam's words are encouraging. In 1957 he opined that "though the results so far achieved to make Kangayam bred a dual purpose animal are not quite encouraging, the potentialities of this breed in that direction have been well established both at Hosur and Palayakottai. With such wealth of data available it must be possible for the "experts" in the field to plan and programme properly and bring about a rapid development of the desired qualities in the not distant future through artificial insemination.

If the architect and my forefather Thiru. Rao Bahadur Nallathambi Sarkarai Mandradiar could, single handedly increase the strength of the pure stock from 50 to 2000 in a span of 50 years, given the rapid development in the knowledge of animal genetics and breed management, like cloning, sex selection which are like Latin and Greek to us, besides the infrastructure available now, it should be possible to achieve best results in quick time. So let us be sincere in our efforts to achieve the above goal which is to make this breed economically viable for it to thrive. This single transformation is enough to save this breed from extinction in addition to the lifting of the ban on activities like "Jallikattu and Rekhla".

Some statistics show that there is an increase in the consumption of the milk of native breeds. Most of it of course is taken to Urban areas. This is due to the organic food movement that has taken form in this part of India. In addition to this a lot of green energy and strategies of reducing the carbon foot print is being discussed. So there is a definite use and need for saving of native breeds.

There should be more awareness programmes involving stake holders such as farmers, the NGOs and the Government to maintain the breed intact. This can be achieved through heritage conservation programmes for School and University students through NGOs. Farmers need to be trained in using the cowdung and urine for agricultural purposes as statistics prove that this art is dying. There is also competing forces which encourage chemicals fertilizers and pesticides. This awareness can be brought in through NGOs. The role of women in agriculture and cattle rearing is phenomenal. Most often in the rural economy the role of women is discounted. Their contribution is enormous. There are a number of women cattle breeders in the Kongu region. More empowerment could be provided to women by training them in many aspects of modern cattle breeding practices.

The Government could also consider marking grazing zones as special zones. Otherwise these grazing lands would be consumed by Real Estate and thereby no habitat for cattle grazing.

Due to the efforts of SKCRF the Govt of Tamilnadu has sanctioned a breeding station for Bargur cattle, in Erode district. In a similar way "Kangayam breed "needs a breeding station in its in situ area. A separate Ministry or a Committee to conserve native livestock in Tamilnadu with members of breeding societies, NGOs can be envisaged.

Annexure 1

Our Appeal to save Jallikattu

Invoking legal status of nations' signatory to Convention on Biological Diversity and Heritage status nations' worldwide practices, it is customary that these ancient traditional practices are left as they are but with rules to organize them.

If this sport is banned, livestock keepers will be forced to abandon the raising of native livestock, which already stand threatened due to extensive use of motor pumps, tractors and mechanized agriculture. If the sport is banned it would be a death knell on the native species. There are many such intangible threats that dictate the continuation of the livestock.

People who want a ban on this are unfortunately far removed from village life and do not know how this chain works. They are rather not only cut off from these realities but also see this event in isolation from the chain. It is imperative to educate them to understand the significance.

It is in our sincere attempt to save the traditional breeds from disappearing, we appeal to you to kindly consider our request to not ban the event and allow this traditional practice. The summary is as follows:

1. The Convention on Biological Diversity (CBD) supports traditional practices to keep the chain intact and thus enables conservation of native breeds
2. As an ancient nation and an ancient practice this is our Heritage and should be seen as one and hence we should to preserve it
3. There is no torture of any animal of any sort and the evidence of which can be seen from live telecast made by media. The time a bull engaged in the sport is less than 30 seconds.
4. Rules can be implemented for safety of animals and men if required

We have lost many breeds and we can't afford to lose any further. It will be a loss to the Nation otherwise.

Annexure 2

Convention on Biological Diversity

According to principles 1, 2 & 3 of the Convention on Biological Diversity (CBD) to which India is a signatory, **further states the following as rights for a livestock keeper:**

Article 8 (j) of the CBD:

"Contracting parties shall…subject to national legislation, respect, preserve and maintain knowledge innovations and practices of indigenous and local communities embodying traditional lifestyles relevant for the conservation and sustainable use of biological diversity…"

Article 10(c) of the CBD

- "customary use of biological resources is protected and encouraged in accordance with traditional cultural practices that are compatible with conservation and sustainable use requirements"..

Chapter 15(4)(g) of Agenda 21 calls on governments at the appropriate level

- "to recognize and foster the traditional methods and knowledge of indigenous people and their communities …relevant to the conservation of biological diversity and the sustainable use of biological resources".

Chapter 15(5)(e) of Agenda 21: Governments should

- "subject to national legislation, take action to respect, record, protect and promote the wider application of the knowledge, innovations and practices of indigenous and local communities embodying traditional lifestyles for the conservation of biological diversity and the sustainable use of biological resources …"

(Please note that India being a signatory to CBD, has enacted the National Biodiversity Act 2002.)

7. STATUS OF FARM ANIMAL GENETICS RESOURCES, CONSERVATION AND IMPROVEMENT IN KARNATAKA

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The Amrithmahal breeding tract is endowed with rich fauna and flora, varieties of plants and vegetation and domestic farm animal genetic diversity as reflected by recognized breeds of cattle viz., Amrithmahal, Hallikar, Khillari, Deoni, Krishna Valley and Malnad Gidda; buffalo breeds such as South Kanara, Dharwari and Gowli, besides non-descript buffaloes which look more or like Surti buffaloes in body size and conformation; sheep breeds such as Bannur, Deccani, Kenguri, Hassan, Bellary and Chitradurga strains of sheep; Nandidurg and Bidri goats; Ankamali pig breed and local varieties of pigs and varieties of local birds. All these livestock genetic resources were locally developed through interaction of man and nature over centuries, and were responsible for transformation of the life style and socio-economic conditions of the people apart from being beasts of burden for agriculture operations including rural transport and also provision of milk, meat and fibres for human welfare throughout the history of mankind.

Total Livestock population in Karnataka from 1997 to 2007

Species	Karnataka (In thousands)			India (In thousands)		
	1997	**2003**	**2007**	**1997**	**2003**	**2007**
Indigenous Cattle	9539	7936	8309	178782	160495	166015
Crossbred Cattle	1293	1602	2193	20099	24686	33060
Total Cattle	**10831**	**9539**	**10503**	**198882**	**185181**	**199075**
Buffalo	**4367**	**3991**	**4327**	**89918**	**97922**	**105343**
Indigenous Sheep	7807	7244	9540	54388	55741	67829
Crossbred sheep	197	12	18	3103	5729	3730
Total Sheep	**8004**	**7256**	**9558**	**57494**	**61469**	**71558**
Goat	**4875**	**4484**	**6153**	**122721**	**124358**	**140537**

Livestock Census of indigenous cattle in 2007 (In lakhs)

Breed	Population (In Lakhs)
Amrithmahal	0.95
Deoni	0.69
Hallikar	20.00
Khillar	4.52
KrishnaValley	0.04
Malnad Gidda	12.81
Non-descript	44.04
Total Indigenous	**83.04**

Livestock Census of sheep and goats in 2007 (In lakhs)

Sheep			**Goats**		
Breed	Total	Total	Breed	Total	
Exotic		1263	Exotic		2.08
Crossbreed		17372	Jamunapari	51065	2.64
Bellary	1733832	4602660	Osmanabadi	208461	
Deccani	1489647		Sirohi	4365	
Hassan	645451		Nandidurg		6.35
Kenguri	438008		Non descript		52.23
Mandya	295722			In Lakhs	61.43
Non descript		4911466			
	In Lakhs	**95.32**			

Some of the recent activities that have taken place in Karnataka State with respect to livestock breeds are as follows.

A. "Survey, Evaluation and Characterization of Mandya (Bannur / Bandur) Sheep Breed" to ICAR, New Delhi through NBAGR, Karnal under Network Project

Recommendations

- Formation of women self-help groups (SHG's) in the arena of sheep farming to encourage and motivate sheep farming activities at the grass root levels in the rural parts of the state.
- Training of the farmers on input precision skills on detection of heat, timely breeding, management of pregnant ewes, rearing of young lambs during weaning period etc.
- Continuous monitoring of the breed with respect to body conformation, physical characteristics, performance traits and breeding practices.
- Cytological, bio-chemical and molecular genetic investigations have to be taken up on large populations in order to identify suitable and breeds specific gene marker characters. In association with these characters, the physical measurements, conformation, body size and performance characters would definitely be useful in distinguishing Mandya breed with its strains or other sheep breeds in the native tract.

As a consequence, a Mega Sheep Seed Project on Mandya Sheep (MSSP-MS) was sanctioned to KVAFSU and is being operated from April, 2012 at LRIC(Sheep), Nagamangala, Mandya /district.

The Mega Sheep Seed Project on Mandya Sheep is structured with the following objectives: (i) improvement of genetic/ productive performance of Mandya Sheep through selective breeding and supply of elite breeding rams in the field and (ii) to impart necessary skills and knowledge on organized sheep husbandry practices to the participatory shepherd families, so that their socioeconomic status could be improved on the long run.

At the farm, true to type Mandya sheep breed seed flock is being maintained under uniform management and feeding practices suitable for breeding purpose. The

Survey and characterization of Hallikar cattle

Information gathered on the trends of Hallikar population and their genetic makeup as per the version of the farmers, breeders and people in general in the native tract retrieved through interactive discussions during the visit by the research team, indicated that the quality and number of Hallikar cattle is decreasing.

The implementation Cattle Breeding policy of Karnataka which envisages the importance of conservation and improvement of indigenous cattle breeds is not on the desired lines. Systematic selection and breeding programme has not been practiced at field level for identifying and producing superior breeding germplasm. Excellent animals are still available with farmers which need be identified and further propagated by the strategic efforts of government bodies and NGOs.

C. Network Project on Animal Genetic Resources for Undertaking Survey, Evaluation and Characterization of Amrithmahal Cattle

- Karnataka state had been facing daunting and recurrent droughts continuously over the years and this was rampant during the last three consecutive years (1999-2000 to 2002-03) with the net result the farmers were forced to sell away their stock due to scarcity of fodder and water resources despite the Government of Karnataka undertaking measures to mitigate the drought occurrence and to overcome the drought effects which happens to be one of the major reasons for declining of the Amrithmahal cattle at an alarming state in the breeding tract.
- All those factors responsible for decline in numbers of Amrithmahal cattle and dilution of its characters have to be looked into seriously for reviving and revitalizing the Amrithmahal cattle breed. Therefore, there is an urgent need to arrest the dilution and genetic erosion of the breed and reverse the trend of fast declining in its population size through planned breeding policy for their genetic improvement.
- Efforts need to be taken up on war footing to restore and develop all available community pasture and grazing lands through watershed developmental programmes involving farmers and NGO's on participatory approach. This will certainly go a long way in the conservation, breeding and genetic upliftment of Amrithmahal cattle for future generations.
- Conservation of Amrithmahal cattle breed in its original form is essential is to be taken up on top priority in view of the declining in numbers of the breed. Hence, conservation of live animals in small herds – *in situ* conservation within their production system and native ecology may be worthwhile to consider and be established at the, which falls within the breeding tract of the breed.

Recent developments as an outcome

a. Herd registration & field performance recording in Amritmahal cattle at Department of Animal Genetics and Breeding, Veterinary College, Hassan.

Objectives

1. To identify genetically superior quality germplasm of Amrithmahal cattle breed in their breeding tract.
2. To develop appropriate breed descriptor for Amrithmahal breed.
3. To develop suitable selection criteria and standards for choosing the genetically female breeding stock as parents of next generation to produce superior quality progeny.
4. To create awareness and consciousness among the breeders / farmers in the breeding tract for overall improvement of breed as well as to improve the socio-economic status of the farmers / breeders.

b. A nucleus herd of Amrithmahal cattle has been established at LRIC (Amrithmahal), Konehally, KVAFSU, Bidar.

D. Recognition of Malnad Gidda as an established cattle breed.

ABSTRACTS

TS-IV-01

ALTERATION IN SERUM TOTAL PROTEIN AND ENZYMES DURING SUB-CLINICAL MASTITIS IN CROSSBRED COWS

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To investigate the alteration in serum total protein and enzymes during sub-clinical mastitis in crossbred cows, eighteen crossbred cows (control=9 and sub-clinical mastitic=9) of 3rd and 4th parities were selected from the local farms. Sub-clinical mastitic animals were screened by modified California mastitis test, bromothymol blue test and milk somatic cell counts. Blood samples (10 ml/animal) were collected from all the animals in sterile heparinised vacutainer tubes from jugular vein, posing minimum disturbance to the animal and subsequently subjected to separation of serum by standard procedure. Milk somatic cell counts were performed microscopically. Serum total protein was determined by Biuret method. The serum alkaline phosphatase (ALP) activity was measured by method using 4-amino antipyrine. The SGOT and SGPT activities in serum were estimated according to the manufacturer's instructions of commercially available kit of Span Diagnosis Ltd., Surat, India using 2,4-Dinitrophenyl hydrazine (DNPH). Milk SCC was found to be significantly ($P<0.01$) higher in sub-clinical mastitic cows than control. Serum total protein level in sub-clinical mastitic cows was found to be lower than control cows though the difference was non-significant. Serum SGOT level in sub-clinical mastitic cows was found to be significantly ($P<0.05$) higher than control cows. There was no significant variation observed in serum SGPT level in control and mastitic crossbred cows. In sub-clinical mastitic cows, the serum ALP was found to be significantly ($P<0.01$) higher than control cows. This study concluded that there were considerable increase of serum SGOT and ALP during sub-clinical mastitis which can be used as a tool for diagnosis of sub-clinical mastitis in crossbred cows.

TS-IV-02

GENETIC IMPROVEMENT OF KANKREJ CATTLE THROUGH ASSOCIATED HERD PROGENY TESTING PROGRAMME

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The AICRP on Indigenous Breed Project is being co-ordinated by the Central Institute for Research on Cattle, Meerut since 2009 and is aimed at undertaking selection of indigenous bulls through associated herd progeny testing and to provide superior germplasm for the genetic improvement of indigenous cattle breeds viz., Sahiwal, Kankrej and Gir. The present study was undertaken to assess the performance of Kankrej cattle registered under the germplasm (GP) and field data recording (DR) units operating at Livestock Research Station of Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat and its surrounding areas for the years 2012 and 2013. A total of 17 Kankrej bulls (9 in the first set and 8 in the second set) selected on the basis of breed characteristics, body conformation and dam's milk production were introduced for breeding from the date of inception. In the first set, a total of 2206 inseminations were done in cows maintained by farmers and in Gaushalas which resulted in 1137 pregnancies (51.54% conception rate). Similarly in the second set, of the 2294 inseminations, 1118 cows got pregnant (48.73%) leading to an overall average conception rate of 50.11 per cent. The overall age at first calving (days), first lactation milk yield (kg), first lactation length (days), dry period (days) and service period (days) evaluated during the year 2012 were 1348.62, 2431.99, 299.68, 119.75 and 133.17, respectively while

the corresponding estimates during the year 2013 were 1238.33, 2634.00, 295.05, 105.18 and 131.93 days indicating the improvement in the performance of Kankrej animals over the year. The best first lactation milk yield in the year 2012 and 2013 were recorded as 4390.61 and 3546.21 kg, respectively. The study thus suggests that genetic improvement programme implemented is effective for increasing the production and reproduction performance of Kankrej cattle as a result of selection of superior bulls and recording proper pedigree and performance data.

TS-IV-03

EMPIRICAL APPLICATION OF RESPONSE SURFACE METHODOLOGY FOR INCREASING THE LIFETIME MILK YIELD THROUGH OPTIMIZING THE PRODUCTION AND REPRODUCTION TRAITS IN SAHIWAL CATTLE

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The response surface was developed for lactation total milk yield (LTMY) in Sahiwal cattle with five explanatory or independent variables *viz.*, age at first calving (AFC), first lactation milk yield (FLMY), first lactation length (FLL), first service period (FSP) and parity using the SAS software. The second-order polynomial model developed was found to be suitable to develop a response surface as the lack of fit was not significant and all the five variables had significant effect on LTMY. The R-square value was 84.30 per cent indicating that the present response surface model explained a major part (84.30 per cent) of the total variation in LTMY. The test of significance revealed that the linear (Independent effect of AFC, FLMY, FLL, FSP and parity), quadratic (AFC*AFC, FLMY*FLMY, FLL*FLL, FSP*FSP and parity*parity) and their interactions (AFC*FLMY, AFC*FLL, etc.) were significant contributors in explaining the variability of the LTMY and the existence of major linear relationship between LTMY and other traits. The mixture of positive and negative eigen values indicated that the stationary point was a saddle point. The highest absolute eigen value was obtained for AFC (1898.36) followed by parity (1290.67), FLMY (776.98), FLL (373.22) and FSP (74.54) indicating their decreasing order of importance in altering the LTMY. Ridge analysis revealed that maximum LTMY (19819.00 kg) can be achieved with a combination of optimum levels of AFC (1226.43 days), FLMY (2647.28 kg), FLL (312.52 days), FSP (222.89 days) and parity (9.88). Based on the above results it may be suggested that the response surface methodology is useful in finding the relationship between the explanatory and dependent variable and can be used to evaluate the optimum independent values for increasing the LTMY.

TS-IV-04

GENETIC IMPROVEMENT OF CROSSBRED CATTLE THROUGH FIELD PROGENY TESTING

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Field Progeny Testing (FPT) project is run by ICAR-CIRC, Meerut for genetic improvement of crossbred cattle under field conditions at various agro-climatic conditions of the country. The present study was conducted on data available with various units of the project *viz.* GADVASU, Ludhiana, KVASU, Thrissur, BAIF, Pune and GBPUAT, Pantnagar from January 2013 to December 2013. A total of 10415, 3981, 5338 and 1778 AIs were carried out at Ludhiana, Thrissur, Pune and Pantnagar units respectively with the highest conception rate (56.20%) at Pantnagar unit followed by Pune (47.35%), Thrissur (45.60%) and Ludhiana (43.60%). A total of 1589 female calves were born at Ludhiana unit followed by Pune, Thrissur and Pantnagar units with 577, 483 and 317 female calves respectively.

The means for 305-day milk yield were 3699 kg at Ludhiana, followed by 3088 kg at Pune, 3281 kg at Pantnagar and 2725 kg at Thrissur units. The mean age at first calving were 1030, 1024, 926 and 774 days respectively at Ludhiana, Thrissur, Pune and Pantnagar. FPT is the best tool to faster multiplication of superior germplasm under the field conditions and enhance the productivity of livestock.

TS-IV-05

MULTIVARIATE ANALYSIS OF PHENOTYPIC DIFFERENTIATION BETWEEN KANKREJ, SANCHORI AND NARI CATTLE POPULATIONS OF RAJASTHAN, INDIA

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A total of 734 indigenous cows of Kankrej (407), Sanchori (152) and Nari (175) were utilized to discriminate three cattle populations based on 12 morphometric traits using size free canonical discriminant analysis. Different morphometric traits revealed that size of Sanchori cows was larger, Kankrej was intermediate and Nari was smallest. Variance component (REMP) analysis indicated that the percentage of intra-breed variation (66.09) was larger than the inter-breed (33.91). This showed that most of the variability was due to within breed differences. The stepwise discriminate analysis showed that distance between hip bones, heart girth, horn length, face width, ear length, face width, horn dia, height at withers, tail length without switch, tail length and body length were the most discriminating traits between these three cattle populations. The Mahalanobis distances between these cattle populations indicated that they are three distinct populations. The dendogram based on the average linkage method showed that there are two clusters; cluster one includes Nari and Sanchori cows and cluster two Kankrej cows, those are clearly separated from cluster one. The individual assignment to different cattle populations by the cross-validation classification approach showed that 100% of the Kankrej cows, 98.08% of Sanchori cows and 98.98% of Nari cows were correctly assigned into their source populations. The present study revealed that the size free canonical approach is proved useful and informative in differentiating between three cattle populations and suggested that Sanchoori and Nari may be established / registered as distinct breeds. Further, these cattle populations may be improved through selective breeding programs so intermixing may be checked / stopped.

TS-IV-06

COMPARISON OF DIFFERENT LACTATION CURVE MODELS IN DIFFERENT PRODUCTION BASED GROUPS IN SAHIWAL COWS

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A total of 11966 monthly test-day milk yields records of first four lactations pertaining to 691 Sahiwal cows sired by 54 bulls, spread over a period of 51 years (1961- 2011), maintained at NDRI, Karnal were used for comparison of different lactation curve models viz. inverse polynomial function, Wilmink's exponential function and mixed log function in Sahiwal cows. Based on their production, Sahiwal cows were grouped into three different groups viz. high, moderate and low producing using cumulative square root method. The above mentioned models were fitted and relative efficiency was compared. The higher coefficient of determination values (R^2) and lower root mean square values (given in parentheses) were the criteria for judging a model to be best fit. In high producing group the R^2 values were found to be ranging from 86.58% (0.165 kg) for Wilmink's function in first lactation to 99.99% (0.028 kg) for inverse polynomial function in second lactation; in moderate producing cows, the R^2 values were found to be ranging from 78.93% (0.153 kg) for Wilmink's function in first lactation to 99.97% (0.050 kg) for inverse polynomial function in second lactation; and in low producing group, the R^2 values were found to be

ranging from 80.95% (0.134 kg) for Wilmink's function in first lactation to 99.87% (0.312 kg) for inverse polynomial function in third lactation, were obtained. The R^2 values for different lactation curve models showed that the inverse polynomial function was found to be best fit followed by mixed log function; whereas Wilmink's function was found to be least fit in all three production based groups in Sahiwal cattle. Hence it can be concluded that inverse polynomial function is the model of choice for estimating the trend of milk production in Sahiwal cattle.

TS-IV-07

EFFECT OF NON-GENETIC FACTORS ON 305-DAY OR LESS MILK YIELD UP TO FOURTH PARITY IN SAHIWAL

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The present study was undertaken on first to fourth lactation 305-day or less milk yield records pertaining to 562 Sahiwal cows sired by 54 bulls maintained at NDRI, Karnal over a period of 51 years (1961-2011). The data were classified according to season and period of calving, age groups and dry periods to study the effect of non-genetic factors on 305 days or less milk yields up to fourth parity. The overall average first lactation 305-day or less milk yield (FL305DMY), second lactation 305-day or less milk yield (SL305DMY), third lactation 305- day or less milk yield (TL305DMY) and fourth lactation 305-day or less milk yield (FRL305DMY) in the present study were found to be 1885.60 ± 25.44, 1895.65 ± 36.80, 2081.27 ± 44.53 and 2165.46 ± 48.07 kg, respectively. The effect of period of calving on 305-day or less milk yield was found to be highly significant ($P \leq 0.01$) for all four lactations except significant effect ($P \leq 0.05$) on TL305DMY; whereas the effect of season of calving on 305- day or less milk yields was found to be non-significant on all four lactations except highly significant ($P \leq 0.01$) effect on FRL305DMY; whereas effect of age groups was found to be non-significant on 305- day or less milk yields for all four lactations. The effect of various dry periods on all ensuing lactation traits was found to be non-significant except highly significant ($P \leq 0.01$) effect on SL305DMY.

TS-IV-08

STUDY OF GENETIC AND NON-GENETIC EFFECTS ON FIRST LACTATION PRODUCTION TRAITS IN CROSSBRED CATTLE

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Data for the present investigation were collected from history sheets of crossbred cows at Instructional Dairy Farm of G. B. Pant University of Agriculture and Technology, Pantnagar. The data pertained to 1198 crossbred cows from 102 sires over a period of 48 years from 1966 to 2014. Cows with abnormal and incomplete records were excluded from the study. The overall least-squares means of first lactation traits *viz.* AFC, FLMY, FLP, FDP, FCI, and FCI were estimated to be 1153.10 ± 24.84 days, 2733± 73.14kg, 320.46± 5.52 days, 113.06± 5.12 days, and 433.542 ± 7.91days respectively. Sire effect was significant on all the first lactation traits. In contrast, different seasons of calving were found to have non-significant influence on all the traits except first service period; similarly, genetic group was also found to have non-significant influence on all the traits except first lactation milk yield. The period of calving was found to have significant influence on all the traits except first lactation milk yield. The heritability estimates of different first lactation traits were observed to be low to high. The genetic and phenotypic correlations among all the traits were observed to be very low to high. The results of present study pointed out that most of variations in the traits were due to non-additive genetic variance. Therefore, improvement in these traits can be brought by better management practices at the farm.

TS-IV-09

COMPARATIVE STUDY OF ESTIMATED BREEDING VALUE OF SIRES BY DIFFERENT SIRE EVALUATION METHODS USING FIRST LACTATION TRAITS IN CROSSBRED CATTLE

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The data for present investigation were collected from history sheets of crossbred cows at Instructional Dairy Farm, Nagla of G. B. Pant University of Agriculture and Technology, Pantnagar. The data pertained to 1170 crossbred cows from 65 sires over a period of 35 years from 1970 to 2004. Cows with abnormal and incomplete records were excluded from the study. Breeding value of sires were estimated by four methods *viz.* Daughter's average, Least- squares, Simplified Regressed Least-squares and Best Linear Unbiased Prediction methods. By Daughter's average method, the estimated breeding values for age at first calving ranged from 1124.00 to 1589.63 days; for first lactation milk yield 2391.00 to 3681.88 kg; for first lactation period 302.75 to 462.95 days; for first dry period 64.33 to 305.00 days; for first calving interval 411.00 to 634.73 days; for first service period 251.50 to 281.67 days. By Least-squares method, the estimated breeding values for age at first calving ranged from 1108.95 to 1599.69 days; for first lactation milk yield 2159.28 to 3729.77 kg; for first lactation period 293.63 to 437.29 days; for first dry period 71.17 to 310.41 days; for first calving interval 415.64 to 658.46 days; for first service period 251.15 to 284.05 days. By Simplified Regressed Least-squares method, the estimated breeding values for age at first calving ranged from 1169.18 to 1555.23 days; for first lactation milk yield 2331.96 to 3634.12 kg; for first lactation period 305.29 to 430.33 days; for first dry period 92.92 to 295.43 days; for first calving interval 450.05 to 635.60 days; for first service period 256.25 to 281.14 days respectively. By Best Linear Unbiased Prediction method, the estimated breeding values for age at first calving ranged from 1293.11 to 1410.24 days; for first lactation milk yield 2944.47 to 3332.41 kg; for first lactation period 344.08 to 375.10 days; for first dry period 158.07 to 204.67 days; for first calving interval 517.89 to 561.57 days; for first service period 261.25 to 277.79 days respectively. The breeding values of sires estimated for first lactation traits by all four methods revealed that EBV's of sires estimated by BLUP method showed small genetic variation in comparison to other three methods.

TS-IV-10

RANKING OF SIRES ON THE BASIS OF ESTIMATED BREEDING VALUES OF SIRES FOR FIRST LACTATION AND LIFETIME TRAITS

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The data for present investigation were collected from history sheets of crossbred cows at Instructional Dairy Farm, Nagla of G. B. Pant University of Agriculture and Technology, Pantnagar. The data pertained to 1170 crossbred cows from 65 sires over a period of 35 years from 1970 to 2004. Perusal of the results indicated association between the Best Linear Unbiased Prediction (BLUP) and other methods of sire evaluation which ranged from 0.7219 to 0.9547 (product moment correlation) and 0.7186 to 0.9693 (rank correlation) for first lactation traits and from 0.7433 to 0.9502 (product moment correlation) and 0.7441 to 0.9380 (rank correlation) for lifetime traits. All the estimates of simple and rank correlation were highly significant ($P<0.01$). The results of the present investigation are supportive of the theoretical expectations that the best linear unbiased prediction method is considered to be the best method followed by least-squares method. These methods have been found as the best

and second best methods in practical evaluation of sire breeding value in the present study as well as for other herds maintained under Indian farm conditions. There were changes in the rank of first few top sires by different methods of sire evaluation. These results indicated that all sires would not rank the same for first lactation and lifetime traits. However, the rank of sires for different traits revealed that 4.5% of top sires almost had similar rank for first lactation and lifetime traits. These results suggested that to improve lifetime productivity, major culling of bulls and cows should be done on the basis of their daughter's first lactation milk yield. The EBV's of sire revealed that BLUP method showed small genetic variation in comparison to Daughter's average, Least-squares and Simplified Regressed Least-squares methods. Because of its desirable properties, the BLUP method may be considered to be more appropriate than that of Daughter's average, Least-squares and Simplified Regressed Least-squares methods.

TS-IV-11

COMPARATIVE STUDY OF EFFICIENCE OF DIFFERENT SIRE VALUATION METHODS IN CROSSBRED CATTLE

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The data for present investigation were collected from history sheets of crossbred cows maintained at Instructional Dairy Farm, Nagla of G.B. Pant University of Agriculture and Technology, Pantnagar. The data pertained to 1085 crossbred cows from 57 sires over a period of 35 years from 1970 to 2004. Cows with abnormal and incomplete records were excluded from the study. The data were subjected to LSLMW and MIXMDL package of Harvey (1990) and DFREML package of Meyer (1998) to estimate the least-squares means, genetic and phenotypic parameters of first lactation and lifetime traits, estimated breeding value of sires by different sire evaluation methods and ranking of sires on the basis of their estimated breeding values for first lactation and lifetime traits. Estimated breeding value of sires were estimated by four methods *viz.* Daughter's average, Least-squares, Derivative Free Restricted Maximum Likelihood and Best Linear Unbiased Prediction methods. The estimated breeding values of sires estimated for first lactation and lifetime traits by all four methods revealed that EBV's of sires estimated by LSA method showed small genetic variation in comparison to Daughter's average, BLUP and Derivative Free Restricted Maximum Likelihood methods. Because of its desirable properties, the LSA method may be considered to be more appropriate than that of Daughter's average, BLUP and Derivative Free Restricted Maximum Likelihood method. Perusal of the results indicated association between the least-squares analysis method and other methods of sire evaluation ranging from 0.994 to 1.00 (product moment correlation) and 0.994 to 0.998 (rank correlation) for first lactation traits and from 0.996 to 1.00 (product moment correlation) and 0.984 to 0.998 (rank correlation) for lifetime traits. All the estimates of simple and rank correlation were highly significant ($P<0.01$). The results of the present investigation are supportive of the theoretical expectations that the least-squares analysis method is considered to be the best method followed by BLUP and DFREML methods. These methods have been found as the best and second best methods in practical evaluation of sires breeding value in the present study as well as for other herds maintained under Indian farm conditions. There were changes in the rank of first few top sires by different methods of sires evaluation. These results indicated that all sires would not rank the same for first lactation and lifetime traits. However, the rank of sires for different traits revealed that 4-5% of top sires almost had similar rank for first lactation and lifetime traits. These results suggested that for improvement of lifetime productivity of animals sires should be selected on the basis of their daughter's first lactation milk yield.

TS-IV-12

PREDICTION OF STANDARD LACTATION MILK YIELD BASED ON FORTNIGHTLY TEST DAY RECORDS IN SAHIWAL CATTLE

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The sires and cows are presently evaluated based on 305-day standard lactation milk yield which requires daily milk recording of cows. The daily milk recording of dairy cattle involves heavy expenditure and is cost prohibitive under field conditions particularly under the Indian condition where most of the farmers are small and marginal. The use of fortnightly test day (TD) milk yields of daughters tend to shorten the time required to take the decision for early selection of sires if early test day milk yield records are involved and this leads to reduction in the cost of recording also. Earlier studies conducted have revealed fairly large predictability by the use of test day milk yields because of high association between test day milk yields and standard lactation milk production records. An attempt has been made to predict the standard lactation milk yield in Sahiwal cattle using fortnightly test day milk yield records. The present investigation was carried out using data of first lactation fortnightly test day milk yields and standard lactation milk yield record of 643 Sahiwal cows sired by 51 bulls from 1961 to 2009 maintained at National Dairy Research Institute, Karnal, India. The test day milk yields were recorded from 6 to 291 day of lactation at fifteen days intervals and they were used to predict standard lactation milk yield by simple linear regression analysis with only one independent variable at a time and stepwise backward multiple linear regression analysis. Based on simple linear regression analysis with individual test day record, the regression coefficients ranged from 101.22 (TD-1) to 233.99 (TD-11). The regression coefficients showed a consistently increasing trend up to TD-11 and thereafter consistently declining trend up to 20th fortnightly test day milk yields. However, the accuracy of prediction (R^2) of 305-day milk yield based on individual test day milk yields ranged between 17.2 (TD-1) and 74.9 per cent (TD-11). Based on fitting of stepwise backward multiple regressions, the regression equation with six variables *viz.*TD-1, TD-2, TD-4, TD-5, TD-6 and TD8 was considered most appropriate for prediction of standard lactation milk yield with 80.6 per cent accuracy and 8.16 per cent error of prediction.

TS-IV-13

EFFECT OF SEASON ON SEMEN QUALITY OF KANKREJ BULLS

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A study on sexual behaviour in Kankrej bull was carried out at the Semen Processing Unit of Livestock Research Station, Sardarkrushinagar with the objective to study the effect of season on seminal attributes. The period of investigation was divided into three seasons viz., summer (March to June), monsoon (July to October) and winter (November to February). Eight apparently healthy Kankrej bulls of 4-5 years of age were selected. For each bull, fortnightly observations of semen collection were recorded and a total of 192 collections, 64 from each season were recorded and evaluated. The average score (1-4 scale) for semen colour was recorded as 3.71±0.03, indicating more inclination towards creamy white colour. The mean semen volume was 4.99±0.11 ml with a range of 4.41 to 5.42 ml per ejaculate. The pH of semen ranged from 6.61 to 6.79, with an average value of 6.71±0.01. The mean mass activity score (0-5 grade) of semen was recorded 4.10±0.05. The initial motility was in the range of 80.31 to 85.94 per cent with mean value of 83.39±0.38 per cent. The average sperm concentration (millions/ml) was ascertained to be

1391.99±35.90 with a range varying from 1178.43 to 1559.51. The live sperm percentage of semen was in the range of 87.0 to 93.06 with a mean value of 90.30±0.32. Among all the seminal attributes, seasonal variation was observed only in initial motility percentage of sperm. Bulls produced semen with significantly ($P<0.05$) higher motile sperm during summer season (85.39±0.70 per cent), compared to monsoon (81.95±0.67 per cent) and winter (82.81±0.51 per cent). No significant difference in initial motility of sperm was observed during later two seasons. However, effect of season was comparable for other seminal attributes viz., colour, volume, pH, sperm concentration, mass activity and per cent live sperm. It was concluded that Kankrej bulls have good sexual behaviour, with better semen quality and quantity throughout the year. However, semen quality was far better in summer months.

TS-IV-14

APPRAISAL OF TEST DAY MODELS FOR SELECTION OF DAIRY SIRES

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Evaluation of sires for milk production has generally been done on lactation yield of daughters. The genetic progress depends upon complete recording of lactation milk yields on sufficient number of daughters which is not possible under field conditions. Selection of sires on the basis of test day models provides a better alternate because of reduced generation interval, cost effectiveness and accuracy of selection. The paper discusses various test day models which utilizes test day records for evaluation of sires. Test day model consider all genetic and environmental effects directly on a test day basis. The use of test day yield depends upon the relative genetic variation during lactation. It maximizes the amount of information to be collected for each animal and it avoids the use of factors to extend partial lactation records. It also includes management group within a herd on a test day. Test day model reduces the cost of milk recording by making fewer measurements. Most commonly used model is repeatability test day model in which consecutive test day samples are considered as repeated observations on the same traits. Random regression model allows fitting of lactation curve to individual lactation for better description of animal genotype. Another important model is multiple traits reduced rank test day model which decreases memory requirements and improves convergence is iteration when solving mixed model equations. It was observed that under local conditions the most recommended model could be the multi-trait multiple regression test day model (MT-RRTDM) for the purpose of reduction in generation interval and accuracy of selection.

TS-IV-15

GENETIC AND NON-GENETIC FACTORS AFFECTING LACTATION YIELD IN SAHIWAL CATTLE

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The present study was conducted on Sahiwal cows maintained at Uttar Pradesh Livestock- cum- Agriculture Farm, Chakganjaria, Lucknow. A total of 2985 records on total lactation yield (TLY) of cows sired by 128 bulls spanning over a period of 63 years (1949 to 2011) was subjected to least-squares analysis using suitable statistical model taking sire as random effect, while period, season and parity as fixed effects. The breeding value of Sahiwal sires were estimated for first three lactations by mixed model method. The least-squares mean of TLY was estimated to be 2069.22± 18.69 kg. The least-squares analysis revealed significant effect of sire ($P \leq 0.01$), period ($P \leq 0.01$), season ($P \leq 0.05$) and parity ($P \leq 0.05$). The heritability estimate of total lactation yield was found to be 0.105 ± 0.035. The phenotypic and genetic trend for TLY was – 116.26 and -4.46 kg, respectively. The result showed that the breeding value of almost 50 per cent sires (63/128) was below than the average for TLY. The negative trend for the present trait stressed the need for ameliorative management practices and effective and clearly set selection criteria to identify animals with superior breeding values on the farm. Thus, it can be inferred that along with better management practices, selection of sire should be undertaken for genetic improvement of the trait.

TS-IV-16

AVERAGE RATE OF INBREEDING IN AN INDEGENOUS CATTLE (VECHUR) CONSERVATION UNIT

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Vechur is the most popular indigenous breed of cattle in Kerala, the number of which were drastically reduced after the large scale crossbreeding in the state. The efforts for conservation of this small native breed of cattle were initiated early in 1989 by the Kerala Agricultural University and subsequently taken over by Kerala Veterinary and Animal Sciences University. The effective and successful *in situ* conservation of any breed depends largely on the herd size and genetic diversity of the animals maintained. The most important challenge under the conservation project is the limited population size and the adverse effects of inbreeding. Thus the present investigation was conducted with the pedigree records of 557 Vechur cattle maintained at the Vechur Cattle Conservation Project, CASAGB, Mannuthy under the Kerala Veterinary and Animal Sciences University, to evaluate the average rate of inbreeding over the years using the Pedigree Viewer programme. Out of the 557 animals 509 were with known sire and dam. Since the conservation project started with procured animals from the field, the number of unlisted sires and dams were 14 and 34, respectively. Thus the analysis was conducted with assumption that the inbreeding coefficient of base population is zero. The total number of sires and dams in the known part of the pedigree were 49 and 137, respectively. The maximum paternal family size was 67 and maximum maternal family size was 14, as per the records. The range of inbreeding coefficient in the herd was 0.0 to 0.3125 with a mean inbreeding coefficient of 0.0167. The whole pedigree data were classified into seven tiers and the numbers of individuals in these seven tiers were 37, 51, 88, 143, 138, 90 and 10, respectively. The average inbreeding coefficients in the first two tiers were zero. The average inbreeding coefficients in third to seventh tiers were 0.0185, 0.0050, 0.0241, 0.0354 and 0.0440, respectively. The results of the present investigation reveal that the inbreeding coefficient is gradually increasing over the generation which is generally expected in a closed herd. This also demands the need of incorporation of few more unrelated breeding bulls with superior breed characteristics for long term and effective conservation of our valuable native breeds like Vechur.

TS-IV-17

ESTIMATES OF VARIANCE COMPONENTS AND GENETIC PARAMETERS OF PEAK YIELD OF CROSSBRED CATTLE

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Variance components and genetic parameters were obtained for peak yield of Jersey crossbred cattle, maintained at the Eastern Regional Station of National Dairy Research Institute, Kalyani, Nadia, West Bengal, India, over a

period of 35 years (1981 through 2015). Analyses were carried out by restricted maximum likelihood (REML), fitting an animal model and ignoring or including maternal genetic or permanent environmental effects. Six different animal models were fitted for all traits. Model 1 was a simple animal model fitting animals' direct additive genetic effects only i.e. ignoring any maternal effects. Model 2 allowed for a maternal effect in addition, but attributed it solely to the permanent environmental effect of the dam. Model 3 assumed that all maternal influence was of genetic origin. Model 4 allowed for a respective non-zero covariance. Models 5 and 6 were corresponded to models 3 and 4, respectively. But fitted both dams' genetic and permanent environmental effects i.e. three random factors altogether. Data on 1102 records of 508 Jersey crossbred animals, descended from 65 sires and 232 dam, were used. The best model was chosen after testing the improvement of the log-likelihood values. Direct heritability estimates were inflated for all traits when maternal effects were ignored. Direct heritability estimates ranged from 0.41 to 0.52 for peak yield depending on the model applied. The additive maternal effects varied from 0.0 to 0.07 for this trait in different models, whereas the estimates of the fraction of variance due to maternal permanent environmental effects accounted for 0-3% of the phenotypic variance, irrespective of the models used. Estimated genetic correlation between additive direct and additive maternal genetic effects for this trait was -0.79, depending on the model used. Results suggested that both direct and maternal effects were important for these traits and further, there is an ample scope of genetic progress through selection for these traits.

TS-IV-18

TIME SERIES ANALYSIS OF INDIGENOUS AND CROSSBRED POPULATION AND MILK PRODUCTION IN TAMILNADU

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Tamilnadu ranks eighth in milk production in India with the production record of 7.05 million tonnes during the year 2012-13. In this study, an attempt was made to analyse the growth of indigenous cattle and crossbred cattle population and milk production in Tamilnadu. The data on population and milk production of indigenous cattle and crossbred cattle for a period of twenty years (1993-2013) were collected from secondary sources. The data were analysed by compound growth rate analysis and conventional analysis in the form of averages and percentages. The study period was divided into two phases (1993-94 to 2002-03 and 2003-04 to 2012-13). The overall growth rate was positive in crossbred population and milk production whereas indigenous cattle population and milk production showed a negative growth rate. Milk production from indigenous and crossbred cattle contributed 47.01 per cent and 52.99 per cent to the total milk production in the first phase whereas in the second phase the contribution from indigenous cattle was declined to 18.40 per cent and crossbred cattle was increased to 81.59 per cent. The contribution of indigenous cattle population to the total cattle population was 71.44 per cent in the first phase whereas in the second phase, it has declined to 36.9 per cent. The decline in indigenous cattle population and milk production may be due to the introduction of crossbreeding technology in which crossbred animals yield high milk production, higher conception rate, early maturity and less intercalving interval than indigenous animals.

TS-IV-19

FACTORS AFFECTING STANDARD LACTATION MILK YIELD IN JAFFARABADI BUFFALOES

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The production records on 467 complete lactations of 156 Jaffarabadi buffaloes sired by 39 buffalo bulls, for 24 years (1987–2010) were studied. The data were analyzed to study the effect of period and season of birth, period and season of calving and parity as fixed effects and sire as random effect on Standard Lactation Milk Yield (SLMY). Mixed model of SAS 9.3 was used to carry out the analysis of data. The least-squares means of SLMY was found to be 3174.79 ± 27.26 kg. Analysis revealed significant effect of period of birth, period and season of calving and parity on SLMY while season of birth didn't show any significant effect on SLMY. Highest SLMY was found during fourth parity (3423.55 ± 111.35 kg). SLMY for 1st to 8th parity was not differing significantly, which reveals the sustained production potential of the animals over different parities. The buffaloes refreshing during summer season were found to be high in SLMY (3220.38 ± 141.41).

TS-IV-20

PREDICTION OF BIMONTHLY TEST-DAY MILK YIELDS USING FOUR DIFFERENT LACTATION CURVE MODELS IN INDIAN MURRAH BUFFALOES

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Lactation curve is the graphical representation of milk yield against time. Dairy cattle and buffaloes with more stable lactation curve are more persistent than those which show a rapid increase in the daily milk yield from calving to peak followed by a rapid decline. Data on 5078 bi-monthly test day milk yield (BTDY) records during first lactation of 916 Murrah buffaloes were used to predict the 305-day milk yield from different lactation curve functions. The average BTDY ranged from 3.98±0.05 kg (BTDY-1) to 7.99±0.06 kg (BTDY-2). The relative efficiency of four lactation curve models via. Gamma-type function (GF), Exponential function (EF), Mixed log function (MLF) and polynomial regression function (PRF) were compared. PRF described the highest coefficient of determination (99.81%) and with least value (0.03 kg) of root mean squares error (RMSE), whereas, least coefficient of determination (95.11%) was observed in EF having maximum (0.14 kg) RMSE value suggesting PRF the best mathematical model for prediction of BTDYs in Murrah buffaloes.

TS-IV-21

HERITABILITY ESTIMATES FOR TOTAL LACTATION FAT YIELD IN MURRAH BUFFALOES

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Present study was conducted with an aim to estimate the heritability of total lactation fat yield in Murrah buffaloes. Production performances of 914 buffaloes sired by 77 bulls over a period of 21 years (1993-2013) were recorded from institute's cattle yard maintained at NDRI. The data were classified according to period of birth, season of calving and parity of animal. Effects of non-genetic factors are studied for significant effects, using mixed model least-squares and maximum likelihood computer program PC-2. Traits recorded were monthly test day fat per cent and total milk yield of each animal. Least-squares means obtained for total lactation fat yield was 181.75 ± 1.91 kg. It was concluded that total lactation fat yield was significantly ($p \leq 0.05$) affected by sire, period of birth and parity of animals, whereas season was having a non-significant effect. Heritability estimate for total lactation fat yield obtained by paternal half sib method was0.328 ± 0.100 indicating that total fat yield in Murrah buffaloes is moderately inheritable (~32%) and can be used as genetic estimate in different selection criteria used in Murrah buffaloes.

TS-IV-22

EFFECT OF FUNCTIONAL TRAITS ON SUBSEQUENT REPRODUCTION PERFORMANCE OF MURRAH BUFFALOES IN INDIA

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A study was conducted on 1585 calving records of Murrah buffaloes maintained at NDRI, Karnal, India spread over a period of 18 years (calved from 1993-2010) to study the influence of various functional traits on subsequent reproductive performance. The major groups of functional traits considered were calving abnormalities, uterine health problems, female fertility problems and udder health problems. The effects of these functional traits on calving to first service (CFS), service period (SP), dry period (DP) and calving interval (CI) were studied by least-squares method using SAS package (Enterprise guide 5.1). Significantly higher CFS, SP, DP and CI were observed in the animals affected with any of the calving abnormalities in comparison to the non-affected group. The increase in CFS, SP, DP and CI was 27.07, 18.71, 96.74 and 6.70 per cent, respectively. Subsequently, the average milk yield per day of calving interval was found to be reduced (from 4.91 to 2.10 kg/day) in these animals in comparison to the normal calvers. A highly significant increase in average CFS, SP, DP and CI was found among animals susceptible to metritis (16.93, 73.88, 53.92 and 20.04 per cent, respectively). The decrease in average MY/CI was 18.55 per cent in comparison to the animals resistant to metritis. Incidence of pyometra was also associated with significant reduction in MY/CI (14.38 per cent) and highly significant increase in CFS (33.08 per cent), SP (39.24 per cent), DP (33.87 per cent) and CI (11.82 per cent). The increase in average CFS, SP, DP and CI associated with anoestrus was 51.58, 94.35, 47.56 and 23.84 per cent, respectively. The average MY/CI was observed to be 16.47 per cent lower in the anoestrus affected animals in comparison to normal animals. The increase in average SP, DP and CI associated with repeat breeding cases was 162.63, 87.58 and 50.15 per cent, respectively. The increase in average DP and CI due to incidence of mastitis was 10.48 and 4.26 per cent, respectively. The increase in average dry period associated with the incidence of mastitis during early stage of lactation (1-60 days) was 13.63 per cent. The incidence of overall

mastitis and mastitis during early stage of lactation significantly reduced the average MY/CI by 5.50 and 14.20 per cent, respectively. The significant decline in production and reproduction performance revealed the need of better management practices for those affected buffaloes to alleviate the expected adverse effects.

TS-IV-23

GENETIC STUDIES ON ECONOMIC TRAITS OF SURTI BUFFALOES AT ORGANIZED FARM IN MAHARASHTRA

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The data on productive and reproductive traits of Surti buffaloes from 287 lactation records of 125 Surti buffaloes maintained at Buffalo Breeding Farm, Hingoliin Maharashtra were considered for the study. Data spread over a period from December, 1988 to December, 2010 wereanalyzed using SYSTAT version 7.0 by SPSS INC. The overall means forage at first calving, lactation length, dry period, calving interval, lactation milk yield, 305 days lactation milk yield and peak yield in Surti buffaloes were found to be 1373.52±21.76 days, 254.30±4.75 days, 212.36±11.50 days, 456.09±10.34 days, 898.80±25.06 kg, 1180.9±20.01 kg and 7.934 kg respectively. The effect of period of birth was observed significant on age at first calving, similarly significant effect of period of calving was observed on lactation milk yield, 305-day lactation yield, lactation length, calving interval and peak yield respectively. Significant effect of season of calving was observed on lactation yield and 305-day lactation yield and significant effect of parity was observed on lactation length, calving interval, lactation yield and 305-day lactation yield. The heritability estimates were 0.226±0.154, 0.446±0.554, 0.332±0.158, 0.55±0.13 and 0.95±0.020 for age at first calving, lactation length, dry period, calving interval and 305-day milk yield respectively. The genetic correlation of 305-day milk yield and lactation length with lactation yield, were found to be positive and highly significant. However, the genetic correlation of dry period and AFC with lactation length, lactation yield and 305-day milk yield in Surti buffaloes were found to be significantly negative. The phenotypic correlation of LL with ICP, LY, 305-day milk yield was found to be positive and significant Whereas AFC was found to have significantly negative phonotypic correlation with all the production traits except dry period.

TS-IV-24

PREDICTION OF LACTATION MILK YIELD BASED ON PART LACTATION PERFORMANCE IN SURTI BUFFALOES

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The data of 287 lactations of 125 Surti buffaloes from the milking records available at Buffalo Breeding Farm, Hingoli was utilized for the present study. Single and multi-variable linear regression with constant were estimated for prediction of lactation milk yield based on part lactation traits *viz.* 30 days, 60 days, 90 days, 120 days, milk production after correction of lactation records for significant effect of non-genetic factors using SYSTAT version 7.0 by SPSS INC. The correlation coefficient between lactation milk yield and first to tenth monthly milk yield were 0.343, 0.386, 0.615, 0.634, 0.284, 0.413, 0.463, 0.448, 0.458 and 0.612 and with first to ten cumulative monthly milk yields 0.343, 0.470, 0.579, 0.663, 0.613, 0.610, 0.590, 0.592, 0.663, and 0.714 respectively. The correlation coefficient between 305-day lactation milk yield and first to tenth monthly milk yield were 0.258, 0.423, 0.509, 0.546, 0.393, 0.473, 0.539, 0.425, 0.395, and 0.417 respectively whereas with first to tenth cumulative monthly milk yield 0.258,

0.437, 0.529, 0.591, 0.646, 0.657, 0.677, 0.645, 0.708, and 0.720 respectively.The phenotypic correlation between part and total lactation records will be efficient but more economic gain could be achieved if selection is made on the basis of fourth monthly yield and cumulative milk yield. Prediction equation for total lactation milk yield based on fourth monthly milk yield (R^2 =0.402) and fourth cumulative monthly milk yield (R^2 =0.440) showed higher accuracy of prediction value while for predicting the 305-day lactation milk yield, four monthly milk yield (R^2 =0.298) and seventh cumulative monthly milk yield (R^2 =0.459) showed higher accuracy of prediction value than advanced part lactation records.

TS-IV-25

GENETIC AND NON-GENETIC PARAMETERS INFLUENCING WEEKLY TEST-DAY MILK YIELDS AND FIRST LACTATION 305-DAY MILK YIELD IN MURRAH BUFFALOES

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India has about 51 million milch buffaloes (19th Livestock Census) contributing 51% of the total milk produced in the country. In order to find out an alternative to daily milk yield recording, which is a costly and time consuming proposition under field conditions, the present investigation was undertaken with the objective to study influence of various non- genetic and genetic factors on weekly test-day and first lactation 305-day milk yield in Murrah buffalo. The data on 39,059 weekly test-day (TD) milk yield records during first lactation of 961 Murrah buffaloes calved from 1977 to 2012 and sired by 101 bulls maintained in an organized farm at National Dairy Research Institute, Karnal were analysed using least-squares maximum likelihood programme to study the effect of genetic and non-genetic factors [period, season and age at first calving (AFC) groups]. The least-squares means for first lactation 305-day milk yield was found to be 1853.49±15.88 kg. The least-squares means of overall weekly test-day milk yields ranged from 2.44±0.07 kg (TD-43) to 7.95±0.06 kg (TD-8). Effects of period, season and AFC groups were found to be highly significant ($P<0.01$), significant ($P<0.05$) and non-significant on first lactation 305-day milk yield, respectively. The h^2 estimate of first lactation 305-day milk yield was 0.25±0.09. The estimates of phenotypic and genetic correlations between 305-day milk yield and different weekly test-day milk yields ranged from 0.52 to 0.84 and from 0.19 to 0.98, respectively and were higher in the middle segment of lactation suggesting that these test-day yields could be used as the selection criteria for early evaluation and selection of animals.

TS-IV-26

GENETIC EVALUATION OF BUFFALOES BASED ON TEST DAY MILK YIELD

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In recent years, interest in test-day (TD) records has increased among dairy geneticists and among members of the dairy buffalo breeding industry. One reason for this interest is a trend among all countries having major dairy buffaloes to reduce costs of recording dairy buffalo performance. A test-day model (TDM) improves the accuracy of genetic evaluation, provides better modelling and extending of part lactation is no more needed. The test-day models have been suggested as the method of choice for the analysis of milk yield traits in order to maximize the use of all available information. Test-day models can predict total production more accurately by accounting

for time-dependent environmental effects. Main objective of any breed improvement program is to bring about genetic improvement by selection of superior sires and dams. Generally, sires are evaluated on the basis of first lactation 305-day or less milk yield of their daughters which result in lower genetic gain per unit of time due to longer generation interval. Daily milk recording is costly and time consuming proposition. To overcome these limitations of 305-day milk yield records some methodological approaches have been proposed to adjust repeated observations during a period of time, such as the milk yield. Test-Day Models are defining as the measuring parameter is the total milk yield during the test day, named 'test day milk yield' (TDMY). Based on predicted milk yield from test day records, the animal can be selected for future breeding. By using the TDMY there is no need to enlarge the lactation period for animals not reaching 305 lactation days.

TS-IV-27

FIELD APPROACH TO ESTIMATATE BODY SURFACE AREA IN BUFFALO

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Estimation of body surface area at field level can help in better quantitative understanding of body size and define quantitative approach for body condition of animal. Further, it is likely to be useful for relating body size with feeding and performance in terms of body surface area. Scanty reports available on estimation of 3 dimensional animal body surface area using either 2 dimensional visuals or by using different body measurements are restricted to data generated from swamp buffaloes on organized farms. An attempt was made to estimate 3D body surface area using body measurement data on 30 buffaloes of age ranging between 5 and 6 years maintained at BAIF Central Research Station Farm. Body measures were taken and mean body height, heart girth, shoulder width, iliac width, ischial tuberosity width, the length between shoulder and ileac wing, the length between ileal wing to ischial tuberosity and the length between shoulder to ischial tuberosity, body weight. The mean values were 124.9±1.03cm, 180.94±2.22cm, 38.37±1.53cm, 46.38±0.83cm, 28.39±1.49cm, 93.49±1.60cm, 29.95±0.70cm, 108.26±1.86cm and 330±11.51kg respectively. The correlation between traits measured were calculated and presented. The approach suggested by Hurnik and Lewis (1991), Heycock (1978), Mosteller (1987) and DuBois and DuBois (1916) and Burhankar*et al.* (2012) were examined for estimating body surface area using the measurements taken. It was noted that the correlation between the body surface areas estimated by different methods was found ranging from 0.661 to 1.0. Based on the study, it was recommended that approach suggested by Hurnik and Lewis Could be used to estimate body surface area under field conditions.

TS-IV-28

GROWTH DIMENSIONS OF BUFFALO MILK PRODUCTION IN TAMILNADU

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India ranks first in the world milk production which went up to 132.43 million tonnes in 2012-13 and it plays a prominent role in the Indian economy. Tamilnadu, the southern most state of India, is one of the top ten milk producing states in the country. The total buffalo milk production in Tamilnadu in the year 2012-13 was 0.71 million tonnes and the milk production was mainly from Murrah, Surti and upgraded Murrah breeds of buffaloes. Time series data for 20 years (1993-2013) on milk production of buffaloes in Tamilnadu were collected from secondary sources. The data were analysed by compound growth rate analysis and conventional analysis in the form of averages and percentages. The study period was divided into two phases (1993-2002 and 2003-2013). Buffalo milk production showed a positive growth during the first phase; whereas in the second phase, it showed a negative growth rate. Overall buffalo milk production had a negative growth rate. Phase-wise analysis by average proportion indicated buffalo milk production contributed 40.19 per cent to the total milk production in the first phase; whereas it had declined to 14.6 per cent in the second phase. In overall, the buffalo milk has contributed 27.43 per cent to the total milk production. The negative growth rate could be due to decreasing buffalo population which was 16.48 lakh in 1993 and 7.83 lakh during 2013. The introduction of crossbreeding technology in cattle leading to increase in milk production might have also contributed to the decline in milk production to total milk production. The reason for declining buffalo population could be due to management constraints associated with buffalo rearing such as aggressive behaviour, repeat breeding problems, silent heat and non-availability of wallowing facilities.

TS-IV-29

IMPROVEMENT OF BUFFALO PRODUCTIVITY: FIELD DATA RECORDING AND CONSERVATION PROGRAMME

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Buffalo diversity is available for the sustainable intensification of food and agriculture production. Continuous rise in food prices has been posing a serious policy challenge in India. The high growth in demand for milk and milk products is increasing in the domestic and international markets with domestic supply not keeping pace. This is due to negligible improvement in animal productivity over the past six decades, increasing cost of production, decreasing trend in productivity of adult females and also significant decrease in quality male germplasm in 2012 as compared to 2007 buffalo population census. Therefore, measures need to be relooked at to study the entire animal production ecosystem. The targets set by the Government of India revealed that the domestic demand for milk would reach 191MT by 2020. This effectively requires an incremental production of 53 million tons in the next seven years from the level of 137.97 million tons in 2013-14 with a CAGR of 5.50 per cent. It is to be noted that the previous incremental quantity of 53 million tons of milk was achieved in 12 years (2001-02 to 2013-14). Therefore, based on past trend in milk production growth, 5.50 per cent increase in milk production per annum is difficult to achieve. Buffalo accounts for about 38.82 per cent population as compared to cattle and contributes about 53 per cent of total milk produced in the country. This indicates significant contribution in milk production and buffalo is recognized as more efficient producer of milk. But, the limiting factors for improvement in milk production performance of buffaloes are insufficient genetic inputs in the form of availability of genetically superior breeding bulls, absence of field data recording and progeny testing infrastructures. Also the private buffalo dairy farms in metros' maintained superior quality Murrah, Mehsana and Banni buffaloes, but about 85 to 90 per cent calf mortality and around 25 per cent buffaloes culled annually due to uneconomical returns to the dairy owners. These figures indicated that large number of calves and buffaloes are removed from the production cycle and departure of valuable germplasm from the herd, because of forcefully killing of calves and slaughtering buffaloes, looking at the short term benefits by the dairy owners. Therefore, for improvement in milk productivity of buffaloes and to accelerate the genetic progress, the best options are: launching mission mode field data recording to identify elite females, identification of elite males in field and to establish calf rearing centres in metros'. The performance of buffaloes in field indicates that buffalo have excellent production potential even better than elite crossbreds. The information on buffalo performance and production potential in field and strategies for conservation of elite germplasm will be discussed and presented in the symposium.

TS-IV-30

AN IMPACT OF CONSERVATION OF KILAKARSAL SHEEP AT ITS NATIVE TRACT

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Kilakarsal sheep, one of the registered Indian breed (Accession Number: INDIA_SHEEP_1800_KILAKARSAL_14024), is distributed in the southern districts of Tamilnadu state of India. They are medium-sized with compact body conformation and reared for meat purpose. It is hardy, heat tolerant and has the capacity to utilize coarse feed materials efficiently, traits that are beneficial in drought prone areas. This sheep breed also has the capacity to cover long distances in search of pasture for grazing. Due to lack of quality Kilakarsal sires and indiscriminate breeding methods adopted by the farmers, this sheep population has come down drastically. Hence, *in situ* conservation efforts were carried out since 2006 by the Tamilnadu Veterinary and Animal Sciences University, Chennai in association with National Bureau of Animal Genetic Resources, Karnal. The main objective of the scheme was to enhance the Kilakarsal germplasm in the farmers' flocks thereby re-establishing the breed in the native tract. Through this effort, a Kilakarsal flock was established at Instructional Livestock Farm Complex, Veterinary College and Research Institute, Tirunelveli. From this unit, a total of 89 Kilakarsal breeding rams were distributed to the farmers and 1541 (740 male + 801 female) Kilakarsal progenies were recorded during the scheme period. The Kilakarsal breed which was restricted to a narrow area of Tirunelveli was made famous by various extension activities. Through these efforts, one ordinary breeder has won "breed savior" award. Supply of more number of Kilakarsal rams to the field, production of elite rams in associated flocks and exchange of rams among themselves are the recommendations for sustainable utilization of the breed.

TS-IV-31

EXPECTED RESPONSES IN GROWTH MEASURES TO SELECTION FOR BODY WEIGHTS AT VARIOUS AGES IN DORPER CROSSBRED SHEEP

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The present study was conducted on different body weight traits of Dorper crossbred sheep. Data on 355 sheep over a period of 12 years from 2001 to 2013 were analyzed to estimate expected direct and correlated responses in different body weight traits like birth weight (BWT), weaning weight (WWT), 6-month body weight (6-BW), 12-month body weight (12-BW) and mature body weight (MBW). Data were analyzed by LSMLMW computer programme using Harvey (1990). The expected direct and correlated responses for single trait selection were estimated following the procedure described by Falconer (1989). The estimates of heritability for the present study in Dorper crossbred sheep varied from medium to high and were 0.247±0.144, 0.345±0.170, 0.891±0.286, 0.926±0.291 and 0.747±0.260 for BWT, WWT, 6-BW, 12-BW and MBW, respectively. The expected direct responses in different body weights were 0.110 kg, 0.655 kg, 1.801 kg, 1.998 kg and 1.458 kg, respectively. The maximum correlated responses of 1.901 kg in one generation was observed in yearling weight if selection is applied to 6-BW. Among several selection criteria, MBW had positive correlated responses with all the body weights in the present study. However, MBW cannot be used as selection criterion for practical situations due to higher overhead costs of maintenance and generation interval will also increase. It is concluded that selection based on 6-BW would be the most ideal selection criterion to improve the body weight performances of Dorper crossbred sheep as it will not increase generation interval.

TS-IV-32

GENETIC STUDIES ON GROWTH TRAITS IN DORPER CROSSBRED SHEEP

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Data on growth traits of 701 animals used in the present study were collected from history sheet of Dorper crossbred sheep maintained at Government Sheep Breeding Farm, Panthal, Reasi, J&K, India. Traits included in the study were birth weight (BWT), weaning weight (WWT), 6-month body weight (6-BW), 12-month body weight (12-BW), mature body weight (MBW) and annual wool production (AWP). The statistical analysis was carried out using LSMLMW computer programme. The overall least-squares means were 2.771±0.051 kg, 14.887±0.293 kg, 17.397±0.264 kg, 22.362±0.282 kg, 29.656±0.231 kg and 0.963±0.041 kg, respectively for BWT, WWT, 6-BW, 12-BW, MBW and AWP. Genetic group had significant effect on all the traits except for WWT. Period of lambing had significant effect on all the traits except for BWT. There was no definite trend for different traits over different periods except for 12-BW, where increasing trend was obtained. Sex had significant effect on all the traits except for 6-BW and 12-BW. The estimates of heritability for the present study in Dorper crossbred sheep varied from medium to high and were 0.480±0.162, 0.381±0.271, 0.893±0.225, 0.727±0.202, 0.679±0.195 and 0.189±0.225 for BWT, WWT, 6-BW, 12-BW, MBW and AWP, respectively. The highest genetic and phenotypic correlations were obtained between 12-BW and MBW. All the phenotypic correlation values were significant barring exception for WWT and AWP, where, non-significant phenotypic correlation was obtained. Six month body weight (6-BW) had high heritability and genetic and phenotypic correlations with other growth traits indicate that 6-BW can be used as a selection criterion.

TS-IV-33

NON-GENETIC FACTORS AFFECTING GROWTH TRAITS OF BHARAT MERINO SHEEP IN SUB-TEMPERATE CLIMATE OF KODAI HILLS

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Bharat Merino (BM) sheep is one of the fine apparel wool breeds of India, known for its adaptability to the temperate and sub-temperate environment and potential for wool as well as meat production. Data were subjected

to analysis of variance using the generalized linear model (GLM) procedure of SPSS to determine the effects of season, year, sex, type of birth and dam age on the body weight from birth to twelve months and greasy fleece yield. The data for this study represents a total of 1649 BM lambs, progeny of 144 sires over the year from 2000 to 2014 were included for the analysis. The data were collected from the breeding flock of BM sheep maintained at the Southern Regional Research Centre, CSWRI, Mannavanur, Tamilnadu at a longitude of 77º-78ºE, latitude of 10º-11ºN and an altitude of 2030 m above mean sea level in the hilly region of South India. The different economic growth traits used for the analysis were birth weight (BWT), weaning weight (3WT), 6 month weight (6WT), 12 month weight (12WT) and greasy fleece yield (GFY). The overall least-square means for body weights (kg) were 3.289 ± 0.02, 19.08 ± 0.23, 25.00 ± 35, 34.79 ± 0.59 and 2.13 ± 0.07 for BWT, 3WT, 6WT, 12WT and GFY respectively. Year, season, sex, type of birth and dam age were highly significant ($P<0.01$) on BWT and 6WT. However above said factors were highly significant ($P<0.01$) on 3WT except season of birth which had no effect. Year, season and sex had significant effect at 1 % level on 12WT whereas type of birth and dam age did not have significant effect. Also, analysis of variance showed that the year and sex of the lambs were important sources of variation ($P<0.01$) on GFY but season variation had significant at ($P<0.05$) and no effect of variation on type of birth and dam age. Results showed that non-genetic (environmental) factors have an important role in expression of genetic potential in the growth traits of BM sheep. Performance records of animal should be adjusted to reduce or discount known environmental differences between animals, so that genetic differences among animals can be recognized and used for effective breeding plan for their improvement.

TS-IV-34

ESTIMATION OF GENETIC PARAMETERS OF BODY WEIGHT TRAITS AND EFFECT OF INBREEDING IN BHARAT MERINO SHEEP

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Genetic parameters of weight at birth (BWT), weaning weight (WWT) and six months weight (6WT) of Bharat Merino sheep being maintained at Southern Regional Research Centre (Central Sheep and Wool Research Institute), Mannavanur, Kodai hills under sub-temperate climate at an altitude of 2030m above MSL were estimated. The present study was carried out using the data generated over the last 15 years, from 2000 to 2014 with records on 1658 progenies descending from 174 sires and 649 dams. A total of seven sire lines are being maintained and utmost care is taken to avoid inbreeding and stray mating. All the animals in this flock were kept under semi-intensive management system. Males were selected based on six months body weight. Selection of ewes was relaxed and culling was done only on the basis of health status and low production. Lambing takes place in two seasons, spring (January to March) and autumn (August to October), where 42% and 58% of lambing took place, respectively. Animals were treated uniformly in both the seasons with respect to management and concentrate supplementation. The mean and standard deviation of the traits (no. of observations in parentheses) namely BWT, WWT and 6WT were 3.71±0.66 kg (1658), 19.64±3.83 kg (1345) and 26.17±4.59 kg (977) respectively. The causal components of variance were estimated by DFREML method using WOMBAT software from which narrow sense of heritability was estimated. The heritability estimates with standard error of the traits namely BWT, WWT and 6WT were 0.52±0.05, 0.16±0.05 and 0.17±0.06 respectively. The inbreeding did not affect the body weight traits significantly. The average inbreeding co-efficient with standard error for the truncated pedigree data over the years from 2000 to 2014 is 0.0018±0.015. It is concluded that the minimum level of inbreeding optimizes the selection programme by accounting simultaneously for the desired traits so as to maximize the response.

TS-IV-35

GENETIC DIVERSITY OF AVIKALIN SHEEP THROUGH PEDIGREE ANALYSES

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The objective of this study was to evaluate genetic diversity in the Avikalin sheep maintained under standard farm management conditions over 39 years. Avikalin was evolved by stabilizing the exotic inheritance at 50 % level in the crosses of Rambouillet x Malpura sheep at ICAR-Central Sheep and Wool Research Institute, Avikanagar. The wool produced by Avikalin is suitable for manufacturing superior carpet. The data on 7483 individuals spanning over 19 generations was used for pedigree analysis using ENDOG version 4.8. The pedigree information estimated by the number of equivalent generation traced was good (5.17). For reference cohort, effective number of founders (f_e) was 58, representing 8.15 % of the potential number of founders. The effective number of ancestors (f_a) was 53 and the genetic contribution of the 20 most influent ancestors explained 50% of the genetic variability in reference cohort. The realised effective population size of the flock computed via individual increase in inbreeding was 103.33±6.18. The ratio f_e/f_a which expresses the effect of population bottlenecks was 1.09. Pedigree completeness for the data spanning over 19 generations revealed 90.49% completeness for the data. The animals born in the last 5 years (2010–2014) were considered as reference population for calculation of inbreeding. The average inbreeding coefficient for complete population was 2.02%, however for the reference population (2010-2014) it was 4.11%. The average relatedness coefficient between individuals of the whole population was 3.84%, however for reference population it was 5.13%. The inbreeding coefficient increased with the addition of each generation to the pedigree. In the population, 5.32% individuals had more than 6.25% F_i. For the current population (2008-2011) the generation interval was lowest for ram daughter pathway (2.94±0.85 years) and highest for ewe to son (4.19±1.70 years). The average genetic conservation index (GCI) for the complete population was 15.46. Our work revealed satisfactory level of genetic variability for Avikalin sheep. Use of sires with the lowest possible average relatedness coefficient and the use of appropriate mating strategies are recommended to keep inbreeding at acceptable levels and increase the genetic variability.

TS-IV-36

GENETIC PARAMETER ESTIMATES FOR GROWTH TRAITS IN MECHERI SHEEP USING RANDOM REGRESSION ANIMAL MODELS

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The genetic parameters for growth traits in Mecheri sheep were estimated with REML using random regression animal models. The data (1991-2006) on birth, weaning (3 months), 6, 9 and 12 months weight were extracted from available production records at the Mecheri Sheep Research Station, Pottaneri, Salem District, Tamilnadu. The period, sex, season of lambing and age of dam at mating were considered as fixed effects. The random additive direct genetic and individual permanent effects were fitted. The data were analyzed using random regression animal model to estimate the (co) variances and the genetic parameters. The heritability estimates for birth, 3, 6, 9 and 12 months body weights were 0.215, 0.357, 0496, 0.480 and 0.349 respectively, and were high for all traits.

Genetic correlation between birth weight and other traits (3, 6, 9 and 12 months weights) were 0.985, 0.933, 0.782 and 0.437 respectively; weaning weight and other traits (6, 9 and 12 months weights) were 0.981, 0.879 and 0.587 respectively; 6- months weight and other traits (9 and 12 months weights) were 0.954 and 0.731 respectively and between 9- and 12-months weights was 0.903. It was concluded that the high estimates of heritability and strong genetic correlation provide the scope for improvement in growth traits by direct selection and further the possibility of using earlier growth measures for improvement of market weight by indirect selection.

TS-IV-37

CONSTRAINT ANALYSIS OF SHEEP REARERS IN CHITTOOR DISTRICT OF ANDHRA PRADESH

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A survey was conducted with a sample of 38 sheep beneficiaries selected randomly from selected mandals in Chittoor district, A.P. The constraints that disrupt the successful rearing of sheep were identified and ranked. Out of the 10 constraints identified, majority of the shepherds opined that poor credit facility from the government sector with special reference to banks was their prime choice with a mean score of 70.15. Second constraint expressed by beneficiaries was lack of veterinary care with a mean score of 65.81. Limited availability of quality breeding stock was ranked 3rdwith a mean score of 63.28. Most of the farmers reported that high lamb mortality was another concern for them and the constraint ranked 4th with a mean score of 58.28. The next constraint faced by beneficiaries was shrinkage of grazing lands, which ranked 5th with a mean score of 51.94. Disease attack was ranked 6th with a mean score of 50.52 followed by drinking water scarcity (7th) with a mean score of 45.65. Frequent drought attacks ranked 8th with mean score of 44.07. Inadequate marketing facilities and non-availability of farm labour ranked 9th and 10th with mean scores of 27.02 and 22.42, respectively.

TS-IV-38

SEMEN CHARACTERISTICS OF NELLORE JODIPI RAM

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Nellore is the tallest Indian sheep breed and is well known for mutton production. Nellore Jodipi also called 'Jodimpu' is one of the three variants of Nellore breed. Nellore Jodipi rams are relatively large and has a graceful appearance with thick horns, directed backward and then forward in most of them. Three rams with good libido stationed at Livestock Research Station, Palamaner were utilized to study semen characteristics. The normal fresh semen characteristics such as mean ejaculate volume, mass activity (0-5 scale) and sperm concentration in Nellore Jodipi sheep were 0.62±0.03 ml, 3.98 ± 0.08 and 4037.66 ± 42.75 million per ml, respectively. While, the mean percentages of individual motility, live spermatozoa, normal sperm and head, mid piece and tail abnormalities and intact acrosomes in fresh semen were 70.75 ± 0.53, 63.22 ± 0.48, 93.83 ± 0.30, 1.02 ± 0.11, 0.10 ±0.04, 5.08 ± 0.22 and 95.47 ± 0.20, respectively.

TS-IV-39

NORMAL BIOCHEMICAL VALUES IN DIFFERENT GENETIC LINES OF MUZAFFARANAGRI EWES

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This study was performed to evaluate the effect of restricted breeding on normal biochemical values in healthy adult, non-pregnant non-lactating Muzaffaranagri ewes. Blood samples for biochemical analysis were withdrawn from 20 (10 local Muzaffarnagri; 10 improved Muzaffarnagri) healthy, non-pregnant non-lactating ewes. Serum biochemical analysis included total protein, albumin, blood urea nitrogen, creatinine, glucose and ß-hydroxybutrate. Improved Muzaffarnagri had significantly higher ($p<0.05$) serum total protein, cholesterol and triglycerides, but significantly lower ($p<0.05$) ß-hydroxybutrate, BUN and creatinine values compared to the local Muzaffarnagri ewes. While, there were significant differences in the biochemical values between the local and improved lines of Muzaffarnagri ewes and the values were within the normal ranges for healthy sheep.

TS-IV-40

GROWTH PERFORMANCE AND HETEROSIS EFFECT IN GMM X PATANWADI SHEEP AND ITS RECIPROCAL CROSSES

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The records for body weights of GMM X Patanwadi and Patanwadi X GMM crosses for the period during 2010-2014 maintained at CSWRI, Avikanagar were utilized for the present study. The GMM animals have 75% Malpura and 25% Garole inheritance. The overall least-squares means for birth weight, 3-month weight, 6-month weight and 12-month weight of GMM X Patanwadi was 3.58±0.05, 16.86±0.34, 24.79±0.55 and 30.99±0.77 kg, respectively. Corresponding weights in the reciprocal crosses i.e. Patanwadi X GMM were 2.54±0.05, 12.98±0.31, 19.76±0.50 and 25.35±1.06 kg, respectively. The effects of sex of lamb, type of birth and regression of ewe's weight at lambing were significant, while effect of season of birth was non-significant for all the body weights in GMMX Patanwadi crosses. For reciprocal crosses, effect of year of birth was found significant for all the body weights and effect of type of birth and regression of ewe's weight at lambing were significant for birth, 3-month and 6-month body weight. The GMM X Patanwadi lambs have 40.94%, 29.89%, 25.45% and 32.72% higher body weights at birth, 3-month, 6-month and 12-month, respectively than reciprocal crosses. This may be attributed to heavier Patanwadi ewes and more incidences of multiple births in GMM ewes. The heterosis effect was positive for GMM X Patanwadi crosses and negative for the reciprocal crosses. The GMM X Patanwadi lambs have 21.86, 2.85, 8.46 and 3.20 % higher body weight compared to their parents average body weights at birth, 3-month, 6-month and 12-month of age respectively. In contrast, the Patanwadi X GMM lambs had 30.35, 33.40, 24.15 and 23.53 % lower body weight compared to their parents average body weights at birth, 3-month, 6-month and 12-month of age respectively. From the present findings, it may be concluded that the GMM X Patanwadi crosses have the potential for superior growth performance than its reciprocal crosses and can be developed as an efficient mutton production strain of sheep.

TS-IV-41

GENETIC AND NON-GENETIC INFLUENCES ON PRE-WEANING DAILY WEIGHT GAIN IN SIROHI KIDS UNDER FIELD CONDITION OF SOUTHERN RAJASTHAN

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Records belonging to 2898 Sirohi kids maintained under AICRP on goats in Nathdwara, Railmagra and Devegarh clusters of Rajasamand district, Bhadsoda cluster of Chittorgarh district and Vallabhnagar cluster of Udaipur district of Rajasthan, spreading over a period of seven years (2006-2012) were analyzed to identify genetic and non-genetic factors affecting pre-weaning average daily weight gain. The genetic effect of sire and non-genetic effects of cluster, year, season, type of kidding and sex of kid on pre-weaning average daily weight gain observed as significant ($P<0.01$). While parity of dam did not affect the pre-weaning average daily weight gain of kids. Kids at Bhadsoda location gained more weight than the other locations. Year of birth had shown gradual decrease in initial year but thereafter increased in average daily weight gain. Kids born in winter gained more body weight than the rainy and summer seasons. Kids born as single gained more daily weight than born as multiples. Male kids gained weight at a faster rate (128.96±4.57 gm/day) than females kids (119.20±4.57 gm/day).

TS-IV-42

POPULATION STRUCTURE AND PEDIGREE ANALYSIS IN BARBARI GOAT

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The Barbari is one of the most prolific, dual purpose goat breed which is being extensively used for commercial goat farming in different regions of India. Goats of this breed are maintained under AICRP on Goat Improvement since 1981 at CIRG, Makhdoom. These goats are kept in semi-intensive system of management. The objective of this study was to evaluate genetic diversity in the Barbari goat over 33 years. The data on 10450 individuals were used for pedigree analysis using ENDOG version 4.8. The pedigree of 10450 animals born between 1981 and 2014 were available, out of which 7923 were in the population reference for which estimates were obtained. For reference cohort, effective number of founders (fe) was 53, representing 8.98% of the potential number of founders in population reference. The effective number of ancestors (fa) was 43 and the genetic contribution of the 16 most influent ancestors explained 50% of the genetic variability. The effective population size of founders was 73.16. The ratio fe/fa which expresses the effect of population bottlenecks was 1.232. Pedigree completeness for the data spanning over 18 generations revealed 85.94% completeness for the data. The average inbreeding coefficient for the whole analysed pedigree and for inbred animals was 2.27% and 4.4%, respectively. The average relatedness coefficient between individuals of the population was estimated to be 4.09% and mean maximum generations estimated was 1.72. The inbreeding coefficient increased with the addition of each generation to the pedigree. In the population, 7.53% individuals had more than 6.25% Fi. The average genetic conservation index (GCI) for the complete population was 6.52. Present finding of the study revealed satisfactory level of genetic variability for further genetic improvement through selection in this flock of Barbari goat. Introduction of new sires with the lowest possible average relatedness coefficient and the use of appropriate mating strategies are recommended to keep inbreeding at acceptable level and to increase the genetic variability.

TS-IV-43

NON-SURGICAL EMBRYO TRANSFER IN NATIVE PIG: A SUCCESS STORY

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Increased interest in conservation and transfer of valuable genetic germplasm with reduced health risks has encouraged the development of non-surgical embryo transfer (nsET) technologies in pigs. Here we report successful birth of piglets 'Rani C-I' through nsET in pig, achieved for the first time in the country at ICAR-National Research Centre on Pig, Guwahati. Native Ghungroo gilts were selected as donor and recipient, and synchronized using exogenous gonadotropins. The animals were tested for standing reaction twice daily and donor animal was artificially inseminated using liquid semen twice at 8-12 hours after the onset of standing reaction and again after 8 hours following first insemination. On day seven following insemination, embryos were harvested. The *in-vivo* derived embryos were transferred to the synchronized recipient using a deep intra-uterine transfer catheter without sedation. The recipient Ghungroo gilt gave birth to 11 piglets on Feb 07, 2014. Out of 11 piglets born, seven have grown healthy in the Institute pig breeding farm, two were stillborn and two piglets died few days after birth. The encouraging result reveals that the use of this cost effective technology will be helpful for multiplication and propagation of endangered native pig germplasm as well as conservation of critically endangered species like pygmy hog (*Porcula salvania*) with the additional standardization for cryopreservation of embryos.

TS-IV-44

EFFECT OF GENETIC AND NON-GENETIC FACTORS ON LITTER SIZE AND LITTER WEIGHT AT BIRTH AMONG DIFFERENT CROSSBRED PIGS

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The success of swine farming is greatly dependent on litter size and litter weight of piglets, as they influence the survival and subsequent growth. Records of nine different genetic grades of pigs from the year 1994 to 2010 maintained at Livestock Farm, Birsa Agricultural University, Ranchi under All India Co-ordinated Research Project (AICRP) on Pigs were analysed. Least-squares analysis of variance was performed to study the effects of genetic and non-genetic factors on litter size of piglets. There were significant effect of different genetic groups and on litter size and litter weight. The highest litter size at birth was found in Tamworth X T&D (9.72±0.33), while the litter weight at birth in T&D was 8.87±0.19. Classification of swine population into two lines viz. High and Low responder to Sheep Red Cells (SRBCs) and identified association of different genetic groups with the reproductive traits can be useful for designing selection and breeding strategies for genetic improvement of swine population.

TS-IV-45

NATIVE CHICKEN RESOURCES FOR LIVELIHOOD SECURITY IN THIRUVALLUR DISTRICT – A CASE STUDY

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Native chicken rearing is an integral part of rural household. Native chicken keeping is a tool for sustainable livelihood and nutritional security in rural families. A study was conducted in Aayalur village in Thiruvallur district of Tamilnadu to document the management practices and performance of native chicken under back yard system. A total number of 30 households were selected randomly in the village who were actively involved in native chicken rearing for the past five years. The data on number of chicken owned, sex ratio, feeding, health cover, housing and incubation practices were collected with the questionnaire and personal observation. In this study, majority of the native chicken were reared by women folks (55%). All the chickens were of non-descript type. The mean brood size was 10.72±5.12 with a sex ratio of 1:15 to 20. The birds were provided with a *kutcha* type of enclosures in all the farms. The laying percentage and the hatchability percentage were 30.8 and 38.0 respectively. The farmers provided sand, husk over that the leaves of *nochi* were put for natural incubation of eggs. None of the farmers were aware of candling of eggs. The birds were sent freely in the morning to go around and in the evening they were supplemented with broken rice. The farmers were not aware of concentrate feed. None of the farmers vaccinated their birds. Raniket disease, theft, heat stroke, mongoose, bandicoots and stray dogs were the main constraints reported by the farmers for mortality of the birds. It was interesting to note that all the farmers reported that the eggs were kept for incubation and the surplus chicken were not sold, but utilized for consumption by the family members. With the supply of recognized native chicken germplasm and proper training of farmers in scientific management practices will make way for sustainable development of native chicken keeping in rural areas.

TS-IV-46

CONTRIBUTION OF WOMEN IN ADOPTION OF RECOMMENDED DISEASE MANAGEMENT PRACTICES IN BACKYARD POULTRY

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Backyard poultry is a part and parcel of human culture in our country since ages. Though *desi* birds are disease resistant, it is essential to adopt the recommended disease management practices to keep the birds healthy. Keeping this in mind, the study was conceptualized with an objective to study the knowledge and adoption level of recommended disease management practices and contribution of women in keeping backyard poultry healthy. The study was conducted at Palakkarai, Chinna Veerasangili and Periya Veerasangili villages of Perundurai block in Erode district, Tamilnadu considering its highest backyard poultry population. A total of 120 respondents were selected by applying proportionate random sampling technique comprising 73, 37 and 10 backyard poultry farmers from these three villages respectively. Data were collected individually through a structured and pre-tested interview schedule from respondents. The results of data analysis revealed that 94.17 per cent of the respondents possessed very high knowledge level on disease management practices in backyard poultry. Further, it showed that cent per cent of the respondents were cleaned the floor regularly, an overwhelming majority (96.67 per cent) isolated the sick birds away from the healthy birds and disposed the dead bird properly, over four-fifth (82.50

per cent) consulted nearby veterinarian and vaccinated their birds, nearly two-third (63.33 per cent) delouced their birds and contrastingly, a meagre (6.67 per cent) dewormed their birds and applied disinfectant on the floor. The contribution of women in disease management practices was 94.83 per cent in the backyard and 36.36 per cent in away-from home activities. This study can foster the policy makers to improve their prudent strategies with specific emphasis on contribution of women and intensify their strenuous efforts to make backyard poultry farmers to adopt all the recommended disease management practices.

TS-IV-47

GENETICS OF GROWTH AND PRODUCTION TRAITS IN RHODE ISLAND RED CHICKEN UNDER LONG-TERM SELECTION PROGRAMME

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Rhode Island Red (RIR) is a brown-egger dual-purpose chicken breed having likings of small poultry farmers in the backyard and rural system. Periodic evaluation of its performance is necessary for economic farming and developing multi-coloured strains for rural poultry production. This investigation was carried out on 325 single-hatched RIR chicks of a strain that has undergone 30 generation of selection based on 40-week part-period egg production. Data on growth traits, viz., body weight at 16 (BW16), 20 (BW20), 40 (BW40) and 64 (BW64) weeks of age and layer economic traits viz., age of sexual maturity (ASM), egg weight at 28 (EW28), 40 (EW40) and 64 (EW64) weeks, egg number up to 40 (EN40) and 64 (EN64) weeks of age, were analyzed using mixed model least-squares analysis of variance. Sex had significant ($P<0.001$) effect on all body weights; males were heavier than females. Overall least-squares means of BW16, BW20, BW40 and BW64 were 1362.62±21.42g, 1791.60±24.53g, 2184.58±26.19g and 2433.80±34.17g, respectively. Corresponding body weights in males were 1492.88±24.01g, 2040.28±28.08g, 2624.41±31.33g and 2784.51±41.28g, and in females 1232.35±25.49g, 1542.91±30.16g, 1744.75±33.66g and 2083.10±42.91g. Least-squares means of ASM, EW28, EW40, EW64, EN40 and EN64 were 134.52±0.86days, 44.81±0.34g, 47.73±0.38g, 51.47±0.71g, 118.27±1.21 and 214.53±4.82, respectively. Heritability estimates for growth traits were 0.55±0.22 (BW16), 0.42±0.19 (BW20), 0.29±0.18 (BW40) and 0.36±0.21 (BW64), respectively and for economic traits were 0.007±0.30 (ASM) 0.17±0.30 (EW28), 0.09±0.32 (EW40), 0.52±0.45 (EW64), 0.02±0.28 (EN40) and 0.86±0.43 (EN64). The correlations among body weights were high and positive. Varied genetic and phenotypic correlations of ASM with body weights, egg weights and egg production were estimated which may be due to smaller sample size. Overall growth and egg production performance of RIR chicken was found to be excellent which suggested the usefulness of RIR for development of multi-coloured rural poultry.

TS-IV-48

FERTILITY, HATCHABILITY AND EARLY MORTALITY IN RHODE ISLAND RED CHICKEN UNDER LONG -TERM SELECTION

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Rhode Island Red (RIR) is a brown-egger dual purpose chicken breed, which is well adapted to local environment and being considered useful in development of multi-colored poultry for rural and backyard poultry production system. RIR at this institute is being maintained as selected strain undergoing long-term selection for

40-weeks part-period egg production. Reproductive parameters like fertility and hatchability are most important parameters for evaluation of reproductive performance of any chicken breed towards its regeneration and propagation. Present investigation was carried out to evaluate the reproductive performance of selected strain of Rhode Island Red (RIRs) that has undergone long-term selection based on 40-week part-period egg production using family index. A total of 462 eggs of RIRs strains were set in four hatches under standard incubation and hatching conditions and a total of 286 chicks were obtained. The per cent fertility and hatchability were estimated as per the standard procedure. Per cent fertility ranged from 71.28 to 84.55; overall per cent fertility being 76.98%. The per cent hatchability estimates on total egg set (TES) ranged from 55.96 to 65.85% and on fertile eggs transferred (FET) basis ranged from 76.25 to 83.28, overall being 61.44% and 79.85%, respectively. Chicks were maintained under standard management conditions and institute's vaccination schedule was followed. The overall per cent mortality was 5.24% during 0 to 6 weeks of age. The overall estimates were in consonance with the earlier reports and thus suggestive of usefulness of RIR selected strain in development of backyard poultry.

TS-IV-49

DEVELOPING A MULTI COLOUR SYNTHETIC BROILER CHICKEN (NANDANAM B_3) SUITABLE TO RURAL BACKYARD POULTRY FARMERS OF TAMILNADU

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A synthetic multi-coloured broiler strain was developed for rural backyard poultry farmers by Poultry Research Station, TANUVAS with good meat quality characteristics. The base population (Nandanam B_2) with body weight of 859±80g (male) and 728±70g (female) was utilized for this purpose. A cross was made between Vencobb (as male line) and Nandanam B_2 (as female line) by artificial insemination. Thirty breeding pens were formed with sex ratio of 1:6. With the replacement stock of 2000 day-old straight run chicks (Approximately 70 chicks from a family in five hatches) in each generation individual selection was practiced based on 8th week body weight as selection criteria with selection pressure of 1 in 6 for females and 1 in 33 for males. On completion of fifth generation, the hatch weight was 42.09 ±0.15 g and attained eight week body weight with over all mean (μ) of 1144.83±17.35 kg with feed efficiency of 2.66 and livability of 91.23 per cent. The average dressing yield was 70.44±1.35 in males and 70.13±1.01 in females with pooled average of 70.28±0.77. The cut-up parts yield viz., the breast, back, thigh, drumstick and wing weight was 16.56 ±4.78, 14.25±0.49, 10.39±0.99, 6.77±1.06, 8.25 ±0.82. The meat has primed in all sensory attributes especially taste relished by all consumers.

TS-IV-50

INDIA'S MISSING BREEDS: DO WE HAVE AN AnGR INFORMATION MANAGEMENT SYSTEM?

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Officially, India has anywhere from 141 breeds (NBAGR) to 298 breeds (FAO) of livestock. Some of these breeds have been developed through modern scientific means but most breeds are the result of years of efforts by the countries diverse livestock rearing communities. Many of these communities are pastoral and nomadic and have selected, raised and bred these animals over several generations. As these communities are nomadic and mobile, some of them do not feature in any official records of the country such as birth and death registers, voter identification cards, census etc. As a result, their animals also do not feature in the 5 year quinquennial livestock census and there is considerable missing information on livestock type, numbers, breeds kept by these mobile

communities. Other data regarding current status of breeds, varieties within breeds, breed production parameters *etc.* is also not available. The objective of this was study was to ensure how breeds kept by pastoral communities could be recognized and to look for missing information. Field work was undertaken in Maharashtra amongst the Dhangarsa shepherding community who rear the Deccani sheep and the Maldharis, a cattle and buffalo raising community who raise Gir cattle and who have migrated into Maharashtra. Data on the public domain about breeds was also collected. The results of the analysis show that these communities live on the fringes of society and there is little or no record of their existence or that of the animals they rear. An effective MIS system on Animal Genetic resources will have to look, build in suitable ways of recognizing mobile communities and the animals they rear.

TS-IV-51

YAK BREEDING IN THE HIMALAYAN REGION OF UTTARAKHAND

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The yak is a long-haired bovid found throughout the Himalayan region of South Central Asia, the Tibetan Plateau and as far North as Mongolia and Russia. Most yaks are domesticated Bos grunniens. There is also a small, vulnerable population of wild yaks, Bos mutus. In the 1990s, a concerted effort was undertaken to help save the wild yak population. Yak physiology is well adapted to high altitudes, having larger lungs and heart than cattle found at lower altitudes, as well as greater capacity for transporting oxygen through their blood due to the persistence of foetal haemoglobin throughout life. Conversely, yaks do not thrive at lower altitudes, and begin to suffer from heat exhaustion above about 15°C (59°F). Further adaptations to the cold include a thick layer of subcutaneous fat, and an almost complete lack of functional sweat glands. Yaks mate in the summer, typically between July and September, depending on the local environment. Females enter oestrus up to four times a year, and females are receptive only for a few hours in each cycle. Gestation lasts between 257 and 270 days, so that the young are born between May and June, and results in the birth of a single calf. At present Himal Prakriti, along with a group of herders in Paton maintains a breeding herd of Yaks in the Ralam Valley (3715 mts) East in the Kumaon region of Uttarakhand. This is the only known breeding population of Yaks in the entire state of Uttarakhand. The purebred herd of Yaks is maintained mainly for producing male yak calves who are then farmed out to high altitude villages. These male yak calves are bred along with cows to become “Stud Yak” bulls which then go on to mate with their cows. The resultant F1 generation offspring has many characteristics that are valuable to alpine dwelling trans-humant communities. The male F1 called Zho or Jibu is sterile and is a very strong, gentle and an easily maintained draught animal. Yak hybrids are more tolerant to heat and make better work animals. Further the milk from the female F1 generation Zhomo is said to be of better quality than normal cow milk. Zhomos are fertile and can be back-crossed with either yaks or bulls. However, repeated back-crossing results in a progressive loss of the desirable characteristics.

TS-IV-52

IMPACT OF SELECTION ON DRAUGHTABILITY OF INDIAN CAMEL BREEDS

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Camel is well known for the draughtability in desert areas of the world for centuries because it can thrive well on meagre resources under extremes of climatic conditions. The draught potential of the camels is difficult to measure. However, the studies have shown that draught potential of a camel is positively correlated with the body length, heart girth and height at wither. Therefore, for the improvement of draughtability of Indian camel breed, indirect selection utilizing body parameters was practised. The male camels were selected for breeding using selection differential method for body length and independent culling level for heart girth and height at wither for a period of 8 years. The overall least-squares means of heart girth, height at withers and body length were estimated to be 208.99 ± 1.28, 198.76 ± 0.58 and 158.79 ± 0.78 cm, respectively. The heritability of body length, heart girth and height atwithers was estimated to be 0.172±0.209, 0.284±0.224 and 0.213±0.215, respectively. In order to assess the impact of selection on body parameters the genetic, phenotypic and environmental trends were estimated. The phenotypic and environmental trends for the body length, heart girth and height at wither were largely positiveand the genetic trends were fluctuating. This was expected because of lowerheritability estimates ofthe traits under study. Overall the selection resulted in gain in phenotype for the selected traits and hence the draught potential of the camels.

TS-IV-53

MATHEMATICAL FUNCTIONS FOR THE PREDICTION OF BODY WEIGHT OF CAMEL FOR MEDICATION

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The knowledge of body weight helps veterinarians in deciding the doses of medication during treatment. At times, the owner doesn't have much idea of the weight of his animal, as well weighing of large animals like camel, may not be feasible. However, the age of a camel can easily be estimated by dentition and we decided to use this information for the estimation of body weight in camels for appropriate use. Looking at the nature of growth in camels, the body weight was analysed for both sexes at three months interval from birth to 3 years of age and at one year interval from 3 to 20 years of age. Mathematical functions to explain the growth pattern in the camel right from birth to 20 years of age were derived. The linear, quadratic, cubic, exponential, inverse and logarithmic curves were initially fitted on body weight data taken at a uniform interval of one year. The R^2 values reflecting the closeness of fit obtained were 0.849, 0.923, 0.595, 0.975, 0.982 and 0.671, respectively in linear, logarithmic, inverse, quadratic, cubic and exponential functions. Looking at the R^2 values, the cubic equation $Y = 43.192 + 29.815x + 0.406x^2 - 0.028x^3$ (x is age in months) can reliably be utilized for the prediction of body weight of Indian dromedary. Further, separate equations for the two sexes were derived utilizing the full set of data.

TS-IV-54

A STUDY ON THE GROWTH PERFORMANCE OF NEW ZEALAND WHITE RABBITS

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Data on growth traits of 610 New Zealand White bunnies born out of 89 litters sired by 25 bucks mated to 46 does maintained at Rabbit Research Centre, College of Veterinary Science, Hyderabad were utilized for the present study. Mean litter size was 5.91 ± 1.73 at birth and 3.64 ± 1.72 at weaning. Litter size at birth had a significant influence on all the body weights studied with bunnies from smaller litters recording higher weights than those from larger litters. The overall means for body weight at birth, 1, 2, 3, 4, 6, 8, 10, 12, 14 and 16 weeks of age were49.39 ± 0.50, 108.60 ± 1.77, 149.18 ± 1.81, 189.57 ± 4.96, 397.27 ± 14.15, 546.00 ± 16.65, 733.91 ± 21.05, 951.37 ± 21.84, 1,168.79 ± 22.96, 1,361.20 ± 26.55 and 1,636.48 ± 40.39 g., respectively. Heritabilities for body weight at birth, 1, 8, 10, 12, 14 and 16 weeks were estimated to be 0.52 ± 0.22, 0.75 ± 0.24, 0.67 ± 0.23, 0.49 ± 0.22, 0.59 ± 0.23, 0.51 ± 0.22 and 0.61 ± 0.23, respectively;while the heritabilites for body weights at 3, 4, 5 and 6 weeks were outside the normal range. The phenotypic correlations among pre-weaning body weights ranged from 0.29 to 0.67 while that among post-weaning body weights ranged from 0.21 to 0.85. Substantial phenotypic association among body weights and medium heritability recorded by body weights hint at the possibility of improving the performance of New Zealand White rabbits.

TS-IV-55

FACTORS INFLUENCING LITTER TRAITS AT BIRTH OF BROILER RABBITS IN KERALA

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Broiler rabbit rearing is a supplementary income source especially among rural women and marginal farmers in Kerala. The broiler performance indicators like high prolificacy and fast growth rate of temperate rabbit breeds were observed to be adversely affected by warm and humid tropical climate of Kerala. The present study investigates the effects of breed and season of kindling on the litter size and litter weight at birth in four purebred temperate broiler rabbit breeds- Grey Giant, White Giant, New Zealand White and Soviet Chinchilla. Data on litter production traits of does involving 482 litters, raised from 41 sires, reared under uniform farm conditions were used in the analysis with an average of 11.76 ± 1.13litters/ sire. Linear mixed model analysis with sire as random effect was conducted to evaluate the effects of breed and season of kindling on litter size and litter weight at birth. As the litter weight is greatly dependent on the litter size, it was considered as a co-variable in case of litter weight. The effects of breed and season of kindling was observed to be non-significant only for litter size at birth. However, significant ($p<0.05$) effect of season of kindling and highly significant ($p<0.01$) effect of breed were observed on litter weight at birth. The litter size was also influencing the litter weight as expected. Paired comparisonsof litter weights during different seasons using Bonferroni test revealed that a significant difference ($p< 0.05$) between summer season (March- June; 231.07 ± 2.98g) and rainy season (July- October; 217.75 ± 4.11g). Similar comparison among the four breeds revealed a highly significant ($p<0.01$) difference between White Giant (216.40 ± 4.21g) and New Zealand White (236.05 ± 4.11g) rabbits. The results of this study point out to the suitability of New Zealand White as the broiler rabbit breed of choice for Kerala state.

TS-IV-56

LIVESTOCK AND POULTRY- FUTURISTIC ENERGY ALTERNATIVE FOR RURAL INDIA

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India is the 4th largest electric power producer in the world but with dismally low per capita energy availability i.e., 883 kWh as compared to world's average of 2892 kWh and for many of developed countries the figure is as high as 10,000 -15,000 kWh. Future energy requirements and available energy sources should be matched to meet the power demands. Bioenergy is a viable alternative and seems promising enough to attain sustainable source of energy without adversely affecting the environment. Bioenergy can help government to minimize both the

import of fuel derivatives and curtail solid waste processing cost. A biogas plant was installed to generate clean environment and develop mechanism (CDM) through the uses of renewable energy from dung and droppings. The biogas plant comprising of two 90 cu m PAU modified fixed domes type has been constructed at the Dairy Research Farm, GADVASU, Ludhiana. Each dome has a diameter of 20', depth 24.5', and wall thickness of 9 inches. This biogas plant has a capacity of 4500 kg (daily) of cow dung and poultry droppings. This plant produces 240 kWh of energy per day, and with this much energy a 40 kVA biogas operated Genset is being run for 6 hours daily to produce electricity. The electricity so produced from this Genset is used for carrying out farm activities like chaffing of green fodder, machine milking of animals and to operate fans, coolers and foggers installed in the animal sheds. The estimated cost of power generated is about Rs.1200-1500/day. The slurry obtained from biogas plant which is nearly odorless and is used as manure in the agricultural fields and has proved to be more potent fertilizer than conventional farm yard manure. The nitrogen, phosphorous and potash content of the slurry was found to be significantly higher than farm yard manure and yielded 50-75% organic humus. A tractor operated vacuum tank is being used very efficiently for direct spray of slurry into the fields. Furthermore, the biogas is a valuable fuel that is already being used in a variety of applications such as cooking and home heating. It can also be converted into compressed natural gas (CNG) after a scrubbing process that removes carbon dioxide and hydrogen sulfide. The installation of biogas plant is an important step towards meeting zero energy input dairy farming and paved a way for its use in far flung rural areas having deficient power supply.

TECHNICAL SESSION – V

Abstracts for Young Scientist Award

ABSTRACTS

TS-V-01

GENETIC PARAMETERS FOR MILK PRODUCTION OF SAHIWAL CATTLE USING RANDOM REGRESSION TEST DAY MODEL WITH A HOMOGENEOUS RESIDUAL VARIANCE

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Studies investigating the use of random regression models for genetic evaluation of milk production in Indian cattle are scarce. A total of 5890 first lactation monthly test day records of Sahiwal cows calved between years 1961-2012 at ICAR- National Dairy Research Institute, Karnal were taken in the present study. The monthly test day milk yield data was modelled using a random regression model (RRM). Different combinations of Legendre polynomial order were fitted for the additive genetic effect and the permanent environmental effect to find suitable random regression model. Among the RRM fitted for the model with third order fit for additive genetic effect and sixth order fit for permanent environmental effect had lowest BIC value as well as residual variance and thus selected as best model. First two eigenvalues of additive genetic random regression coefficient matrix explained more than 99% of the additive genetic variation whereas four eigenvalues were needed to explain about 98% of the permanent environment variations. The heritability estimate was low and it ranged from 0.01 to 0.10. The values of genetic correlation ranged from -0.17 to 0.99. The value of permanent environment correlation ranged from 0.29 to 0.99. The genetic correlations between two adjacent test days were high (≥ 0.88). The main egienfunction corresponding to largest egienvalue did not show any large change during lactation suggesting selection based on this would lead to uniform selection for all part of lactation.

TS-V-02

MOLECULAR CHARACTERIZATION OF MURRAH BUFFALOES USING MICROSATELLITE MARKERS

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A total of 30 microsatellite markers selected from the list suggested by FAO were used to characterise Murrah buffaloes. All the 30 microsatellites were successfully amplified by polymerase chain reaction and observed number of alleles ranged from 4 (CSSM032 and ILSTS005) to 12 (CSSM033 and ILSTS028) with a total of 239 alleles across the 30 loci. The overall mean observed heterozygosity, expected heterozygosity and unbiased expected heterozygosity values were 0.439, 0.826 and 0.841 and ranged from 0.000 to 0.967; 0.709 to 0.899; and 0.754 to 0.915, respectively. The overall mean PIC was 0.803. All the 30 primers used in the present study were found to be polymorphic and highly informative with the PIC values ranging from 0.656 to 0.879. The overall mean inbreeding coefficient and the outcrossing rate obtained in the present study were 0.483 and 0.464, respectively. Out of 30 microsatellite markers studied, 29 markers showed significant deviation from Hardy - Weinberg equilibrium which might be because of heterozygote deficiency. The sufficiently high mean values of observed number of alleles, observed heterozygosity and PIC for various microsatellites in the present study supported their suitability for genetic diversity studies. Results of the present study have contributed to the knowledge of genetic information on Murrah buffaloes.

TS-V-03

GENETIC VARIABILITY IN NATIVE DOG BREEDS OF TAMILNADU THROUGH MICROSATELLITE ANALYSIS

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Microsatellite analysis of four indigenous dog breeds of Tamilnadu namely Rajapalayam, Chippiparai, Kanni and Kombai was carried out at 29 loci using 175 samples to assess the genetic variability and relatedness among them. In this study, a total of 297 alleles were observed with an overall mean number of alleles as 10.24 ± 0.61 per locus. The number of alleles in the markers differed substantially (5 in AHTk211 to 19 in LEI2D2) indicating that these microsatellite loci showed high variability in the native dog breeds of Tamilnadu. These microsatellite alleles were of size ranging from 80 (AHT121) to 484bp (FH2148). The overall PIC value observed in the present study ranged from 0.6337 (INU030) to 0.8914 (LEI2D2) with a mean value of 0.7704 ± 0.01.The average observed and expected heterozygosities pooled over different markers in the four dog breeds were 0.7334 ± 0.02 and 0.7997 ± 0.01 respectively, indicating the presence of high amount of genetic variation in all the four dog populations. The overall F_{IS}, F_{IT} and F_{ST} values observed in this study were 0.0319, 0.0785 and 0.0481 respectively for all the four dog populations. An analysis of Nei's genetic distance, phylogenetic tree, principal component analysis and multidimensional scaling pinpointed the uniqueness of Rajapalayam and Kombai dogs as well as the closeness of Chippiparai and Kanni dogs. Structure analysis revealed that Chippiparai and Kanni dogs had more admixtures between them; while Rajapalayam and Kombai were more distinct with lesser amount of breed admixture.

TS-V-04

MICROSTELLITE GENOTYPES INFLUENCE RELATIVE EXPRESSION LEVEL OF TOLL LIKE RECEPTOR-4 GENE IN BURSA OF RHODE ISLAND RED CHICKEN

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Genes for toll-like receptors (TLRs) play a central role in innate immunity in poultry. TLR4 gene is mapped to micro-chromosome E41W17 linkage group out of 50 linkage groups in consensus linkage map of chicken genome. TLR4 is linked to resistance to infection to *Salmonella enteric* serovar Typhimurium in chickens. Four microsatellite loci, ADL0149, HUJ0002, ADL0293 and MCW0330 are mapped around TLR4 gene. This investigation was carried out to assess the effect of polymorphism at these closely mapped microsatellite loci on relative mRNA expression of TLR4 in bursa tissue of Rhode Island Red (RIR) chicken. Twelve birds were genotyped for four microsatellites after resolving PCR products on 3.4% metaphor agarose. Relative mRNA quantification of TLR4 gene in bursa of the same birds was performed by qRT-PCR using DyNAmoColorFlash SYBR Green qPCR Kit® and CFX 96®- Real Time PCR detection system. Mean ΔC_t values were calculated by subtracting C_t of reference gene (β-actin) from C_t of target gene and then $40\text{-}\Delta C_t$was determined. Influence of genotypes at each of four microsatellite loci on mRNA expression of TLR4 was analysed by least-squares analysis of variance of $40\text{-}\Delta C_t$ data using SAS, 2010, which revealed significant ($p \leq 0.12$) effect of genotype at MCW0330 locus. Mean $40\text{-}\Delta C_t$ values for DD (35.411±2.066) and CC (34.580±3.866) genotypes were significantly higher than other genotypes viz., AA (25.120±5.468), AC (22.950±5.468) and BD (21.840±5.468), indicating that microsatellite MCW0330 could be a marker for TLR4 gene expression. Thus, MCW0330 genotyping can be effectively used to predict TLR4 gene expression and play important role in genetic resistance to Salmotnellosis in poultry.

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SOCDAB EVENTS- AT A GLANCE

S No.	Event	Theme	Date & Year	Host Institute	Organizing Secretary
1	1st National Symposium	Livestock Biodiversity vis-a-vis Resources Exploitation: An Introspection	Feb 11-12, 2004	NBAGR, Karnal	Dr. R.K.Pundir
2	2nd National Symposium	Domestic Animal Diversity: Status, Opportunities and Challenges	Feb 10-11, 2005	NBAGR, Karnal	Dr. B.Prakash
3	Workshop	Crossbreeding at the Cross-roads	Oct 22, 2005	Veterinary College, Banglore	Dr. M.G.Govindaiah
4	3rd National Symposium	Conservation and Improvement of Animal Genetic Resources Under Low Input System: Challenges and Strategies	Feb 9-10, 2006	NBAGR, Karnal	Dr. P.K.Singh
5	4th National Symposium	Role of Animal Genetic Resources in Rural Livelihood Security	Feb 8-9, 2007	Birsa Agricultural University, Ranchi	Dr. D.K.Singh 'Dron'
6	5th National Symposium	Redefining Role of Indigenous Animal Genetic Resources in Rural Development	Feb 15-16, 2008	Veterinary College, Banglore	Dr. M.R.Jayashankar
7	6th National Symposium	Livestock Biodiversity Conservation and Utilization: Lessons from Past and Future Perspective	Feb 12-13, 2009	NBAGR, Karnal	Dr. D.K.Sadana
8	7th National Symposium	Challenges to Domestic Animal Biodiversity and Action Plan for its Management and Utilization	Feb 10-11, 2010	Anand Agricultural University, Anand	Dr. D.N.Rank
9	8th National Symposium	Animal Genetic Resources for Sustainable Livestock Sector in India	Feb 18-19, 2011	Orissa Livestock Resources Development Society (OLRDS), Bhubaneswar	Dr. Sanat Mishra
10	9th National Symposium	Role of Indigenous Animal Genetic Resources in Rural Food Security vis-a-vis Climate Change	Feb 24-25, 2012	BAIF Development Research Foundation, Pune	Dr. A.B.Pande
11	10th National Symposium	Integrated Development of Vast biodiversity of Indigenous Livestock for Long Term Rural Livelihood Security	Feb 7-8, 2013	GBPUAT, Pantnagar	Dr. C.V.Singh
12	National Seminar	Technological and Policy Interventions for Sustainable Cattle Breeding in India	March 14, 2013	PDC, Meerut	Dr. Umesh Singh
13	11th National Symposium	Harmonizing Phenomics & Genomics for sustainable management of livestock vis-a-vis upliftment of rural masses	Feb. 6-7, 2014	NBAGR, Karnal	Dr. N.K.Verma


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