National Symposium on
Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income
&
XV Annual Convention of
Society for Conservation of Domestic Animal Biodiversity (SOCDAB)

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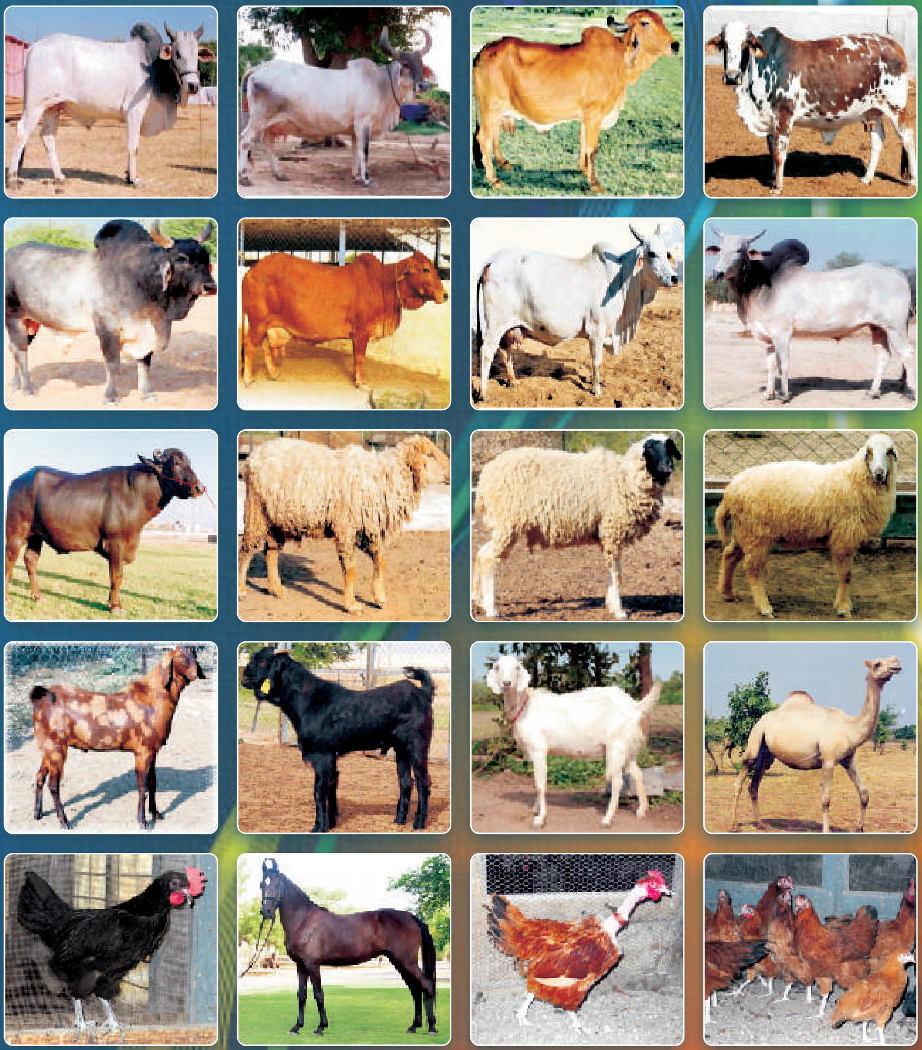

at
College of Veterinary & Animal Science
Rajasthan University of Veterinary & Animal Sciences, Bikaner (Rajasthan)

Organised by
Rajasthan University of Veterinary & Animal Sciences
BIKANER (Rajasthan)-334001 India
&
Society for Conservation of Domestic
Animal Biodiversity (SOCDAB) NBAGR, Karnal

National Symposium on Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income
& XV Annual Convention of Society for Conservation of Domestic Animal Biodiversity (SOCDAB)


M J F College of Veterinary & Animal Sciences


पशु चिकित्सालय


EMERGENCY
HOSPITAL

। पशुधनं नित्यं सर्वलोकोपकारकम् ।

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Published by
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सत्यमेव जयते

कल्याण सिंह
राज्यपाल, राजस्थान
राजभवन
जयपुर 302006

संदेश

मुझे यह जानकार प्रसन्नता हुई है कि राजस्थान पशु चिकित्सा और पशु विज्ञान विश्वविद्यालय, बीकानेर द्वारा दिनांक 8 से 10 फरवरी, 2018 को 'सस्टेनेबल मैनेजमेंट ऑफ लाइवस्टॉक एण्ड पोल्ट्री डाइवरसिटी फॉर एनहैनसिंग द फार्मर्स इनकम' विषय पर राष्ट्रीय संगोष्ठी का आयोजन किया जा रहा है।

संगोष्ठी की सफलता के लिए शुभकामनाएँ।

(कल्याण सिंह)

सत्यमेव जयते

VASUNDHARA RAJE
Chief Minister Rajasthan

Message

I am glad to know that Rajasthan University of Veterinary and Animal Science (RAJUVAS), Bikaner is organizing a national Symposium on 'Sustainable Management of Livestock and Poulty Diversity for enhancing the farmer's income' on February 8-10, 2018 at Bikaner.

Livestock sector holds great economic significance in the state as it plays important role in increasing household incomes in rural areas. I am sure that this symposium shall come up with important recommendations and suggest ways to make livestock rearing more remunerative.

I wish the event all the best.

Vasundhara Raje.

(Vasundhara Raje)

प्रभुलाल सैनी
मंत्री
राजस्थान सरकार
कृषि (कृषि विपणन सहित)
उद्यानिकी, पशुपालन एवं मत्स्य विभाग
6322, मंत्रालय भवन, शासन सचिवालय
जयपुर 302005 (राजस्थान)

Message

I am happy to learn that RAJUVAS, Bikaner and SOCDAB, Karnal are jointly orgainising a Three day National symposium on ''Sustainable Management of Livestock and Poultry Diversity for enhancing the farmers' Income'' at Collage of Veterinary & Animal Science, Bikaner from February 08-10, 2018 and compendium is published on this occasion.

The theme chosen for the conference is of poor farmers' interest. Livestock and poultry sector play a vital role in improving the socio-economic conditions of rural masses. The productivity of Livestock beings depends on the management under which the livestock are reared. The farmers are the real custodian of the livestock. The interaction of farmers with the scientific community can improve the management of livestock for sustainable production. Farmers' knowledge has an important role to play in bringing about sustainable innovations in livestock productivity.

I Congratulate the Organisers for providing a platform for this interaction through this Conference. I have no doubt that the suggestions made by the speakers to increase livestock farmers' income will be well taken and implemented by the concerned authorities. I wish the conference a great success.

(Dr. Prabhu Lal Saini)

। पशुधनं नित्यं सर्वलोकोपकारकम् ।

Prof. Dr. B.R. Chhipa
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Message

It is a matter of great pleasure that RAJASTHAN UNIVERSITY OF VETERINARY & ANIMAL SCIENCES (RAJUVAS), is organizing a national Symposium on 'Sustainable Management of Livestock and Poulty Diversity for enhancing the farmers' income' at College of Veterinary & Animal Science, Bikaner, from February 08-10, 2018 in collaboration with the Society for Conservation of Domestic Animal Biodiversity (SOCDAB), NBAGR, Karnal.

RAJUVAS is premier institute established on 18th May, 2010, has been playing a crucial role in the development of livestock sector as an instrument of rural development through its multifarious activities. The nine Livestock Research Stations of University are acting as centers for development of Indigenous breeds and a dependable source for supply of breeding stock of high genetic to the farmers' and Gaushalas in their breeding tracts. RAJUVAS is promoting the conservation and development of six indigenous cattle breeds such as Rathi, Tharparkar, Kankrej, Sahiwal, Gir and Malvi, two goat breeds Marwari and Sirohi, two sheep breeds Marwari and Magra, and developed the RAJUVAS strain of the poultry.

I feel that the participation and deliberation of leading Scientists, NGOs and stake holders will help to formulation of scientific approach for sustainable management of livestock production and safeguard the use of livestock to double the farmers' income in The Hon'ble Prime Minister's mission by the year 2022.

Best wishes to the Organizing Committee of Successful Event.

(Prof. B.R. Chhipa)
Vice-Chancellor

Message

India is mega centre for domestic animal biodiversity, which is reflected in terms of number of mammalian and avian species and breeds/lines within each species. In a country like India where livestock and poultry genetic resources are the lifeline of agriculture based economy, the value of output from livestock sector was Rs. 8,12,352 crores in 2015-16. So far, India has registered 169 livestock and poultry breeds developed in different agro-climatic zones of India. These indigenous breeds possess unique qualities of disease resistance, heat tolerance and ability to survive and produce under low input production system. Therefore, the effective management of domestic animal diversity requires not only the conservation of domestic animal diversity but also continuous enhancement of their productivity so as to keep them sustainable under present Indian livestock production system. Keeping in view the role of livestock in rural livelihood security and livestock keeper's income, it is imperative to discuss and formulate adequate strategies for better management of huge population of livestock and poultry of India.

Society for Conservation of Domestic Animal Biodiversity was established in 1998 and has been continuously making efforts for better management of domestic animal diversity. The strength of life members of the society has gone to 1074, which indicates that the SOCDAB is one of the most vibrant Society in the field of livestock and poultry development in India. It has already organized one International Symposium, 13 National Symposia, one National Seminar and one workshop to discuss various issues relating to the management of animal genetic resources. It is indeed matter of great satisfaction that SOCDAB is organizing it 15th National Symposium on a very relevant theme "*Sustainable Management of Livestock and Poultry Diversity for enhancing the farmers' income*" in collaboration with RAJUVAS, Bikaner during 8-10th Feb 2018. Enhancing the income of farmers is a need of hour and livestock can play a significant role in it.

The society always promotes quality presentation especially by the young professionals. I am confident that this symposium will provide a strong platform for deliberations among various stakeholders including policy planners, researchers, NGOs, gross root level technocrats, livestock keepers from different organizations, which will help them in formulating adequate programmes and policies for developing livestock sector in totality so as to increase the income of livestock keepers and farmers. The realistic recommendations during the symposium will certainly help the stakeholders in development and conservation of animal genetic resources of India. I am grateful to all the guests and delegates of the symposium for sparing their valuable time in the interest of our livestock and poultry.

As a President of the Society, I cordially welcome all the delegates and guests attending symposium and extend my best wishes for the grand success of the symposium.

16/III/17

[Arjava Sharma]

। पशुधनं नित्यं सर्वलोकोपकारकम् ।

Dr. G. C. Gahlot
Organizing Secretary
SOCDAB
National Symposium 2018
RAJUVAS, Bikaner, India
M: 9414426554

From the Desk of Organiser

It gives me enormous delight to welcome all the eminent speakers and delegates to the National Symposium on “Sustainable Management of Livestock and Poultry Diversity for enhancing the farmers' Income” being held at College of Veterinary & Animal Science, Bikaner from February 08-10, 2018.

We feel it a proud opportunity for organizing this conference. The conference will cover scientific approach to sustainable management of livestock and poultry diversity for enhancement of the farmers' income. The program of symposium SOCDAB 2018 covers three days and includes streams of up to four technical sessions. One technical session is exclusively for the Scientist farmers' interaction. The program is further enriched by keynote presentations offered by world-renowned researchers in the field, and oral presentations that address topics as per the theme of symposium. These sessions are principally designed to enhance the development of the livestock production and enterprise within the country. These annual gatherings enable the building of a productive dialogue between Farmers' and member scientists. They also provide an invaluable opportunity for networking and fruitful contacts between them.

We look forward to an exciting week of insightful presentations, discussions, and sharing of technical ideas with colleagues from around the country. We thank you for attending the conference and hope that you will enjoy your visit to the Bikaner.

I wish to extend a warm welcome to fellow delegates from all over the country. I realize that you will fully dedicated to the sessions that will follow but I do hope you will also take time to enjoy fascinating Rajasthan with its culture, friendly people and multi-cultural cuisines.

The conference would not have been possible without the enthusiastic and hard work of a number of colleagues. This will not be possible without the help of them. I would like to extend my heartfelt gratitude to those who shared their time and efforts in helping us to finish the souvenir program. We are also grateful to all the authors who trusted the conference with their work. A conference of this size relies on the contributions of many volunteers, and we would like to acknowledge the efforts of all members and referees and their invaluable help in the review process.

Gahlot

(Dr. G. C. Gahlot)


सरस गोल्ड
हाई एनर्जी पशु आहार
सरस पशु आहार
(सामान्य)
सरस बाय-पास पशु आहार

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Lead Paper

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Technical Session-I

Management of Livestock and Poultry Diversity.

(Characterization, Evaluation, Inventrization, Conservation)

LP-01

TECHNOLOGICAL AND POLICY INTERVENTIONS IN MANAGEMENT OF ANIMAL GENETIC RESOURCES IN INDIA

Dr Arjava Sharma
National Bureau of Animal Genetic Resources, Karnal (Haryana)

Animal husbandry is an integral component of Indian agriculture supporting livelihood of more than two-thirds of the rural population. This sector also plays a significant role in supplementing family income and generating gainful employment in the rural sector, besides providing cheap nutritional food to millions of people. Livestock provides milk, egg and meat as nutritious food; draught power for agriculture; fibre; manure and domestic fuel; and hides and skin. In 2015-16, this sector contributed 155.5 million tonnes of milk, 82.93 billion eggs, 43.6 million kg wool, and 7.0 million tonnes of meat. 49% of total milk is contributed by buffaloes followed by 27%, 21% and 3% by exotic/crossbred cows, indigenous/non-descript cows and goats respectively. 86.8% of the production of egg is contributed by improved fowl and 11.96 % is from desi fowl, 0.96% from desi duck and 0.28% from improved duck. Nearly 46.5% of the production of meat is contributed by poultry while buffalo, goat, pig, sheep and cattle contributed 23%, 13%, 5.5%, 7% and 5% respectively. According to estimates of the Central Statistics Office (CSO), the value of output livestock sector at current prices was about Rs 5,91,691 crore during 2015-16 which is about 28.5% of the value of output from agricultural and allied sector. At constant prices the value of output from livestock is about 29% of the value of the output from total agriculture and allied sector. Livestock are the best insurance against the vagaries of nature like drought, famine and other natural calamities.

Current status of AnGR diversity in India

Population dynamics: According to the Livestock Census (2012), the country had 512 million livestock population comprising mainly of 191m cattle, 109m buffalo, 65m sheep, 135m goat and 10m pig; and 729 million poultry population. During the last two census periods (2007-12) cattle, sheep and goat population decreased @ 0.8, 1.8 and 0.8 per cent per annum, respectively, whereas buffalo and poultry increased @ 0.6 and 2.5 per cent per annum, respectively. The vast and varied population of animals that country possesses is indigenous while a very small to sizably high proportion is represented by crossbreds between exotic germplasm and native stock. There are very few animals belonging to exotic breeds in the country which are maintained mostly in organized farms.

Species	Livestock Population (millions)		Change (%)
	2007	2012	(2007-12)
Cattle	199.08	190.9	- 4.10
Buffalo	105.34	108.7	3.19
Sheep	71.56	65.07	- 9.07
Goat	140.54	135.17	- 3.82
Pig	11.13	10.29	-7.54

Donkey		0.44	0.319	- 27.17
Horse		0.61	0.625	2.12
Mule		0.14	0.196	43.07
Camel		0.52	0.40	- 22.63
Yak		0.08	0.77	- 7.64
Mithun		0.26	0.298	12.88
Poultry	**Chicken**	617.6	692.65	12.13
	Duck	27.6	23.54	-14.85

Diversity: India has traditionally been a mega biodiversity center and rearing of domesticated animals of different species viz. cattle, buffalo, sheep, goat, pig, camel, horse, donkey, yak and mithun by livestock keepers has been practiced since time immemorial. Presently, there are 169 registered breeds of livestock and poultry in India which includes 41 for cattle, 13 for buffalo, 28 for goat, 42 for sheep, 7 for horses and ponies, 9 for camel, 7 for pig, 1 for donkey, 1 for yak, 18 for chicken, 1 for duck and 1 for geese. in addition to many more not characterized and accredited so far.

Species		**Registered Breeds**
Cattle	Milch	Sahiwal, Gir, Rathi and Red Sindhi
	Draft	Amritmahal, Bachaur, Bargur, Dangi, Hallikar, Kangayam, Kenkatha, Kherigarh, Khillar, Malvi, Nagori, Nimari, Ponwar, Umblachery, Red Kandhari, Siri, Motu, Khariar, Binjharpuri, Ghumusari, Pullikulam, Kosali and Badri, Punganur
	Dual-purpose	Deoni, Gaolao, Hariana, Kankrej, Krishna Valley, Mewati, Ongole, Tharparkar, Gangatiri, Belahi, Malnad Gidda , Vechur and Lakhimi
Buffalo	Large sized	Murrah, Nili-Ravi and Jaffarabadi
	Medium sized	Mehsana, Marathwada, Nagpuri, Pandharpuri, Bhadawari, Surti, Banni, Chilika, Kalahandi and Toda
Goat	Milch	Beetal, Jamunapari, Jhakrana, Surti, Kutchi, Mehsana, Malabari
	Meat	Black Bengal, Ganjam, Konkan Kanyal, Berari and Teressa, Salem Black
	Dual purpose	Barbari, Sirohi, Attapady Black
	Milk/Meat	Gohilwadi, Zalawadi, Marwari, Osmanabadi, Sangamneri, Kannaidu, Kodi Adu and Pantja
	Milk/Meat/ Fibre	Gaddi, Chegu, Changthangi and Sumi-Ne
Sheep	Apparel wool	Nilgiri
	Carpet wool	Gaddi, Rampur-Bushair, Bhakarwal, Poonchi, Karnah, Gurej, Changthangi, Chokla, Magra,
	Meat & carpet wool	Nali, Marwari, Jaisalmeri, Malpura, Sonadi, Patanwadi, Muzaffarnagri, Jalauni, Deccani, Hassan, Coimbatore, Balangir, Bellary
	Meat	Nellore, Mecheri, Ramnad White, Kilakarsal,Vembur, Madras Red, Tiruchi Black, Kenguri, Chhottanagpuri, Shahbadi, Ganjam, Garole , Bonpala, Mandya, Katchaikatty Black, Chevaadu and Kendrapada
Camel		Bikaneri, Jaiselmeri, Malvi, Marwari, Kutchi, Jalori, Mewari, Mewati and Kharai
Horse/Ponies		Marwari, Kathiawari, Zanskari, Bhutia, Spiti, Manipuri, Kachchhi-Sindhi
Pig		Ghoongroo, Niang Megha, Agonda Goan, Tenyi Vo, Nicobari, Doom and Zovawk

Donkey	Spiti
Chicken	Ankleshwar, Aseel, Busra, Chittagong, Danki, Daothigir, Ghagus, Kadaknath, Kalasthi, Kashmir Favorolla, Miri, Nicobari, Punjab Brown, Harringhata Black,Tellichery, Mewari, Kaunayen and Hansli
Yak	Arunachali
Duck	Pati
Geese	Kashmir Anz

Our indigenous animal genetic resources are rich in variability and endowed with many desirable attributes like disease resistance, tolerance to hot and humid stresses, adaptability to different environment and production management systems and ability to utilize coarse roughages and crop residues e.g. Bhadawari buffaloes are known for high milk fat content, dahi from milk of Chilika buffaloes has longer shelf life at room temperature, ghee from Ganjam goat is believed to increase sperm count, meat of Kadaknath chicken is used to enhance stamina, Changthangi goat, Changthangi sheep and Chegu goat produce finest quality of fibre (pashmina), Black Bengal goat produce best quality leather; Kharai camel is adapted to mangrove ecosystem and dry land ecosystem, Chilika buffaloes feed on sea weeds, Teressa goat survives on saline water; Pandharpuri buffaloes are used as walking dairies for door-to-door supply of milk because of multiple let downs; etc. Indigenous goats (Balck Benagl) and sheep (Garole) breeds are being used world over for exploiting fecundity gene of these breeds. Also, milk from Indian zebu cattle and buffaloes contain only A2 allele of *beta*-casein protein which is considered to be safe for human consumption whereas most of *B. taurus* breeds have higher frequency of A1 allele of beta casein which has been implicated in certain diseases, namely type 1 diabetes mellitus (DM1), ischaemic heart disease (IHD), arteriosclerosis and neurological disorders, such as autism and schizophrenia.

In addition to the registered breeds, there are still many animal populations which have not been characterized and accredited so far. These 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.

Possible threats and measure to protect their diversity

Genetic diversity defines not only animal breeds’ production and functional traits, but also the ability to adapt to different environments, including food and water availability, climate, pests and diseases. Diverse animal genetic resources are a key to economic development. Many local livestock breeds continue to represent the lifeline of rural populations. The diversity of these resources makes possible human livelihoods in some of the most inhospitable areas where crop production cannot be exclusively depended upon. While they may not be able to compete with “improved breeds” in milk and meat yields, they fulfill a much wider range of functions and provide a larger range of products. Being able to thrive even with low fodder inputs, their maintenance is ecologically more sustainable, especially in marginal environments. Requiring lower levels of health care and management, they commonly entail a lower workload in comparison with exotic breeds. As is becoming increasingly clear, they often have scope for specialty products and can be essential to preserve habitats and cultures.

However, this diversity is being constantly threatened due to it’s under utilization by not realizing the true values of native AnGR and improper implementation of breeding policies.

The official breeding policy recognized crossbreeding of only non-descript cattle with exotic breeds as a tool for improving milk production. There was no intention to crossbreed pure indigenous breeds but the immediate gains lured the stake holders to go for crossbreeding on a larger scale involving recognized breeds also which resulted in genetic dilution and decline in population of well defined breeds. Social changes have also greatly influenced AnGR especially small ruminants because present generation is not keen to continue their ancestral occupation of rearing livestock in migratory system of grazing. As a result, a large number of farm animal breeds are getting endangered and declining in population at an alarming rate. At the local level, the loss of a breed means the loss of a livelihood strategy and loss of indigenous knowledge.

The priority of state animal husbandry departments is more on improving the productivity of only few economically important breeds rather than conservation and development of the AnGR which are in the process of genetic dilution and degradation. Programmes for identification, evaluation and selection of genetically superior breeding males of indigenous breeds are inadequate. Moreover, it is also difficult to implement the breeding programmes at farmers level, as breeding at farmers' herds or flocks is mostly uncontrolled which results in dilution of genetic purity of the breeds. There is no regular system of monitoring of the breeds at risk. Lack of farmers awareness about the long-term impact of conservation of biodiversity and no or negligible immediate financial benefit also make them less interested in conservation programme. Insufficient trained manpower and infrastructure also hinders the implementation of the programmes. Almost all the conservation programmes on AnGR are funded and implemented by government agencies and participation of farmers and private sector is negligible. Absence of breeders' organization barring few and lack of awareness, participation and motivation of the livestock keepers make the implementation of breed conservation programme more difficult and not sustainable. Squeezing grazing lands and lack of policies for animal grazing in forest areas and development of pastures are some other factors affecting indigenous AnGR.

Management of AnGR and welfare of their custodians i.e. livestock keeping communities, pastoral tribes and other stakeholders has overlapping domains involving plethora of departments and institutions across the ministries like ICAR, SAUs, SVUs, Central and State Departments of Animal Husbandry, Environment and Forests, NGOs, etc. Though the onus for achieving goals of the national programme on conservation, sustainable management and use of animal genetic resources therefore lies with many players, yet there is no mechanism in place for coordination and monitoring different programmes on conservation of native breeds.

Indigenous breeds are generally low producers but contribute in many other ways to the livelihood and social security of their keepers. There is a need to consider as many uses of AnGR as possible and relate these aggregated benefits to the resources used to know the actual utility of a breed. Moreover, many of these breeds have the potential and their production performance can be enhanced substantially by following intensive selection programmes. With the changes in consumer demand, and the enormous challenges posed by climate change and emerging diseases, we may need to rely back on the adaptability and potential of indigenous animal genetic resources to face an uncertain future.

The best way of conservation of the genetic resources is to sustainably utilize them in their ecological niches so that these are continuously evolved to produce while adapting in the changing environments. Long term breeding plans need to be implemented for continuous genetic improvement of indigenous breeds of farm animals. The important role of livestock keepers, pastoralists, and local communities in the use and development of livestock resources need to be recognized. It also emphasizes the need for the active involvement of indigenous communities and the role of local knowledge and institutions in conservation. Economic worth of the indigenous breeds should be enhanced through value addition by propagating environmentally important attributes of different animal breeds and useful pharmaceutical and nutritional properties of their animal products. Searching of such breed specific biomolecules will enhance the utilization and ensure the survival of these breeds. Developing branded animal products and creation of niche markets for such products would be of great significance. This will add value to indigenous animal genetic resources and will ultimately help in their conservation and utilization. Also this sector has great export potential in form of animal products and by-products. The outcome of such programme will also add to the income of farm animal keepers.

Documentation system

Documentation of animal genetic resources encompasses all activities associated with generating information on their identification, qualitative and quantitative description, geographic and demographic distribution, native habitats and production systems, etc. ICAR-NBAGR has taken up this activity through Network approach by involving species specific institutes, SAUs, Department of Animal Husbandry & Dairying both at the National and State level, NGOs, etc. and is continuously striving to document as many as resources as possible. Following activities/ steps have been taken up for inventorization of AnGR of India.

- Technical standards and protocols for characterization of breeds/populations both at phenotypic and genetic level like questionnaires and breed descriptors for collection of information by conducting surveys in the natural habitat of a breed, and a set of 25 highly polymorphic microsatellite markers for all species of livestock and poultry have been developed.
- Almost all the registered indigenous farm animal breeds have been characterized both phenotypically and genetically.
- Molecular genotyping for diversity analysis has been accomplished in different livestock and chicken breeds and *phylogeny* have been established.
- Breed descriptors have been developed for all the breeds and published in various issues of Indian Journal of Animal Sciences.
- Breed bulletins/ Monographs/ Leaflets have been prepared for most of the registered breeds.
- Country Report on AnGR of India has been prepared and included in FAO's State of the World on AnGR.
- Breed-wise census has been initiated by Department of Animal Husbandry, Dairying & Fisheries, Govt. of India.
- Registration of Livestock and Poultry Breeds has been initiated by ICAR-NBAGR in 2007 as a part of documentation system which would provide identity, recognition and protection to the valuable animal genetic resources.
- An 'Information System on Animal Genetic Resources of India (AGRI-IS)' has been developed. This contains characteristics of all registered breeds of livestock and poultry along with two photographs of each breed This is available through a link *'Animal Gentic Resources of India* (*AGRI-IS*)' on website of ICAR-NBAGR (http://www.nbagr.res.in)

Future road map

Activity	Implementing agencies
• *Characterization and inventorization of Farm AnGR*	
(i) Explore the non-descript populations of each livestock species to identify potential breeds/ populations.	DAHD&F, State A.H. Deptt., State Agricultural/ Veterinary Universities/ Institutes, ICAR, NGOs
(ii) Characterize (phenotypically and genetically) the identified populations and register the uniform and stable ones.	DAHD&F, State A.H. Deptt., State Agricultural/ Veterinary Universities/ Institutes, ICAR, NGOs
(iii) Estimate population trends, identification of breeds under threat and preparation of early-warning and response system.	DAHD&F, State A.H. Deptt., ICAR
• *Sustainable use and development of Farm AnGR*	
(i) Production of genetically superior germplasm for genetic improvement and conservation of indigenous breeds	DAHD&F, State A.H. Deptt., State Agricultural/ Veterinary Universities/ Institutes, ICAR, NGOs
(ii) Formation of breed societies for each breed.	DAHD&F, State A.H. Deptt., State Agricultural/ Veterinary Universities/ Institutes, ICAR, NGOs
(iii) Value addition of indigenous breeds for enhanced economic worth.	State Agricultural/ Veterinary Universities/ Institutes, ICAR
(iv) Developing branded animal products of indigenous livestock and creation of niche markets.	State Agricultural/ Veterinary Universities/ Institutes, ICAR, NGOs
(v) Document and validate ITKs related to management of AnGR.	State A.H. Deptt., State Agricultural/ Veterinary Universities/ Institutes, ICAR, NGOs
• *Conservation of farm AnGR*	
(i) Formulate and periodically review species-wise and breed-wise breeding policies by each state with participation of stakeholders.	DAHD&F, State A.H. Deptt.
(ii) Prioritize the breeds for conservation in accordance with early warning and response system.	DAHD&F, State A.H. Deptt.
(iii) Implement conservation programmes for breeds at risk.	DAHD&F, State A.H. Deptt., State Agricultural/ Veterinary Universities/ Institutes, ICAR, NGOs
(iv) Establish/strengthen the National/State Gene Bank as germplasm repository.	State A.H. Deptt., State Agricultural/ Veterinary Universities/ Institutes, ICAR
• *Policies*	
(i) Formulation and periodic review of National and State Livestock Policies.	DAHD&F, State A.H. Deptt.
(ii) A legal framework for registration of animal breeds and protection of Livestock Keepers' Rights.	DAHD&F
(iii) Policy for adequate grazing land to livestock in collaboration with Ministry of Forest and Ministry of Revenue. Establishment of fodder banks/storage system for supply during drought/natural calamities.	DAHD&F/ State A.H. Deptt., Concerned Ministries/Departments

LP-02

RISK STATUS AND CONSERVATION OF CATTLE GENETIC RESOURCES IN SOUTH INDIA

Dr K Anil Kumar
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Introduction

The indigenous cattle genetic resources in Kerala, Karnataka, Tamilnadu, AndhraPradesh and Telangana states accounts for 14.12% of total indigenous cattle resources of India. There are eleven recognized breeds in these South Indian states. Some the breeds like Hallikar, Amrithmahal and Ongole are available good numbers where as some others like Vechur and Punganur are having population size around 2000 only. It is hence clear that the relevance and importance of each breed is different and so also their population and strategies for conservation and multiplication are different. A critical analysis of the Animal Genetic Resources of South India is made. These different breeds or genotypes of cattle have their own special characters and role in the social and cultural aspects of their breeding tract.

Objectives of Conservation

The major objectives of conservation of the different breeds or genotypes are described under five different aspects namely economic, social and cultural, environmental and research. Apart from these an aspect common for all indigenous cattle is as an insurance against unknown situations like diseases and climatic changes. The combination of genes present in most of these indigenous animals may not be having too much significance in the current scenario. But it is likely that on a future emergency like emerging diseases or worse climatic situations or catastrophic events, these combinations can be the answer. They are evolved through natural or artificial selection of hundreds of years and loss of them will be permanent and irreplaceable

1. Vechur

The breed was on verge of extinction thirty years back. The efforts to conserve and multiply the breed were a challenging task for the scientists involved. The efforts to collect the pure specimens were started with combing the cattle populations of its breeding tract. The characters of the breed described by old timers and those available in older books were used to identify the true Vechur animals. The initial effort yielded 12 cows and two bulls. The herd was kept as closed and planned breeding operations were started. Some of the animals bought were pregnant at the time of purchase the male calves born from their calving was also included in the herd, Breeding strategy was so planned to avoid excessive inbreeding. After twenty years of efforts the current population of Vechur and graded Vechur is around 2000. As it a conservation project the improvement aspect was not included. Selection was also limited as the population size was critically small

a) **Economic -** Vechur cattle is adjudged as the most precious livestock of the state of Kerala. The market demand for the same is increasing day by day. The price of milk and ghee of Vechur cows are also in high demand.

b) **Social and cultural -** The breed was part of older documents of erstwhile princely state of Travancore. Apart from that there is no other cultural and social role attributed to Vechur cattle, though it was considered as the best dairy animal of the state in earlier days.

c) **Environmental -** The fragmented land holding of state of Kerala make it difficult for an interested person to keep a crossbred animal as a house cow. The miniature Vechur is an alternative. Apart from this the accepted organic policy for agriculture in the sate opens up possibility for better marketing of dung and urine of indigenous breeds including Vechur. More than 90% of cattle of Kerala are crossbreds. There are problems with adaptation of these breeds to hot humid climate of Kerala. The Vechur is well adapted to the climatic condition of the state and hence is very important for the state.

d) **Research -** The advantage of the breed through are known to the keepers is not well documented. Studies to characterize different loci are proceeding. Whole genome sequence data is already generated. The future research demands availability of the breed and its phenotypic data.

2. Kasargode

The animals are limited to one district of Kerala namely Kasargod. The population of the breed in 1990 s was estimated to be more than fifty thousand. Afterwards these animals were drastically coming down in their numbers. A study to survey and characterize group was undertaken in 2003 and the breed descriptor for Kasargod cattle was prepared. Since then a society for conservation of Kasargod cattle was formed and efforts to preserve the valuable animals are in force.

a) **Economics -** The breed is in high demand as a source of manure and urine for organic agriculture. The milk production is very low and cannot be considered as a major economic return. An unethical practice of sale of these animals as the more precious Vechur cattle is prevalent. As a result the demand and value of these animals are also increasing.

b) **Social and cultural -** The animals are well knitted to the agriculture community of areca farmers who maintain them as a source of organic manure. The deep litter system practiced for these animals is unknown in other parts of the country.

c) **Environmental -** The scarcity of fodder is one of the major problems in breeding tract of these animals. The rock grass and the leaves of areca plant are major fodder sources. They are insufficient to cater the nutritional needs of a crossbred higher producer but sufficient for small sized Kasargode type of animals.

d) **Research -** The importance of these animals and their adaptation to comparative hot arid tropical climate is an advantage for survival of the breed.

3. Other dwarf genetic groups

There are atleast five other dwarf cattle groups in Kerala namely Vatakara, Kurichiatt, Kuttampuzha, Wilwadri and Highrange dwarf. Because of the efforts of conservationists, the educated farmers are sensitized about the importance of local genotypes. As a result they all started to from breed associations for improvement of their cattle. These breed associations were recording animals and were trying to get the incentives and support for rearing these animals. The organic agriculture based practiced lead to increased importance of local genotypes. More than the milk cowdung, urine and other products are fetching the farmers return. Appreciations in value of these animals are also helping to ensure their survival in farmers' hands. An apex body namely "Confederation of breed associations of dwarf cattle of Kerala" is also functional now.

a) **Economics -** The other groups of dwarf cattle of the state are also in demand due to increasing awareness about conservation. These animals are hence an asset for the keepers and they donot like to part with them. The incentives given to the indigenous cattle keepers by Government of Kerala and local self governments are also instrumental in increasing their demand.

b) **Social and cultural -** These indigenous dwarf animals are being kept through generations and are linked to the farmer families as a member. The economic viability is not a factor in their keeping.

c) **Environmental -** Major purposes of keeping dwarf cattle in Kerala are twofold. They supply the milk for the family and provide dung and organic manure for agriculture. Organic agriculture especially vegetable cultivation recognizes these animals as an integral part. Their dung, urine and other products are used extensively for production of bio-fertilisers and bio-pesticides.

d) **Research -** They are more adapted to the climate and fed conversion is expected to be more efficient compared to higher producing crossbreds. As disease incidence is low, and fat content of milk is more, the farmers are happy to keep them. Each of these groups of animals process unique characters which need further studies. These animals are hence considered as the valuable resource for various genes.

4. Umblachery

Umbalachery cattle breed is spread over in Nagapattinam, Thiruvarur & Thanjavur Districts of Tamilnadu State. Bullocks are mainly used for wet and ploughing and transport of goods using bullock cart. Umblachery animals are suitable for marshy rice field of Cauvery river delta region.

a) **Economics -** The persistency in lactation and comparatively medium production ensures consistent returns for the keepers. The breed keepers are also getting remuneration from Penning of the stock during night hours.

b) **Social and cultural -** The breed is closely associated with social and cultural life of people of the breeding tract. Major risk identified for the breed is increase in maintenance costs due to restrictions in grazing and mechanization of farm operations.

c) **Environmental -** Keeping the animals in the farmers' agricultural fields enriches the land with manure and urine. This in turn is reducing the requirements of inorganic fertilizers. The animals are degrading the forests with over grazing. This is causing conflicts with forest officials.

d) **Research and training -** As for the other indigenous genetic resources, Umblachery is also not well documented on its good traits. Hence it is essential for future research.

5. Amrith Mahal

The breed is seen mainly in Chikmagalur, Davanagere, Shimoga, Hassan, Chitradurga, Tumkur districts of Karnataka. It was evolved from the Hallikkar cattle and is having the characters of Mysore breeds.

a) **Economics -** Value of the animals are going down due to the number of reasons. The ban on transport of animals had created a situation where the culled and weak animals are also retained in the herd. This is causing huge burden on the keepers.

b) **Social and cultural -** The breed was developed by Mysore Kings 400- 500 years back (1572 to 1636 AD) and are part of social and cultural heritage of the breeding tract.

c) **Environmental -** There is lands earmarked for keeping of these animals and these Kaval lands are important for the environmental equilibrium of breeding tract. Depletion of Kaval lands is putting pressure on Amrith Mahal keepers as grazing become difficult for these stock.

d) **Research -** The animals were at one time heavy milkers but present stock are not those productive. The body size and ability to graze in adverse conditions need further investigation.

6. *Malanad Gidda*

Primarily present in Uttara Kannada, Dakshina Kannada, Udupi, Shimoga, Chikmagalur, Haveri and Hassan, Kodagu districts of Southern Karnataka. They are maintained by farmers as a source of organic manure.

a) **Economics -** Animals are maintained under zero input system.

b) **Social and cultural -** Malanad means highland and Gidda mean dwarf. The name itself shows the significance of the breed in cultural and social life of its breeding tract.

c) **Environmental-** The freely roaming Malanad Gidda cattle are identified as one of problems in forest areas.

d) **Research -** The dwarf characters and feed efficiency together with adaptability to the climate are important and need be studied in detail. Restrictions on grazing are also detrimental for the survival of the animal.

7. *Punganur*

The breed is of Chittoor district of Andhra Pradesh. These small animals are very sturdy and fat content of the milk is very high. They have most of the dairy characters of Indian breeds.

a) **Economics -** The high demand for the milk and ghee is highly remunerative for the keepers. The value of the animals also makes it highly sought after commodity.

b) **Social and cultural -** Punganur breed very much connected with religious rituals of temples like Lord Thirupathy temple. These animals presence is considered as very auspicious and hence are kept by many persons.

c) **Environmental -** The Punganur cattle are mostly limited to organized herds or as house cows and is not causing any environmental problems.

d) **Research -** Punganur cattle is very small in size and fat content of milk is very high These characters need be studied in depth.

8. *Pulikulam*

These animals are known for their ferocious nature and are maintained by migratory herders in Sivagangai and Madurai districts of Tamilnadu. Though it was developed as a draught breed, in present situation its major significance is for bull riding (Jellikettu).

a) **Economics -** The returns from Pulikulam cattle are through sale of male calves either as bullocks or for bull riding. The milk production is negligible and is not a major source of income. The keepers are getting money for penning the animals for night in farmers' fields.

b) **Social and cultural -** The breed is closely knitted to the social and cultural life of the communities if not the Tamilnadu state as a whole. The Jellikettu is the bull riding sport event where the bulls of Pulikulam cattle are used. These specially trained bulls are even worshiped at some places.

c) **Environmental -** The grazing of these animals are mostly from the forest areas and it is harming the forest and is prevented by forest officials.

d) **Research -** The animals are selected for Jellikettu is hence having ferocious nature and is said to have a mind of its own. These characters of the breed namely the competitive spirit and ferociousness need be studies in detail.

9. Bergur

The red and white Bergur animals are seen in Krishnagiri district and Bergur foot hill of Athiur taluk of Erode district. They are reared under semi wild conditions.

a) **Economics -** Bergur cattle is mainly used for agricultural operations in the hilly terrain of western Tamilnadu. Cows yield reasonable quantity of milk and it is another income for the keeper. The herd size is large and during night hours the cattle are kept in "pattys".

b) **Social and cultural -** The breed is kept by Kannada speaking Lingayats of Tamilnadu state of these animals.

c) **Environmental -** Though grazing is done in forest areas conflict with forest officials are not a major issue.

d) **Research -** These animals are described as dual purpose by the farmers and hence their characters need be analysed further.

10. Kangayam

The pride of Erode and Coimbatore districts of Tamilnadu is the Kangayam breed. The breed is having some characters of Mysore breeds like emergence of horn from top of the poll and long pointed horns.

a) **Economics -** These animals are fetching very huge prizes the annual Kangayam fair at Palamkottai. Some of the best male calves are sold for making Jellikettu bulls.

b) **Social -** Pattigar of Palamkottai was instrumental in revival of fortunes of this breed. The selection and subsequent marketing strategies are linked with the social life of its breeding tract.

c) **Environment -** The huge animals are fed with crop residues and are no way degrading the environment.

d) **Research -** The size of the animals makes Kangayam an ideal experimental unit for growth studies. Research is needed at molecular level to identify the genes connected with growth traits.

11. Malaimadu

This breed is found in 20 villages of adjoining Westernghats spread over Madurai,Theni, Virudhunagar districts. It is not yet recognized by NBAGR as a pure breed. It is described as hill cattle and rotational grazing system is followed for its keeping in Tamilnadu State.

a) **Economics -** These animals are kept on low input system and are not usually supplemented with concentrates. The returns are mainly from penning the stock for night at farmers field and sale of male calves for bullock production.

b) **Social -** They are integral part of lives of communities maintaining them.

c) **Environment -** The rotational grazing system followed for the breed ensures environmental sustainability and hence is good. Restrictions are placed on grazing in the Giant Squirrel Sanctuary.

d) **Research -** The ability to thrive on-coarse fodder and better feed conversion efficiency need to be studied in detail.

Analysis of Position of the Breed

The present situation of the breeds or genotypes including its strength, weakness, opportunities and threats (SWOT analysis) are necessary to know about the breed status and also to chalk out strategies for future, it also opens up the possibility of evaluating the challenges faced by the breed and the stakeholders for each group. The driving factors for each breed have to be identified and conservation strategies need be identified and prioritized.

1. Vechur

a) **Strength -** The Vechur cattle is a recognized breed of livestock in India. The conservation efforts are more than 25 years old There is a trust working for conservation of the breed namely Vechur conservation trust. Compared to other dwarf varieties, Vechur cattle are well documented and its advantages are known. The semen of the breed is available through department of Animal Husbandry. The huge prices of these animals are also remunerative for the farmers.

b) **Weakness -** The narrow genetic base of the breed can cause problems in fertility and viability. The tendency to name every dwarf cow as Vechur makes it difficult to distinguish true Vechur cows.

c) **Opportunities -** Vechur breed is very rare commodity and fetches more than lakh rupees per animal. The high demand of Vechur and Vechur like animals can be utilisd for conservation of the breed. The literate farmers are keeping the indigenous animals with sufficient knowledge about their management and importance.

d) **Threats -** Livestock improvement Act 1964 doesnot allow keeping of breeding bulls without the permission of Director Animal Husbandry.

2. Kasargode

a) **Strength -** The population is comparatively larger and is in thousands.

b) **Weakness -** The very low milk production is one of the major weaknesses. Dwindling area plantation in the breeding tract makes the very purpose of keeping animals difficult. Non availability of semen is a concern in many parts of the state.

c) **Opportunities -** The awareness among farmers to keep indigenous animals and to use its milk for home consumption can be utilised for its distribution as house cow. Availability and comparatively reasonable prices makes Kasargode cattle affordable to marginal farmers.

d) **Threats -** Shifting of Kasargode animals from its breeding tract to other parts of the state due to high demand reduces its population in breeding tract. The breeding of shifted animals is also a problem.

3. Other Dwarf cattle

a) **Strength -** The demand and concern for keeping them in their breeding tract is very strong. Well organized breed societies is very active in conservation efforts and performance recording. Breed associations for improvement of various genetic groups of dwarf cattle is strength for these animals.

b) **Weakness -** the number of these groups are very small and unsustainable, Breeding bulls are very low in number and cryo- preservation of semen is not done.

- c) **Opportunities -** It is possible to form a identifying and recording system for the animals through the breed societies.

4. Umblachery

- a) **Strengths -** Well adapted to the breeding tract. Umalchery cattle can survive on dry fodder or crop residues and yield 3-6 liters of milk for 6 to 10 months. It is comparatively disease resistant. Breed association and NGOs are working for conservation of the breed. It is good work animal and is suitable for marshy paddy fields for ploughing.
- b) **Weakness -** The introduction of mechanical ploughing reduced the use of bullocks for ploughing. The maintenance of bullocks need not be met by the farmers. The availability of water in the grazing land is also another problem.
- c) **Opportunities -** The long lactation length and sustainable production of milk through out the lactation are major positive aspects for the breed. Support for conservation of the breed by Government and the NGOs are also high.
- d) **Threats -** The grazing lands are getting reduced. The uses of bullocks are not much because of availability of tractors.

5. Malai Madu

- a) **Strengths -** Well adapted to resource scarce breeding tract. Bullocks are used for ploughing and agricultural operations. Another major use is for production of organic manure. The management system can be described as zero input system.
- b) **Weakness -** Productivity is very low. Grazing facility is getting reduced.
- c) **Opportunities -** The enthusiastic keepers want to maintain these animals. The support from NGOs for keeping the grazing rights is also significant.
- d) **Threats -** Declaration of Giant Squirrel Sanctuary and consequent restriction of grazing is the major threat for existence of the breed.

6. Pulikulam

- a) **Strengths -** The Pulikulam animals are kept as a treasure for the keeper. Males are needed for Jellikettu or bull riding and are in great demand.
- b) **Weakness -** Low numbers of the breed and unavailability of good quality breeding bulls make it difficult to maintain the true breed types.
- c) **Opportunities -** Bull riding is being accepted as a ethnic sport and restrictions are getting removed, This will make relevance of the breed more prominent.
- d) **Threats -** The restrictions in grazing aspets in forest areas are the major threat. Availability of drinking water in the tract is also another problem.

7. Punganur

- a) **Strength -** Acceptance of the breed as status symbol and consequent demand are very high for Punganur cattle. The good quality of milk and its high at content are strength of the breed.
- b) **Weakness -** Very low numbers of the breed and absence of a breeding plan are the major weakness for the Punganur animals.
- c) **Opportunity -** The high demand by the public is the major opportunity.
- d) **Threats -** Critically low numbers makes the existence of the breed at risk.

8. Amrith Mahal

a) **Strength -** The adaptability of the breed in the breeding tract is absolute. Sufficient population is available in numbers.

b) **Weakness -** Low milk production and high maintenance costs are major negative aspects.

c) **Threats -** Fast depleting Kaval areas are causing problems with grazing and sustenance of the breed.

9. Bergur

a) **Strength -** Major use of these animals are in the hilly terrain of their breeding tract for agricultural operations. These animals are best suited for the same and hence are indispensable for the region. Moderate milk production is also another attraction for the keepers.

b) **Weakness -** The use of these animals are very much restricted to small area.

c) **Threats -** Large scale crossbreeding in the breeding tract is the major threat for the breed.

10. Kangayam

a) **Strength -** It is one of the best draught breeds of India. The high endurance and ability to carry heavy loads make it best working animal. Major use is in pulling carts through roads.

b) **Weakness -** Mechanisation has reduced the relevance of the breed.

c) **Threats -** Fast reducing number of animals threatens the existence of the breed. Extensive crossbreeding in the breeding tract is another threat for the breed.

11. Malanad Gidda

a) **Strengths -** Population and spread of the breed is vast compared to other south Indian breeds. The animals are maintained under low input system and are not a burden to the keepers.

b) **Weakness -** Very low production of the cows is the major problem. Intensive crossbreeding undertaken in the breeding tract is detrimental to the survival of the breed.

c) **Opportunities -** Recognition of the breed by National Bureau of Animal Genetic Resources is most important.

d) **Threats -** Restriction for grazing in forest lands is major threat faced by the keepers.

Risk Analysis of the Genetic Groups

The classification of breeds based on risks faced by the breed in its long time survival is done based on a number of aspects. Of these the most important ones are the breeding females, breeding males and the total population size is important. Based on these three the classification is as follows:

Table 1. Categorization of breeds based on the number of animals

	Class	Number of females	Number of Males	Total population
1	Extinct	No breedable females	No breedable males	
2	Critical	≤ 100	≤ 5	≤ 720
3	Endangered	>100 ≤ 1000	>5 ≤ 20	>720 ≤ 1200
4	Vulnerable	1000-2000	20 -36	1200-2400
5	Not at risk	All others	All others	All others

Another important aspect is to find out where the 75% of the animals are present if it is in an area of less than 12.5 km radius the breed is critical and if it is in between 12.5 to 25 km radius the breed is endangered.

Growth of the number of breed is another aspect. The rate of growth per year is given by

R = (log N_2 – Log N_1) / t where N_1 and N_2 are the number of animals in first and second census and "t" is the interval between the two census.

Table 2: Comparison of population of different breeds of cattle of South India (2007 & 2013 census)

	Name of breed	**2007**	**2012**			**Percent change compared with 2007 population (true animals)**	**Percent change compared with 2007 population (total animals)**
		Number of animals	**True animals**	**Graded animals**	**Total**		
1	Amrith Mahal	96021	105343	123720	229063	+ 9.70	+138.56
2	Kangayam	314817	80620	112825	193445	-74.39	-38.55
3	Bargur	20879	14154	2153	16307	-32.31	-21.90
4	Umblachery	217193	39050	33460	72510	-82.02	-66.61
5	Pulikulam	34191	7352	2733	10085	-78.50	-70.50
6	Punganur	733	2772	56	2828	+278.17	+285.81
7	Vechur	160	1065	1414	2479	+565.62	+1449.38
8	Malanad Gidda	1282121	899091	150452	1049543	-29.87	-18.14

* GOI 2013

Of the different recognized breeds, Vechur and Punganur have a population around 2000 numbers with number of breeding males very low. The effective population sizes of these breeds are in two or three digits. The increase in population shown is misleading as the recorded population of Vechur in 2007 was only that of organized herds. In case of Punganur also the increase can be attributed to the high demand of the animals and subsequent registration of all Punganur like animals as Punganur.

From the data presented above it is clear that the two Tamilnadu breeds namely Umblachery and Pulikulam are getting reduced at a rate of around 82% and 79%, respectively (on number of true breeds alone) and around 70% each when graded animals are also considered. The situation of Kangayam breed is also almost similar. These fast reductions in number of the three breeds are indicative of keeping them under scanner. The rate of deterioration of Bergur and Malanad Gidda though less than that of above three breeds, is also of much concern. The unrecognized genotypes Kasargode, Other dwarf cattle and Malaimadu were not included in the census or breed survey. The risk status of all these breeds and genotypes are considered as "Not at risk" based on their present population. But because of reduction in their numbers these are also very vulnerable.

Conservation and Sustainable use Strategy for Breeds

While formulating a breeding policy and conservation policy for Vechur and Punganur breeds, two aspects are emphasized. They are inbreeding and risks associated with smaller herds.

1. Increase in inbreeding - The inbreeding of the population is likely to increase over time and the rate of increase can be calculated as $\Delta F = 1/N_e$ where the effective population size is the major influence. This increasing inbreeding of the herd can lead to problems with viability and fertility. Loss of valuable genes is also needing be considered.

2. Risk status - These two breeds are having their presence in limited area and is hence likely to be affected unforeseen diseases or climatic changes or natural or manmade disasters. These can wipe out whole populations.

Breeding Plan

For Vechur and Punganur breeds the broad frame work of breeding strategy can be the same. First step for conservation should be identification of each animal of the breed and DNA fingerprinting of the same. This will ensure the purity of the breed. As the NGOs may not The possibility of developing breed signature is another important step towards breed identification. The continuous performance recording of all animals is most important aspect.

The most important step should be to strengthen the nucleus herd as the epicenter of conservation. The Vechur conservation unit, Centre for Advanced Studies in Animal Genetics and Breeding of Kerala, Veterinary and Animal Sciences University and Livestock Research Station, Palamaner, Chittoor of Sri Venkiteswara Veterinary University has the major herds of the two breeds, respectively. They should be converted as open nucleus herds. As each animal of the breed is registered and recorded, the introduction of animals to the nucleus herd should be easy.

The breeding of animals of the farmers is another important area where interventions are necessary. Availability of semen from true breed bulls has to be ensured. Number of breeding bulls is also very important. Each breed should have atleast 20-25 breeding bulls to ensure low inbreeding.

Inorder to ensure the safety of the breed, exsitu conservation is also recommended. Two methods are to be employed namely cryopreservation and establishment of satellite herds outside the breeding tract. Exsitu conservation of embryos, fibroblasts and other tissues is also a major priority for these.

Genetic improvement programme-

It is not necessary to start genetic improvement programme as number of animals is less and further deterioration of gene pool is not be caused. Hence selection and improvement programme cannot be undertaken under these conditions.

Conclusion

The most of the recognized breeds of South India except Vechur and Punganur are classified under "Not at risk" category as per the current accepted criteria of FAO. But population of these animals are coming down because of a battery of reasons like reduced productivity, changed cultural and social aspects of breeding tract and the crossbreeding policy. These are leading to rapid loss of the valuable germplasm and new strategies are the need of the hour to prevent further genetic erosion of these breeds. The frame work of conservation strategy for the two vulnerable South Indian breeds, Vechur and Punganur are presented, the plan can be used for similar low numbered genotypes like Kasargod, Malaimadu and other dwarf cattle of Kerala.

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LP-03

PROMOTION OF BREEDERS ASSOCIATION AND GROUPS FOR CONSERVATION AND IMPROVEMENT OF LIVESTOCK BREEDS

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India is home to a large number of local livestock breeds that have been nurtured by pastoralist communities – Bakkarwal of Kashmir, the Van Gujjar of Uttarkhand, the Gaddi of Himachal Pradesh, the Raika, Gujjar, Sindhi Muslim and Rajput in Rajasthan, the Maldhari of Gujarat, the Gowli and Dhangar of Maharashtra and Karnataka, the Toda, Kurumbar, Konar and Bargur Lingayat in Tamilnadu are some among them. There are about 151 registered breeds in our country. There are many more that still need to be described.

With the disappearance of India's common lands, pasture lands, tanks and forests, the local livestock breeds are being lost at an alarming rate. Many factors have contributed to the loss of livestock in general and local breeds in particular. With the advent of technological revolution, animal drought power has been replaced with tractors and power operated equipments, making livestock redundant. On the other hand, with agriculture becoming less remunerative, the village youth are going in search of other livelihood options, leaving agriculture and animal rearing. Even the government has contributed to the rural crisis. For example, the rural employment programmes, have added to the labour shortage, which is already prevalent in the villages, thus affecting small farmers and livestock keepers.

Therefore there is a need to conserve and improve our native breeds of livestock in our country while capacity building of efforts initiated by interested groups or persons involved in this narrow area of breed based economy are to be encouraged and strengthened.

Experiences in Breed Conservation by involving local communities

There are good experiences of few NGOs or groups who attempted in organizing those livestock keepers, farmers or pastoralists keeping local breeds which inturn provides livelihoods for them. Brief information of few cases are given below:

1. Conservation of Sahiwal cattle breed by Vishav Namdhari Sangat- Punjab. This is gaushala initiated in 1857 to supply milk to the namdharis who are strict vegeatrians and drink only cow's milk. They have been maintaining about 150 - 200 animals of Sahiwal breed. They sell male calves to Govt agencies for breeding purpose. SEVA has documented their conservation efforts which have been sustaining more than 150 years and Breed Saviour Award has been given to the Vishav Namdhari Sangat. (Details in www.sevango.in Breed Saviour award profile 2011).
2. Umbalachery Cattle Breeders Association was promoted by SEVA an NGO which worked in this area for about 5 years in Nagapattinam District, Tamilnadu during 2001-2005. The main objectives of the association: in situ conservation of Umbalachery cattle breed renovation of animal drinking water ponds and common grazing lands and train livestock keepers on herbal medicine for animals. The Umbalachery cattle breed is

known for wetland ploughing and transport of agricultural produce in rural areas. The cattle are pooled as temporary herds during Jan-June and each herd size is about 400-500 cattle taken for grazing and they are also penned during night time in farmers field to contribute manure to the wetland. There are more than 25 herds in Nagapattinam and adjoining districts. In each herd one or two Umbalachery bull will be maintained for breeding through natural service. SEVA renovated 9 tanks/ ponds for animal drinking water purpose, procured 5 quality bulls and supplied to the herds and both male and female calves distributed to 150 members. The association has removed encroachment in the grazing land and also semen of Umbalacherry cattle is made available in the local veterinary centre due to their pursuance.

3. Conservation and development of Tharparkar Breed of cattle by SURE NGO. The effort of this NGO-SURE resulted in birth of 2091 Tharparkar progenies in 15 villager of Barmer district, Rajasthan.
4. Conservation of Hallikar cattle by Timbaktu Collective an NGO based at Anantapur district of Andhra Pradesh. The farmers revived their land productivity by promoting Hallikar breed which are being utilized as draught animals by the farmers. 500 farmers were supported to procure 1200 Hallikar cows in 35 villages which supply draught animals for the farmers during 2007-2008.
5. SEVA NGO has promoted Pulikulam cattle herders group in 4 villages in Madurai district, Tamilnadu during 2006. SEVA registered this breed which is known for *Jallikattu* a cultural heritage event in Tamilnadu state. This group is negotiating with Govt. for reviving their traditional grazing rights associated with forests, tanks and other common property resources. Bore wells have been dug in 3 places to help the herds drinking water facilities in Madurai and Sivagangai districts. Refer profile of breeders association. (Details in www.sevango.in Breed Savour award profiles 2011).
6. Banni Pashu Uchherak Sangathan (Banni Breeders Association) in Kutch, Gujarat has been promoted by Sahajeevan NGO which works with Maldhari communities and stress the need for conservation of Banni grass land and associated breed viz. Banni Buffalo during 2009. It has been registered as distinct buffalo breed of our country. It linked with Sharad Dairy of NDDB to market the milk through cooperatives inturn offering remunerative price for the milk procured from the buffalo farmers.
7. Kachaikatti Black Sheep breed conservation by sheep breeders association SEVA NGO has promoted the herders association in 5 villages in Vadipatti taluka of Madurai district, Tamilnadu during 2003. The breed has been registered by SEVA and it is taking up the issue of grazing in forest zone of Sirumalai hills of Madurai district. Micro credit is extended for construction of sheep shed and other activities of the herders.
8. Jagruta Kurubar kuri Matu Unni Utpadakara Sahakari Sangh was registered during 1989 with 200 sheep breeders in Belgaum Taluka, Karnataka State. It was initiated by Shramik Abhivrudhi Sangh an NGO based at Belgaum. This is a sheep herder's sheep and wool producers society which focuses on Deccani sheep. The society is providing all services viz. veterinary care, purchasing wool from members, marketing of wool products in north Karnataka.
9. Vembur Sheep Breeders Association has been promoted by SEVA NGO during 2002 and it extends services to members *viz*. construction of sheep shed, drinking water facilities through hand pumps, providing quality male animals to the herds, organising animal

health camps, supply of fodder seeds, seedlings etc. in 10 villages in Virudhunagar, Thoothukudi districts of Tamilnadu. After intervention of SEVA the population of the breed increased.

Role of Breeders Association

Breeds of livestock can be conserved better along with production system or ecosystem conservation. Therefore under the extensive production system of livestock keeping there is a need to preserve and renovate the common property resources for access to grazing land and drinking water. In addition services viz. veterinary care, breeding and marketing of livestock products are to be facilitated in order to sustain the remuneration derived from livestock keeping.

The breeders association shall take up one or more services or activities as indicated below:

1. Land use rights for access to grazing in common lands, revenue lands, forest ends as per Forest Rights Act 2006., access to drinking water source viz. tanks, ponds, dam sites and removal of encroachments in the migratory routes etc.
2. Record keeping system including pedigree keeping for future selection.
3. Arrangements for feed, fodder and medicine for animals.
4. Veterinary services.
5. Breeding services, AI, supply of male animals to herds and replacement of males to avoid inbreeding at regular interval.
6. Marketing of livestock products with or without value addition.
7. Registration of breed if not yet registered.
8. Supply of draught animals to farmers.
9. Upgrading local animals with selective breeding with pure superior bulls of local breed.
10. Reducing the cost of maintenance including imparting training on herbal medicine for animals.
11. Providing microcredit facilities to livestock keepers for purchase of inputs and animal shed construction and for procuring animals, fodder cultivation etc.
12. Providing incentives for breeders including recognition and awards.

There should be some policies to support in establishing breeders associations at village or cluster level in the breeding tract of animals based on such experiences attempted by private groups including NGOs, Gausalas etc. It should be nurtured on long term basis (minimum 10 years or more) and this will in future substitute or play complementary role to state owned breeding farms existing in many states.

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LP-04

LESSER KNOWN ANIMAL GENETIC RESOURCES OF SOUTH INDIA

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South India constitutes five major states viz., Andhra Pradesh, Telangana, Karnataka, Tamilnadu and Kerala. The conditions under which the livestock in south India maintained have been undergoing constant change due to progressive restriction of grazing areas, more extended use of mechanical transport on road and changes in agricultural system. The major known cattle breeds like Ongole, Amrithmahal, Kangayam, buffalo breeds like Toda, sheep breeds like Nellore, Deccani, Mandya and goat breeds like Malabar are few examples of the livestock biodiversity in southern India. In addition to these recognized breeds of different species, the South Indian states also include several lesser known or unrecognized livestock biodiversity, which in turn are contributing to the total animal biodiversity of the country. Some of these genetic groups might disappeared before their significance is realized. Hence, systematic phenotypic and genetic characterization of the lesser known germplasm is needed so that breeding plans can be formulated and efforts can be started to speed up the conservation programmes.

The lack of comprehensive information on population fragmentations and geographical distributions, many animal populations in our country are commonly referred to as "non-descript" or "traditional". These traditional populations, mainly local, often exhibit large phenotypic diversity; are managed by farmers and pastoralists at low selection intensity, but may be subject to high natural selection pressure; pedigree may be partially known or not known; genetic structures are mainly influenced by migration events and mutations; population size is generally large. It is primarily in these regions that phenotypic characterization studies on animal genetic resources (AnGR) are needed. But, assessing the diversity of AnGR is made more difficult by the existence of many animal populations that are not assigned to any recognized breed. Even though parts of these "non-descript" populations are known to be multiple crosses of recognized breeds, some animals might belong to homogenous groups distinguishable from neighbouring populations on the basis of identifiable and stable phenotypic characteristics that warrant them being distinguished as separate breeds. One major feature of such genetic groups is local adaptation which can be characterized by less calf or kid mortality rates and better production. These features are generally perceived by the local inhabitants but unless systematic efforts are not taken up to record their characters in terms of their phenotype and genetic makeup, there is danger that such genetic groups may get extinct. Further, phenotypic characterization is fundamental to the establishment of national inventories of AnGR and usefulfor effective monitoring of AnGR populations.

These lesser known genetic variants can be conveniently called as genetic groups, rather breeds unless they are characterized, so that to differentiate as non-descript or do they qualify to be called as breed. 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 breeders. The Food and Agricultural Organization (FAO) uses the following broad definition of the breed concept, which accounts for social, cultural and economic differences between animal populations and which can therefore be applied globally in the measurement of livestock diversity: *"either a sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity".*

In the present paper, some of the native genetic groups of various livestock species that exist in southern India have been reviewed. Importance of characterizing such native genetic groups and the need for their recognition is emphasized.

Andhrapradesh and Telangana

Cattle breeds

Thurupu: This is a little known species of cattle, from the Mannanur forests in Mahbubnagar district of Telangana state. The animal is also known as Nallamalapoda. The variety can be distinguished through its brown/red spots on white skin or white spots on light brown skin, with straight and sharp horns. The cattle got its name because it is bred in the Nallamala forest in the eastern part towards Mahbubnagar (*Thurupu means east locally*). The cattle of this genetic group are sturdy that were bred over centuries by the Lambada and Golla communities and has evolved to survive the dry weather ecosystem. Hence, low level of inputs is sufficient for maintenance of the animal. The cattle are mostly located in four mandals Amrabad, Achampet, Mannanur and Lingal bordering Nallamala forest area. They possess excellent draught power to work in the region and works from the age of 3-20 years. The genetic strain is under threat due to cross breeding. Recently, the Government of Telangana instructed not to implement crossbreeding in this breed. At present the population is estimated to be about 25000 animals in the Nallamala forest. The livestock Node of Revitalising Rainfed Agriculture (RRA) Network and Watershed Support Services and Activities Network (WASSAN) are involved in physical characterization of the genetic group and the work is in progress.

Jhari: Jhari cattle are seen in Adilabad district of Telangana state. The animals are primarily used for draft, agricultural operations, transport followed by milk and dung. Animals are medium sized with white or brown colour. Forehead is described as concave. Horns are medium to small sized with well developed dewlap and curved forward. Horns are small to medium sized, curved forward, cylindrical and sickle shaped. The milk production in females ranges from 1.5 to 2.0 kg per day. Natural service is preferred by the farmers for breeding their animals. The phenotypic characterization of the breed was initiated as part of National Agricultural Innovation Project (NAIP).

Buffalo breeds

Godavari: The breed is found in Godavari delta region and Krishna delta regions. Godavari buffaloes were evolved through upgrading of local buffaloes with Murrah. Animals are medium statured with compact body. Coat colour is black with sparse coarse brown hair. The horns are not so tightly curved as in Murrah but form a loose ring at the top. Their milk producing ability is comparable with that of Murrah breed but due to grading up, their reproductive efficiency is better compared to Murrah. The tail is described as thin with a white switch.

Goat breeds

Mahabubnagar goats: They are seen in Mahabunagar, Raga Reddy and Nalgonda districts of Telangana state. These animals are bi-coloured (Black, white or brown). Most of the animals have straight head. One third of animals have wattles. ears are pendulous and beard is absent in majority of female animals. Both males and females are horned and horn pattern is straight.

Kanchu Meka / dwarf goat: They are seen in semiarid hilly and coastal parts of Andhra Pradesh. They are known for their reproductive efficiency.

Sheep breeds

Different strains of Nellore: Nellore, Prakasham, Anathpur and Chittoor districts of Andhra Pradesh is the home tract of the breed. Colour is white or brown and is classified to three different types from pure white "Palla" with or without brown spots"; Jodipi" is white with black spotted body and "Dora" is completely brown. Nellore breed have ears described as long and drooping. The Nellore ewes are polled and rams are horned. Majority of the animals have wattles. Tail of these varieties is short and thin. Though Nellore brown is recognized breed by NBAGR, but the other strains of Nellore are of different phenotypes. So the other two strains of Nellore, i.e., Palla and Jodipi are to be characterized and also conserved for future.

Macherla Brown: These animals are seen in Guntur, Nalgonda, Prakasham and Krishna districts of Andhra Pradesh. Colour is described as combination of brown and white. Most of the animals are polled. Forehead is convex with pendulous ears. Muzzle and hoof are black. Tail is described as slender.

Vizianagaram Local: This sheep breed known for high fecundity is seen in Srikakulam and Vizianagaram districts. These sheep, reared mainly for meat purpose have slightly convex head and body colour is White black and black patches around the eyes, perennial region, on the fetlock joints.

Karnataka State

Buffalo breeds

Dharwadi: These animals are seen in Dharwad and adjacent districts of northern Karnataka. Skin of these animals is black with greyish white hairs. Horns are medium sized and orient backward and with a curving to form a half circle. The breed is known for unique taste so very popular among farmers for its milk and flavoured milk products.

South Kanara: These animals are seen in Shimoga, Udupi and Dakshin Kannada districts of Karnataka. South Kanara buffaloes are well built and medium sized animals. They are basically used for agricultural operations in wet fields, especially ploughing, levelling and peddling so as to make the land suitable for paddy transplantation. These animals are also used for racing in water bound fields, famously called as "Kambla" race in this region.

Goat breeds

Bidari: The animals are seen in Bidar district of Karnataka. The animals are described as coloured with brown, black or combination of these two as the colour. It is a dual purpose breed.

Nandidurga: These goats are seen in Chitradurga, Tumkur, Mandya and Davanagere districts of Karnataka and accounts for around 10% of goat population of the state. The colours of the animals vary much from white to pure black or brown or combination of these. Animals are taken for grazing of around 6 - 10 hours a day covering around 10 - 20 km per day.

Kerala State

CattleBreeds

Kasargode: Originated in Northern part of Kasargode district of Kerala, these animals are also small and highly to the dry and hot conditions of their breeding tract. More than a milk producer they are reared for dung, which is essential component of arecanut based agriculture of the region. Kasargode cattle are black or red in colour with occasional white patches usually in face and ventral side of body. Horns are laterally orientated and animals have well developed hump anddewlap.

Vadakara: Vadakara cattle are found in Malabar region in the districts of Calicut and Kannur of Kerala State. They are small and well adapted to the climatic conditions of the region. These animals' are with small hornsless prominent dewlap and hump and can be of different colours. They are conserved through the activities of a NGO registered for the purpose. Their current population is expected to be more than 1000.

Kurichiat cattle: They are the animals reared in tribal settlements of Kurichiat in Wayanad district of Kerala. These animals are kept on a zero input system with no supplementation of concentrates and maintained solely on grass and grazing. Colour of the animals is described as dark brown and some of the animals have white spots. Height of the animals was around 102 cm.

Highrange Dwarf cattle: High range dwarf cattle are present in the tea estates of Iduddi district of Kerala. These animals are small to medium sized and their horns are large. They are not usually milked. These animals serve as an immediate resource for the poor farmers. Their population has been drastically reduced and now may not be more than 250.

Kuttampuzha dwarf: It is described as a forest cow of district of Ernakulam of Kerala. The unique rearing system of these animals is peculiar in leaving them in the forest for months by their Adivasi owners. They are bought back when information about their calving is known to the owner. The fat content of milk was found tobe higher than other such groups. They feed on almost all types of fodder and are resistant to tick and other diseases. They have a body weight of 150 Kg and are known to have capacity to swim across therivers.

Cheruvally cattle: Another small sized genetic group of cattle of the state found in Cheruvally village of Kottayam district. These animals are small sized with smaller sized horns and known for good disease resistance. The colour can be anything. Efforts are on to define the breed through a project sponsored by Kerala State Biodiversity Board by anNGO.

Buffalo Breeds

Kuttand: They are the working animals of Kerala habitat to Kuttanad area. The vast paddy cultivated area needs these animals for agricultural work. They are smaller in size with broad flat and curved horns. Two white markings one around the jowl region and another at the region just above the shoulder are two salient marks of the animal.

Kurichiat: They are the animals reared in tribal settlements of Kurichiat in Wayanad district of Kerala. These animals are having longer horns curving backwards, inwards and are parallel to the neck. Average height of the animals was around 107 cm.

Goat Breeds

Attappady Black: The goats are reared by tribal people of Attappady village in Palghat district of Kerala. Animals are black with few of them having reddish black coat colour. Very few white spotted animals are also seen. They are reared for meat and are very sturdy. They have comparatively longer limbs and thrive on dry tree leaves of their breeding tract.

Tamilnadu State

Cattle Breeds

Malaimadu: They are short and sturdy animals seen in Western Ghats spread over Madurai, Theni and Virudanagar districts of Tamilnadu. They are mostly let loose to forests. Penning during night hours for providing manure for the field is common in the home tract. Male animals are good draught bullocks especially for wetlandploughing.

Goat breeds

Salem black: These animals are found in Salem, Erode and Dharmapuram districts of Tamilnadu. They are black animals with long body suitable for meat purpose breeds. Their height is also more than other goat breeds of the region. Males and females had horns and they are curved upwards and backwards. Most of the animals have tassels.

MolaiAdu: The genetic group of these goats is seen in Gopichettipalayam and Erode districts of Tamilnadu. They are white in colour and females are polled. Ears are long and drooping. Body is compact and low set.

PallaiAdu / SeeniAdu: These goats are seen in Thoothukudi and Tirunelveli districts of Tamilnadu. They are medium sized animals with compact body. Colour is described as yellowish brown. Few white animals and mixture of black and brown coloured animals are also seen. Ears are medium, leaf like and semi pendulous. Horns are present in both the sexes and are thick and long. Females have short, straight and sleek hairs in almost all parts of the body. Males have fairly long, straight and rough hairs on neck and withers.

KodiAdu: The goat breed is seen in districts of Pudukottai, Tanjore, Tirunelveli, Ramanthapuram and Tuticorn districts of Tamilnadu. The animals have white colour with splashes of black on both the sides. The ventral side is usually white. Face, ears and legs are dark or coloured. All the animals are horned. The horns have an upward, backward direction and curve low or up sharply at the tip. Ears are medium in size and slightly drooping. Backline is straight and legs are thin and long. They are used as meat animals.

Sheep breeds

Kachakatty: It is a rare breed of sheep seen in Madurai district of Tamilnadu. The animals are medium sized with compact low set body. Ears of the breed are very peculiar and described as rudimentary though stumpy and leaf like ears are also seen in some animals. Rams have twisted horns and ewes are polled. Colour of the breed varies from black to tan. The males of the breed are used for fighting also.

Conclusion

Animal genetic resources are the result of human interventions and the current populations are genetically very distant from their wild progenitors. New breeds developed each time people introduced livestock populations into new environments and new territories, or when they selected them for new use patterns. These AnGR provide a wide range of products and services including food, transport, fibres, fuel and fertilizer. Over time, a variety of different breeds has been developed to provide these benefits in a wide range of environments. Domestic animal diversity is a reflection of both cultural and ecological diversity which are developed out of the interplay between biological and cultural factors.

The definition of breed in developing countries, as per FAO, should also be considered the social, cultural and economic differences between animal populations. When we are considering the lesser known or local or non-descript varieties or strains, they should fulfil the criteria like common utilization pattern, sharing common habitat, closed gene pool and also the rearers or breeders should consider them as unique or distinct. All the South Indian strains/varieties enlisted here are as per these criteria because many of these listed unknown genotypes are unique and best suited for the societies and places of their origin since several centuries. Hence, these are very valuable and need to be characterized and conserved. Due to lack of awareness and systematic scientific studies, they were under negligence and not got recognition. But in the context of climate change and maintenance of our rich biodiversity, it is necessary to popularize these lesser known breeds.

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LP-05

KNOWN AND LESSER KNOWN DIVERSITY OF LIVESTOCK IN RAJASTHAN STATE

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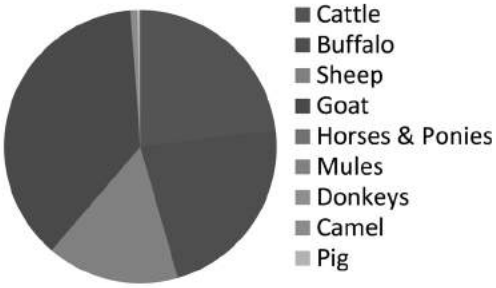
Rajasthan is the largest state of the country with geographical area of 3.42 lac sq. km. About 55% of the total area of the state is under Thar Desert. The livestock sector provides round the year employment opportunity with more than 50% of total house hold income in arid region as against national average of 22.5%. It supports 5.5% of India's human population and about 11% of the country's livestock population and provides livelihood to 66% of the State's population. Because of the limited water resources, most of the agriculture production is rain-fed and as such, the livestock sector assumes more importance. In arid western region, livestock farming essentially works as an insulating factor against vagaries of drought and famines, and provides a kind of stability and sustenance livelihood to the rural poor.

More than 80% rural families keep livestock in their households. Contribution of animal husbandry sector to the GDP of the state has been estimated to be around 9.16 %. About 35% of the income to small and marginal farmers comes from dairy and animal husbandry. In arid areas the contribution is as high as 50%. The sector has potential to create employment in rural areas with least investments as compared to other sectors. As per the 19th livestock census 2012, the State has 133.2 lac cattle, 129.76 lac buffaloes, 90.797lac sheep, 216.66 lac goats, 3.26 lac camels, 2.37 lac pigs and 30 lac poultry. The State faces frequent droughts/ famine, which results in crop failure, because most of agriculture is rain fed. Dairy sector provides sustainable year-round income to large number of farmers and livestock sector is principal source for socio- economic and nutritional needs of rural masses. The National Commission on Cattle has also recommended that in the State of Rajasthan, the emphasis should shift from crops to animal husbandry as a major livelihood option.

Livestock Wealth of the State

The state is endowed with finest drought hardy milch breeds (Rathi, Gir, Sahiwal and Tharparkar), dual purpose breeds (Kankrej and Haryana) and the famous drafts breeds of Nagauri and Malvi. Regarding buffalo breed, Murrah and Surti buffaloes are the preferred breed found in Rajasthan. As per the 19th Livestock census 2012, there are 577.32 lacs Livestock (which include Cattle Buffalo, Sheep, Goat, Horse and Ponies, Mules, Donkeys, Camel, Pig) and Poultry 80.24 lacs. State has about 10.76% of the livestock of the country. State contributes 11% of milk, 35% of goat meat and 30% of wool of the nation's production.

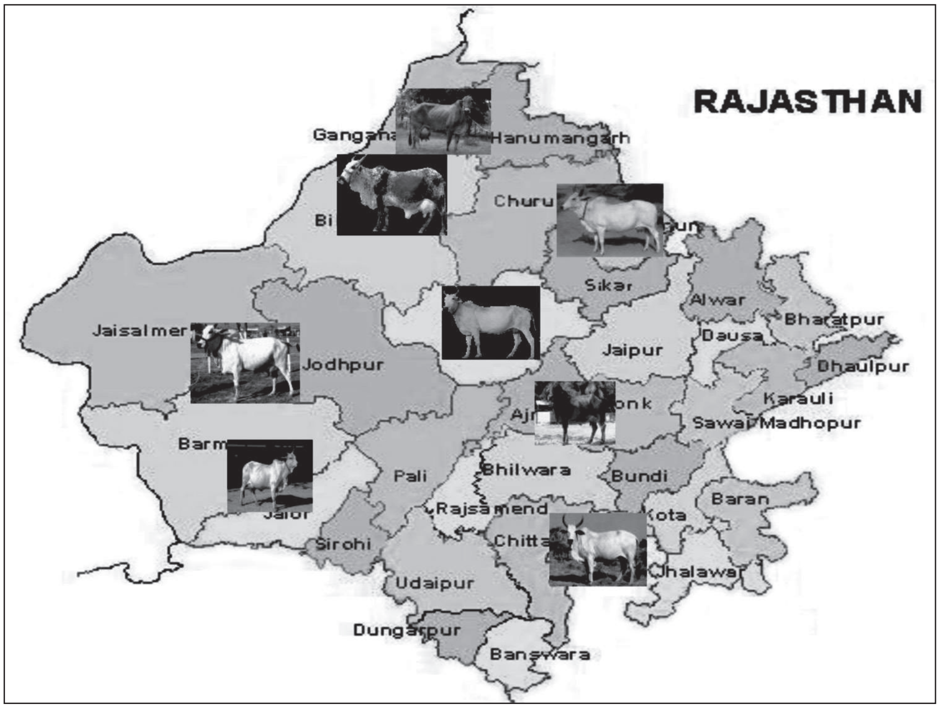


Cattle Breed of Rajasthan

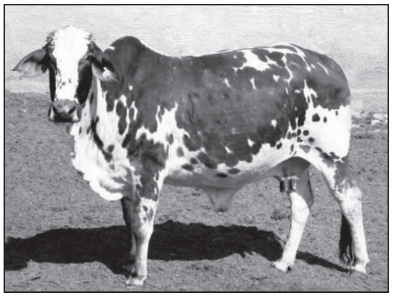
The Rajasthan state has three native cattle breeds viz Rathi, Tharparker and Nagori, having great deal of endurance. Rathi cattle breed is reared for dairy purposes in the northern districts of

ShriGanganagar, Bikaner and parts of Jaisalmer which are irrigated or partially irrigated arid zones with alluvial or loamy soil. The Tharparkar cattle breed is native of the Jodhpur and Jaisalmer districts in eastern region of the state which has arid climate characterised by low rainfall and desert soil. Tharparkar cattle breed reared for dual purpose of draught and milk production as it can produce milk under rigorous feeding and unfavourable environmental conditions. Nagori cattle breed has been named after the Nagaur district which is in central part of the state. The Nagori cattle are sturdy and used for ploughing, cultivation, drawing water from wells as well as transportation of field produce to markets. Earlier they were used as trotters in light iron wheeled carts for quick transportation. There was a good demand of Nagori animals in Bihar but after implementation of Rajasthan Bovine Animal (Prohibition on Slaughter and Regulation of Temporary Migration or Export) Act, the demand has tapered off. In addition to native breeds, Gir, Malvi, Kankrej and Hariana cattle are found in large numbers in the state. In case of buffalo, there is no native breed. However, enormous numbers of Murrah, Surti buffaloes are reared in the region.

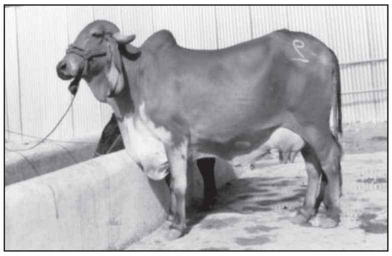
Distribution of Indigenous Cattle Breeds in Rajasthan



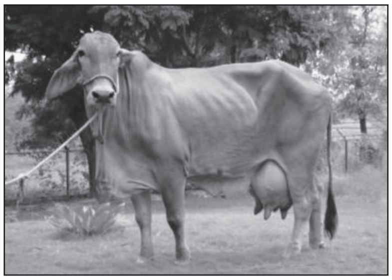
1 **Rathi:** Originated in the region of the state of Rajasthan consisting of Bikaner, ShriGanganagar and Hanumangarh districts. Important milch breed of cattle found in the arid regions of Rajasthan. Rathi cattle are thought to have evolved from intermixing of Sahiwal, Red Sindhi, and Tharparkar. The animals are usually brown with white patches all over the body, but animals having completely brown or black coat with white patches are also seen. The breed is locally known to have two variants, which are Rathi and Rath. The Rathi cattle are a draft breed, and the Rath is a pure milk producing variant. The Rath cattle were domesticated by Rath tribe and the variant originated in the Alwar district of Rajasthan.



2 **Tharparkar:** This breed mainly found in Barmer, Jaisalmer and Jodhpur districts of Rajasthan. Tharparkar (named after the Thar Desert in Rajasthan) is a dual purpose and disease resistant cattle breed. The breed is also known as "White Sindhi", "Grey Sindhi" and "Thari. The breed is medium sized compact with white and light grey coloured coat. Face and extremities are darker than rest of the body. In bulls neck, hump, fore and hind quarters are also dark. The colour gets darker during winter.

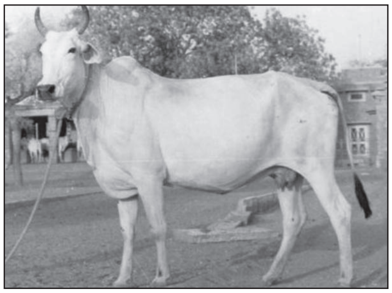


3 **Gir:** Originated in southwest India in the state of Gujarat and have since spread kishangarh (Ajmer) Rajasthan. The Gir is distinctive in appearance, typically having a rounded and domed forehead (being the only ultra convex breed in the world), long pendulous ears and horns which spiral out and back. The breed is known for its distinct appearance, height and weight and natural beauty. Their body is well proportioned and the udder in cows is well developed and round. The body colour is shining red to spotted white. Although, their body colour can vary from pure red to speckles, yellowish red to white with large red spots. Their skin is soft, thin and glossy. Their ears are very long and are an excellent fly and insect swatter. The horns of Gir cattle are set well back on their heads and thick at the base.



4 **Sahiwal:** The breeding tract of the breed is Ferozpur and Amritsar districts of Punjab and ShriGanganagar district of Rajasthan. The cows are brownish red in colour; shades may vary from a mahogany red brown to more greyish red. Extremities in bulls are darker than rest of body colour. Animals have well developed udder, good slope at rump and shorter horns. Due to its unique characteristics, Sahiwal breed is exported to wide list of countries and regions. Heavy breed with symmetrical body having loose skin.

5 **Kankrej:** Originated in Gujarat and also found in Barmer and Jodhpur districts of Rajasthan. The unique characteristics like resistant to tick fever, heat stress, very little incidence of contagious abortion and tuberculosis. Coat colour of the animal varies from silver grey to iron grey and steel black. Unique characteristic of this breed is its large, pendulous ears. The horns are lyre shaped. The cows are good milkers and bullocks are used for agricultural operations and road transport.



6 **Naguri:** Breeding tract of Nagori breed is Bikaner, Jodhpur and Nagaur district of Rajasthan. They are white in colour and are upstanding, very alert and agile animals with long and narrow face. Nagori cattle are fine, big, upstanding, active with white and grey colour. They have long, deep and powerful frames, with straight backs and well-developed quarters. The face is long and narrow but the forehead is flat and not so prominent. The eyelids are rather heavy and overhanging and the eyes are small, clear and

bright. The ears are large and pendulous. The Nagori breed is one of the most famous trotting draught breed of India and are generally appreciated for fast draught activity. They are famous as trotters and are used all over Rajputana of Rajasthan in light iron-wheeled carts for quick transportation.

7 **Malvi:** The breed animals are found in Madhya Pradesh and Rajasthan. Malvi bollocks are known for quick transportation and able to carry heavy loads on rough roads. Bullocks are good for road and field work, economical feeders and have good adaptability.

Small ruminants, sheep and goats, constitute 57.6 % of the total livestock of Rajasthan. There are eight well-defined breeds of Sheep, which produce quality carpet wool, and four breeds of goats. Sheep also occupy an important place in animal husbandry sector of the State. The important breeds of sheep are, Nali, Magra, Chokla, Marwari, Jaisalmeri, Malpura, Sonadi, Pugal and Bagdi. Small land holdings and growth in agriculture has reduced grazing opportunities for the sheep, endangering their existence.

Sheep Breeds of Rajasthan

Some sheep breeds whose populations have shown a decline are the Malpura, Chokla and Jaisalmeri in Rajasthan. The Malpura, which yields a substantial amount of wool, is bred by nomads in Jaipur, Tonk, Sawai Madhopur, Chittorgarh and Bhilwara districts in Rajasthan. These areas fall in the migratory route of Marwari sheep, which yield more wool. Chokla is also known as Chapper and Shekhawati. There is need for conserving the breed, because its numbers are declining for natural reasons and owing to large-scale cross-breeding programmes. Nali is a good carpet-quality wool breed, with the densest and heaviest fleeces among the breeds of Rajasthan and wool of reasonably good carpet quality. It also needs conservation in the light of its falling numbers. Formerly, Magra sheep is also known as Bikaneri Chokhla and Chakri. Pugal has its origin in the Pugal area of Bikaner district in which the breed has its home tract. Malpura breed is very similar to Sonadi but is better in wool production and quality and in body size; this could be due to better environmental and nutritional conditions in the region where Malpura is the predominant breed as compared to conditions in the home tract of Sonadi.

1 **Marwari:** This sheep breed found in Barmer, Jalore, Sirohi, Pali, Ajmer, Jodhpur (excluding Phalodi tehsil), Parbatsar, Merta and part of Didwana and Nawa tehsils of Nagaur. Black faced, stocky and medium built, adult males weighing on an average four legs. This is a highly stabilised breed, capable of undertaking long journeys and possessing high resistance to diseases and worms.

2 **Sonadi:** This dual purpose breed found in E. Udaipur, Dungarpur, Banswara, Chittorgarh, E. Bhilwara, Bundi, Kota and Jhalawar. Appears light brown in colour, weighing more than 60 kg; The Animals are fairly well built, Light brown face with the colour extending to the middle of the neck. Ears are large, flat and drooping; withstands heavy rainfall and can walk through hilly areas. The fleece is white, extremely coarse and hairy.

3 **Malpura:** Its origin in the Alwar, Bharatpur, Sawai Madbopur, Tonk and Jaipur (excluding N.W. adjacent to Sikar and Nagaur). Appears almost completely white 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.

4 **Chokla or Shekhawati:** Originated in Churu, Jhunjhunu and Sikar districts. Very light built, weighing about 26 kg. The animals are light to medium sized. The face generally devoid of wool, is reddish brown or dark brown, and the colour may extend up to the middle of the neck. The skin is pink. The ears are small to medium in length and tubular. Tail is thin and of medium length. The coat is dense and relatively fine, covering the entire body. Chokla grows the finest carpet wool of all the Indian breeds ranging in its quality number from 54s to 60s count.

5 **Nali:** Breeding tract of this breed is ShriGanganagar. Nali sheep breed is medium sized, light brown faced; weighing about 35 kg 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.

6 **Jaisalmeri:** This dual purpose breed of sheep found in Jaisalmer tehsil and in Phalodi tehsil of Jodhpur. Brown and black faced, weighing about 45 kg. Tall, well-built, largest breed in Rajasthan; Typical Roman nose, long drooping ears generally with a cartilaginous appendage; Both sexes are polled; Tail is medium to long. Fleece colour is white, of medium carpet quality and not very dense.

7 **Magra:** Distributed along the borders of Jaisalmer, Churu, Nagaur and Bikaner districts. Medium to large in size. White face with light brown patches around the eyes is characteristic of this breed. Skin colour is pink. Ears are small to medium and tubular. Both sexes are polled. Tail is medium in length and thin. Fleece is of medium carpet quality, extremely white and lustrous and not very dense.

8 **Pugal:** Originated in Pugal area of Bikaner district. Fairly well built weighing about 30 kg. Face is black with small light brown stripes on either side above the eyes; the lower jaw is typically light brown. Ears are short and tubular. Both sexes are polled.

Goat Breed of Rajasthan

The important goat breeds in the State are Sirohi, Marwari, Jhakrana and Barbari breeds, which are reared for milk and meat; Lohi, and Jhalwadi breeds are mainly for meat purpose. These are all hardy species and can withstand the extremes of climate in the region. Goat breeds like the Marwari and Sirohi are all-purpose breeds contributing to livelihoods with both mutton and milk and are hardy species in the area.

1 **Sirohi:** Originated in Sirohi district of Rajasthan. Coat colour is brown, white, and admixture of colours in typical patches; hair coarse and short. Compact and medium sized body. Tail twisted and carries coarse pointed hair. Horns are small and pointed, curved upward and backward. Average body weight of buck is 50 kg and doe is 23 kg.

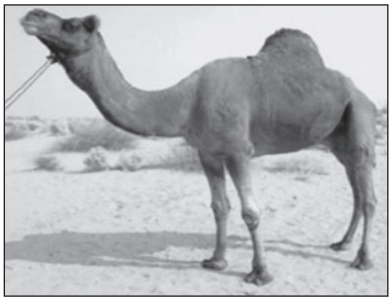
2 **Marwari:** Marwar region of Rajasthan, which is its natural habitat. Marwar region of Rajasthan, comprising Jodhpur, Pali, Nagaur, Bikaner, Jalore, Jaisalmer and Barmer districts. It's a dual purpose goat breed and raised for both meat and milk production. It is a desert goat breed and well known for its tolerance of hot and cold climates. Marwari goat is also well known for its capabilities of disease resistance and capabilities of thriving in very harsh nutritional conditions.

3 **Jakhrana:** Concentrated mainly in surrounding area of Jakhrana village of Behror tehsil of Alwar district in Rajasthan state. Actually, the habitat of this breed is a small hamlet in the Aravali hill ranges. It is an important dairy goat breed of the semi-arid tract of the Rajasthan, India. Jhakrana goats are longer. Their coat colour is black with white spots on the ears and muzzle. Their face is straight with raised forehead. They have short and lustrous hair on their coat. Both bucks and does usually have small horns which are short, stumpy directed upward and backward. The Jakharana goats have leafy and dropping ears that are medium in length. Udder of the Jakharana does is large in size and well developed with long conical teats.

Camel Breed of Rajasthan

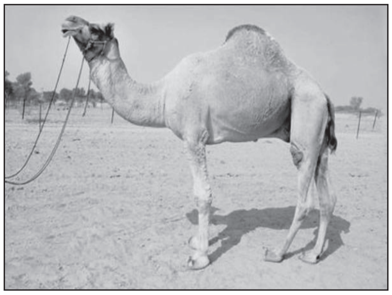
Rajasthan has the monopoly in breeding camels. For the people of Rajasthan, the camel has been more than just a beast of burden. It played an important role in region's economy and heritage and continues to play this role to this day. Many still earn their livelihood from camel breeding, using camel milk, wool, skin and bones for various purposes. Bikaneri, Jalori, Marwari, Mewari, Mewati and Jaisalmeri breeds are considered as the best breeds of camels.

1. **Bikaneri camel:** Bikaneri camels are predominantly bred in Bikaner and nearby districts, such as ShriGanganagar, Hanumangarh, Churu, Jhunjhunu, Sikar and Nagaur of Rajasthan. The



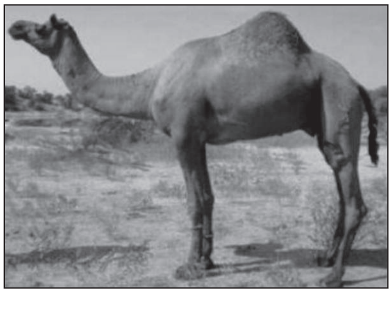
camels of Bikaneri breed are heavily built and are attractive with a noble look. It has good height, strong built and active habits. The colour of the coat varies from brown to black, however in some animals reddish tinge is also found. They have symmetrical body and slightly dome shaped head. The fore head has a well-marked depression (stop) above the eyes, which is characteristic of this breed. Nose is long and extends up to two third of the head. Some camels of this breed have a luxuriant growth of hair on their eyebrows, eyelids and ears; they are called 'jheepra'. The chest pad is well developed and placed between angles of elbow. The shoulders are strong, broad and well set to chest. Neck is thick, fairly erect, with a marked curve giving a graceful carriage to the head. The udder is well developed in females.

2. **Jaisalmeri camel:** The breeding tract of Jaisalmeri breed encompasses the Jaisalmer, Barmer and part of Jodhpur district in Rajasthan. The Jaisalmeri camels are of active temperament and are quite tall with long and thin legs. They have small head and mouth with narrow muzzle. The head is well carried on a thin neck and the eyes are prominent. The forehead is not dome shaped and is without any depression above eyes (stop). Also, there is no luxuriant growth of hairs on their eyebrows, eyelids and ears. The body colour is predominantly light brown. The Jaisalmeri camels have thin skin and short hairs on body. The udder is mostly round in shape. It is a medium sized breed of camel.



3. **Mewari camel:** Mewari breed of camel has derived its name from the Mewar area of Rajasthan found in the Udaipur, Chittorgarh and Rajsamand district. The camels of this breed can also be seen in Bhilwara, Banswara, Dungarpur districts and Hadoti region of Rajasthan. Mewari camels are stouter and a little shorter than Bikaneri. They have strong hindquarters, heavy legs, hard and thick foot pads. Well adapted to travel and carry loads across hills. The body hairs are coarse, which protects them from the bites of wild honeybees and insects. The body colour varies from light brown to dark brown but some animals are almost white in colour, such variation in body colour is generally not seen in other breeds of camel. The head is heavy, set on a thick neck. Unlike the Bikaneri camel, the Mewari camel has no 'stop', but its muzzle is loose. Ears are thick and short, set well apart, tail is long and thick. The milk vein is prominent and the udder is well developed in females.

4. **Jalori:** These are mixture of Marwari and Jaisalmeri. Comparatively smaller than Marwari. They are good quick draught animals and are also good transport animals.



Horse Breed of Rajasthan

Marwari or Malani breed of horses is inhabitant of Badmer, Jalore and Jodhpur districts. it comes in all equine colours, although pinto patterns tend to be the most popular with buyers and breeders. It is known for its hardiness, and is quite similar to the Kathiawari, another Indian breed from the Kathiawar region southwest of Marwar.

1 **Marwari or Malani horse:** The Marwari or Malani is a rare breed of horse from the Marwar (or Jodhpur) region of India. Known for its inward-turning ear tips, it comes in all equine colours. It is known for its hardiness. The Marwari averages between 14.2 and 15.2 hands (58 and 62 inches, 147 and 157 cm) high. They can be bay, grey, chestnut, palomino, piebald, or skewbald.

Chicken Breed of Rajasthan

1 **Mewari chicken:** This breed of chicken is found in Central and Southern part of Rajasthan and is native to Ajmer, Sirohi, Jaipur, Udaipur, Bhilwara, Dungarpur, Banswara, Rajsamand, Chittorgarh and Pratapgarh districts of Rajasthan. It is reared for egg and meat under free range or scavenging system. Adult weight is about 1.9 kg in cocks and 1.2 kg in hens. Annual egg production ranges from 37 to 52. Egg weight is about 53 gm. These birds are reared in backyard both for egg and meat with little or no input i.e. free range/ scavenging system. Average flock size is about 15. Birds are medium to small in size. Plumage colour varies from light to dark brown, and grey. Males have bright gold and bronze feathers forming a "Shawl" or "Cape" over the back of the bird from neck to lower back. The tail is composed of long arching feathers that initially look black but shimmer with blue, purple and green in good light. Comb is red in colour and is of single type. Wattles are red and are large sized in males. Adult weight is about 1.9 kg in cocks and 1.2 kg in hens. Age at first egg is about 6.7 months. Annual egg production ranges from 37 to 52. Egg weight averages about 53 gm. Females are broody in nature.

Lesser known diversity of livestock of Rajasthan

Cattle breeds

Four of the milk produced in the state by cattle (about 80.1%) is contributed by indigenous cattle breeds and non-descript cows. Though the proportion of non-descript cattle in Rajasthan (48.64%) is well below the national proportion of 69.65%, some more cattle population of the state may deserve the status of a breed but so far kept under the non-descript category due to lack of any systematic attempts for their characterization. One such non-descript population locally known as Nari cattle.

i) **Nari cattle:** Originated in Pali and Sirohi districts of Rajasthan. The population of Nari cattle in the breeding tract is expected to be more than 50,000. Nari cattle have compact body and are strong and active. The cows are generally white or grey in coat colour; the bulls are white, dark grey or black in colour. The horns are very long and very strong. The special aspect of the Nari cow is that she is very alert and protective. The age at first calving and inter-calving

period is reported to be 3.0-3.5 years and 12-15 months, respectively. Average peak milk yield is reported from 6 to 18 litres. The lactation length varies from 8 to 12 months. The milk contains 4.5 to 5.0% fat. This cattle population has not been included in the list of recognized cattle breeds of India. In the forest, if one cow is attacked, she will make noise and all the other cows will come and protect her with their horns. Nari cow also protects her owner from wild animals and attackers.

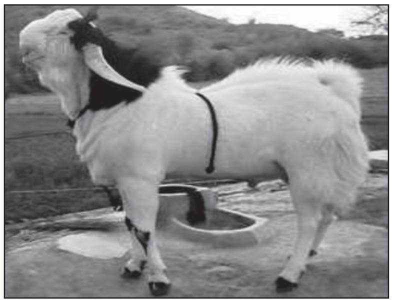
ii) **Sanchori cattle:** Breeding tract of Sanchori cattle includes Sanchor and adjoining tehsils of Jalore district of Rajasthan state. Sanchori cattle are mainly distributed in Sanchore, Bhinmal and Raniwada tehsils of Jalore district of Rajasthan. The animals derive the name Sanchori from the place of their habitat. Sanchor/desi cattle are kept in the herd size varying from 2 to 20 animals in the open houses adjacent to the farmer's house in their agricultural fields called *Dhanis*. The animals are hardy and well survived in all the seasons in the open housing system. Coat colour of animals is generally white and horns are smaller in size and diameter as compared to Kankrej cattle. Bulls are white, grey or black in coat colour. Body is bigger than the Kankrej cattle. Hairs are short and straight. The muzzle colour is black in majority of animals; however, pinkish muzzle is also seen. Hoof colour is invariably black. Tail switch is black, greyish or mixed. The age at first calving and inter-calving period is reported to be 3.0-3.5 years and 12-15 months, respectively. Average peak milk yield is reported from 6 to 18 litres. The lactation length varies from 8 to 12 months. The milk contains 4.5 to 5.0% fat and 8.5 to 8.8% SNF.

Sheep breeds

i) **Chitarangi Sheep of Rajasthan:** Chitarangi is a good carpet wool type sheep population, distributed in Fazilka and Muktsar districts of Punjab, Ghadsana and Anupgarh tehsil of ShriGanganagar districts of Rajasthan and nearby areas. Coat colour is white with reddish brown patches around eyes, muzzle and on ear. Ears are large with serrations at distal end of ear pinna in most of the animals. The Adult body weight of males and females varied from 40 to 95 kg in males and 26 to 74 kg in females. The fleece is good carpet type with fibre diameter 42.22 µ and staple length 5.90 cm.

ii) **Dumba Sheep of Rajasthan:** Dumba is found mainly in Jaipur, Nagour and Ajmer districts of Rajasthan. The coat colour is white and brown mostly. Ears are large in size. The deposition of fat in the tail is a distinct characteristic. Average adult body weights of male and female were 90.92 and 66.33 kg, respectively. Main objective of rearing and keeping these animals by entrepreneur or live animal traders is to fetch a huge sum of money during the Eid festival as they have great aesthetic and religious value. Elite people spend huge money on purchasing these animals. The market price of these animals in Mumbai and other metropolitan cities is very high as claimed by entrepreneurs. Adult males are sold at the rate of Rs 90000 to 150000, female Rs 70000 and lambs Rs 15000-30000 in the market.

Goat breeds



i) **Totapari goat:** This breed is closely related to the sheep as both are in the goat-antelope subfamily Caprinae. Totapari is one of the oldest domesticated species, and have been used for milk, meat, hair, and skins over much of the world. Totapari goats are extremely curious and intelligent. They are also very coordinated and widely known for their ability to climb and hold their balance in the most precarious places. This makes them only ruminant able to climb trees, although the tree generally has to be on somewhat of an angle. Due to their intelligence, once a goat has discovered a weakness in the fence, it will exploit it repeatedly. They are also very coordinated and widely known for their ability to climb and hold their balance in the most precarious places. While goats are generally considered hardy animals and in many situations receive little medical care, they are subject to a number of diseases.

ii) **Sojat goat:** One of the famous meat goat originated in Rajasthan. It is distributed in Sojat, Phalodi, Pipar, Jodhpur and other small regions of Rajasthan. They are heavy in size and tall in height and very well suited for semi-stall feeding having only 2 months of lactation period. It is in high demand during Bakrid. It is cross bred from the Jamnapari goat. It is primarily farmed for its meat as the milk yield is low, giving only 65 kg per lactation period. It is commonly sacrificed during the Bakri-Eid Festival. Skin color is White with spots.

Donkey

i) **Sindhi donkey:** Sindhi donkeys are reared by Kumhar, Sansi and Bhil Communities in Barmer and Jaisalmer districts of Rajasthan. They are well adapted to feed, fodder and water scarcity, endemic to this region. About 1-6 donkeys are kept per household. The Sindhi donkeys are able to carry about 100 kg of load as back pack even on sandy tracts. They are also used extensively in carting and ploughing. The donkeys of Sindhi breeds are of smaller size with leaner built. The predominant coat colour is light brown with small percentage of brown and grey animals. The belly, inner surfaces of legs, ventral side of neck and inner sides of ears are generally of lighter shade or white in most animals. The small manes are present which are usually of darker shade than the rest of the body colour. The face is longer and thinner with an average length of 46.5 ± 3.22 and 45.77 ± 3.1 cm, in male and female, respectively. The forehead is slightly convex. The nasal bone is straight to slightly concave. The heights at withers of male and female animals are 98.8 ± 3.9 and 97.93 ± 4.9 cm, respectively.

SP-01

CHARACTERISATION AND EVALUATION OF THO-THO CATTLE OF NAGALAND

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Surveys were conducted in 24 villages of 4 districts of Nagaland i.e. Kohima, Phek, Zuhneboto and Dimapur to characterise Tho-Tho cattle of Nagaland. A total of 242 cattle of different age and sex including 186 Tho-Tho and 56 desi/non-descript were recorded for physical and ten different morpho-metric traits. To know management and performance of Tho-Tho cattle 76 farmers were interviewed from these districts. It was observed that Tho-Tho cattle mainly reared for beef. In the state people preferred beef over pork. Cattle population of the state showed sharp decline of 51% during the years 2007-2012 and needs immediate attention. Based on different physical and morphometric traits, it may be concluded Tho-Tho cattle are distinct as compared to indigenous cattle of Tripura, Mizoram, Manipur and Siri of Sikkim. Tho-Tho- cattle were larger in size as compared to desi/non descript cattle of the state. Management and performance are more or less similar in the whole north-east region i.e extensive system of management. Multi-variate canonical discriminate analysis using different morphometric traits of indigenous cattle of Manipur, Meghalaya, Mizoram, Nagaland, Sikkim (Siri) and Tripura showed that Siri (Sikkim) and Tho-Tho (Nagaland) were significantly different than other indigenous cattle of the region and it was supported by physical traits also. Therefore, it is recommended that Tho-Tho cattle population may be registered as distinct cattle breed from Nagaland.

SP-02

CHARACTERIZATION OF KONKAN CATTLE POPULATION OF WESTERN GHAT REGION OF MAHARASHTRA

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Konkan cattle are distributed in Thane, Palghar, Raigad, Ratnagiri and Sindhudurg districts of Konkan region of Maharashtra and adjacent parts of Goa. For phenotypic characterization of this cattle population, 11 body measurements and physical traits of 609 animals belonging to different age groups and sex were taken in Ratnagiri, Sindhudurg and Raigad districts of Maharashtra. A total of 152 farmers of these three districts of Maharshtra were interviewed for general management practices followed for cattle husbandry. Data collected from three districts of Konkan area was pooled and analyzed. The farmers keeping Konkan cattle were 11.4% illiterate and rest were literate. The land holding of about 80% farmers was up to 5 acres. Grazing was the main source of the feeding, however, farmers also offer green grasses collected from forest and 1-2.5 kg of concentrate to lactating animals and bullocks. The housing of the animals was closed type (66%) with full/half walls made up of thatched, mud or brick. The roof was slanting in shape made up of thatched (61.5%), earthen type or sometimes concrete (38.5%). The sanitation and ventilation of the animal houses were poor (68.9%). The breeding of animals was generally through natural mating at the time of grazing. The coat colour of animals was generally brownish red (45%)or black (24.5%) however, animals of brown, white or mixed coat were also seen. The colour of muzzle (79.8%) and tail switch (90.9%)was generally black but in some animals carroty/mixed muzzle or creamy tail switch was also seen. The forehead was small and straight, sometimes slightly concave. The horns were straight in most of the animals and orientation of horn was outward, upward and backward. Udders are small in size; teats are small, cylindrical with pointed/ rounded tips. The hump and dewlap are small to medium in size in cows and medium to large in bulls. The animals were small in size with compact body. Body length, chest girth, height at withers, paunch girth, face length, face width, tail length with switch, tail length without switch, horn length, horn circumference and ear length were obtained as 101.48±0.41, 134.10±0.60, 100.78±0.50, 141.05±0.71, 41.09±0.19, 19.43±0.14, 85.37±0.59, 67.82±0.56, 19.82±0.54, 14.11±0.21, 18.30±0.13 cm, respectively in cows and 109.29±0.63, 146.55±0.95, 106.54±0.53, 151.71±1.07, 44.70±0.25, 23.13±0.15, 92.10±0.85, 72.12±0.68, 23.91±0.67, 19.05±0.25, 18.45±0.14 cm, respectively in bull/bullocks. The animals are hardy and well survived in hot and humid conditions of the coastal area. The average daily milk production is 2.23 kg; generally 1-2 kg in a day however; few elite animals with milk production of 5-6 litres were also seen. The age at first calving, calving interval and lactation period were obtained as 49.27±0.56 m, 17.21±0.35 m, 226.53±6.22 d, respectively. The animals are used for the agricultural operations in area. Microsatellite genotyping of 48 DNA samples of Konkan cattle using 25 Microsatellite markers was carried out and data was analyzed. The parameters like actual number of alleles (9.69), expected number of alleles (4.36), observed heterozygosity (0.66), expected heterozygosity (0.73) and PIC values (0.65) were estimated and within and between breed (with the cattle breeds of Maharashtra and Malnad Gidda) genetic diversity were also estimated. The bottleneck analysis indicated absence of any recent bottlenecks in the population. The Nei's genetic distances with 14 Indian cattle breeds indicated that Konkan cattle population was clubbed with Malnad Gidda breed of cattle, which is also a dwarf cattle breed of western ghat area of Karnataka state. The population of Konkan cattle is adequate in its breeding tract and this unique cattle population well deserves for status of a breed and therefore registered as cattle breed of India.

SP-03

PHYSICAL CHARACTERISTICS AND BREED DESCRIPTOR OF KENKATHA CATTLE

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A planned scientific survey of *Kenkatha* breed under ICAR ad-hoc project on the basis of questionnaire developed by NBAGR was conducted in breeding tract and the detailed physical characteristics of the breed were recorded. The body was short, deep and compact.Body colour varied from grey-dark grey (38%) to black (62%). Black colour on neck, shoulder, hump and quarters was the characteristics of the bulls. Cows and bullocks were generally dark grey. Headwas short in length with dished forehead and prominent poll. Muffle was slightly upturned and was black in all the animals. Eyes were placed wide apart with black rims. The eye lids were also black in all the animals. Ears were short, pointed, carried alert and the orientation was horizontal in 78% of the animals. Horns were medium sized emerging from outer angle of polls, going in a markedly forward and upward direction and terminate in sharp points (80%). Usual colour of horns was black (97%). Neck was short, thick and strong. Dewlap was small (41%) to medium (59%) in size and was not pendulous. The hump was small (47%) to moderate (53%) in size; welldeveloped and erect in bulls. Sheeth was generally pendulous and the naval flap was medium (59%) to small (41%). Legs wereshort, straight and strong with hard and black hooves. Tailwas moderate in size, well set on the body ending in a black-bushed switch reaching up to the fetlock in all the animals. Udder was small and round (45%) or bowl in shape (55%). Fore and rear udders were medium to small. Teats were funnel shaped (66%) or cylindrical shaped (34%). Milk veins were medium (38%) to small (62%). The Temperament of majority of animals was moderate (40%) to tractable (55%). Small proportion of animals (3.5%) also displayed wild temperament.

SP-04

GEOGRAPHICAL DISTRIBUTION, MANAGEMENT PRACTICES AND UTILITY OF KOSALI CATTLE AT NATIVE TRACT

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Kosali, the first breed of cattle from Chhattisgarh state has been registered as 36th breed of cattle. These animals are smaller in size and are well adapted to the existing agro-climatic conditions of the region. In the present study, a field survey was conducted to find out the geographical distribution, management practices and utility of the Kosali cattle. This study revealed that Kosali cattle are mainly distributed in the Central Plain Region of the state. They are fed in groups and individually. Kosali cattle owners (96.49%) grow fodder as paddy and gave un-chaffed dry fodder. The concentrate feed, which comprises of broken rice and rice polish (Kodha) may sometimes be supplemented to the lactating cows (at the time of milking) and working bullocks. The green fodder is rarely grown and naturally grown grasses are available during rainy season only and provided to the animals. The general practices recorded were to tie Kosali cattle mostly during night hours (88.69%) in kaccha houses (83%). Natural mating is the only mating system in the entire breeding tract. About 70% farmers are using Kosali animals for milk and agriculture operations. In conclusion, Kosali cattle are well adapted to the existing agro-climatic conditions of the region. They have excellent capacity of heat tolerance and disease resistance and can thrive well under the poor feed stuffs available in the state. Appropriate breeding strategies, management and conservation models should be designed for overall improvement of this breed.

SP-05

PERFORMANCE EVALUATION OF DUMBA SHEEP IN SEMI-ARID REGION OF RAJASTHAN, INDIA

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In India, Dumba sheep are maintained by sheep farmers and live animal traders in Jaipur, Nagaur and Ajmer districts of Rajasthan, Delhi, Malerkotla tehsil of Punjab and Muzaffarnagar district of UP. Characterization of Dumba sheep was undertaken through survey of the flocks in and around Jaipur, Ajmer and Naguar districts of Rajasthan. A number of owners reported that the sheep maintained by them were Turkish Dumba. The fat-tailed Dumba sheep are hardy and able to withstand the tough challenges of desert life. Therefore, these animals exhibit promising growth rate and attain high body weights when maintained under semi intensive and intensive system of management under arid and semi-arid conditions of Rajasthan in India. During the survey information were recorded on phenotypic characters body biometry and performance traits of about 98 animals (64 adults and 34 lambs) from 10 farmers' flocks. The animals are large in size with a fat tail, a characteristic of Dumba sheep. The coat colour is white with brown face and legs. However, animals with black coat colour or with black or brown patches of different shapes and sizes were also observed during survey. The adult body weight of males and females were 90.92 ± 6.39 and 66.33 ± 2.50 kg, respectively, which varied from 54 to 124 kg in males and 47 to 96 kg in females. The overall body length, height, chest girth, paunch girth, face length, face width, ear length and tail length were 74.02± 0.79, 77.97 ± 0.68, 95.12 ± 0.94 96.44 ± 1.03, 21.42 ± 0.21, 9.51 ± 0.10 and 18.71 ± 0.30 cm, respectively. Both the sexes are polled; however, horns were observed in some males. Body weight of lambs in the age groups of 1-3 and 3-6 months ranged between 11-32 and 23 -60 kg, respectively. The sheep keepers reported a huge demand of Dumba animals for the religious tradition of sacrifice during *Bakr-Eid* festival. The market price were reported to range from Rs 60000 to 125000 for males, Rs 10000 to 70000 for females and Rs 25000 to 40000 for lambs depending upon the age, body weight and conformation of the animals, demand in the market and penchant of the purchaser. The adaptation of Dumba sheep to the arid and semiarid climate of Rajasthan, promising growth rate and their market demand indicated a fair scope of its propagation and development in India.

Keywords: Dumba sheep, performance evaluation, body weight, body biometry.

SP-06

STATUS OF WORLD'S UNIQUE ANIMAL GENETIC RESOURCE OF LADAKH

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Nature has its own role to play in selecting the best germplasm which can thrive and which are adapted to extreme type environment. The process of selection though it takes thousands of years but the result is birth of a perfect organism, one such unique example is the highly diverse and unique domestic and wild animals of Ladakh. It is the only typical cold arid zone of our country with extreme climate and hostile condition, the area makes its floura and fauna a unique one and distinct from rest of the country. Around 60% of the farmers of Ladakh are Pastoralist and 40% of the farmers are agriculturist and the majority of the economic income comes from animal rearing in Ladakh. It has some of the world's best animal genetic resource in the form of Pashmina goats, Changthangi Sheep, Semi domesticated Yak, Bactrian (Double Humped Camel) Zanskari horse and *Bos Taurus* in the form of local cattle. All this livestock contribute a lot to the income of the farmers and the Changthang people are completely dependent on this livestock rearing. All this livestock are reared on extensive system on high altitude pastures grasses. Ladakh is a world leader in producing the finest Pashmina (fibre diameter less than 12μ) and a store house of the best germplasm in the form of Changthangi goats. In our country the Changthang region alone produces around 45,000 kgs of raw Pashmina fibre every year from about 2.34 lacs of Changthangi goats, which forms 97% of the total Pashmina production of our country. The Changthangi breed of sheep is famous, for its wool and mutton production however its population has drastically reduced during the past few years from 113554 in the year and presently 34453 only in 2013. In our country Jammu and Kashmir state has the highest population of Yaks and its hybrids especially Ladakh division which has the highest population of Yaks distributed in both Kargil and Leh districts.The yak population has a sharp decline from 18904 in 2007 to 1340 in 2008 in Leh district (SHB 2007-08) similar pattern is also noticed in Kargil district (census 2007-08). Zanskari horse, one of the precious germplasm adapted to the hypoxic conditions of high altitudes of Ladakh, is already endangered and needs immediate attention for its conservation. Its present population is around 3000 only. Another important livestock species is Bactrian camel, which has also a critical population of hardly about 157 and also declining. The local cattle which is a non-descriptive breed is very well adapted to the hypoxic condition of Ladakh, can thrive very well on meagre feed and highly resistant to most of the contagious disease. Certain reports on the local cattle indicate it to the *Bos Taurus* species. There are around 36231 (2008) local cattle in the district. The local poultry layer bird, very well adapted has extinct due lack of conservation programme. Ladakh has been deprived of basic research facilities in animal science sector for so many years due to which these unique genetic resources are declining in terms of numbers as well as in production. If necessary steps are not taken immediately a time will reach that all this precious animals will be lost forever.

Keywords: Ladakh, Animals, Population, Livestock.

SP-07

PRELIMINARY STUDY ON CHARACTERIZATION OF TELENGANA GOATS

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Human prosperity has always been linked with the livestock wealth. Andhra Pradesh has some of the richest livestock resources in the Country and is one of the most advanced states in Animal Husbandry activities. The state has the world famous breed of Ongole cattle, Aseel breed of poultry, Nellore breed of sheep. Presently Andhra Pradesh stands first in poultry (1005.80 lakhs) and sheep population (210.15 lakhs), second in buffalo population (107.68 lakhs), seventh in goat population (64.27 lakhs), and eighth in cattle (94.24 lakhs) and pig population (5.49 lakhs) in the Country. Although, the state has good number of goats which may be consisting of several smaller sub populations. So far, no uniform or homogenous population has been reported which can be a suitable candidate for breed status assignment. With the objective of searching population having homogeneity, the study has been taken on characterization of goats of Telengana state which is newly created (29th) state from Andhra Pradesh. The survey was started with recording of information on goats of Mahabubnagar, Nagarkurnool and Jogulamba Gadwal districts of Telengana. Here, goats are reared mainly by SC/ST communities having no or little land holdings. Flock size observed ranged from 4 to 70. The phenotypic traits like coat colour, type of ears, horn, head profile and other face features were recorded on 150 goats belonging to different farmers (or flocks) in different villages. The biometric traits and body weights were also recorded. It has been observed that goats with coat colour black, white, brown, with or without spots, splashes, with or without facial stripes existed in the flock. Animals are with long tapering mouth, medium sized drooping ears, long and thin legs, thin and pointed horn curving backward. Wattles are present in some animals. Nose is either roman or flat. Muzzle is black/brown. Horn and hooves are grey. The average measurements (cm) for height at withers, length, chest girth, paunch girth, face length, horn length, ear length and tail length of 97 adult females (> 18 months) were 70.33±0.59, 66.64± 0.54, 80.39± 0.62, 81.74± 0.76, 18.49± 0.21, 13.98 ± 0.44, 10.80± 0.64, 12.89± 0.16 and 72.88±1.00, 67.13± 1.01, 79.79± 1.35, 79.67± 1.32, 18.17± 0.41, 14.30± 1.10, 13.83± 0.34, 13.33± 0.40, respectively of 24 males. The average body weights (kg) were 37.09± 0.71 and 38.65± 1.85 in females and males, respectively. Prolificacy is good with singlet in first kidding and 60 % twining in subsequent kiddings. Triplets in few cases but quadruplets rare were seen. Goats reared purely on jungle/pasture grazing. Breeding is through natural mating. The study is in progress to cover more animals from other districts.

SP-08

GOAT PRODUCTION IN UTTARAKHAND: PRESENT STATUS AND FUTUR PROSPECTS

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Uttarakhand has a total geographic area of 53,483 square km, of which 86% is mountainous and 65% is covered by forest. Goat farming can be ideal for the state like Uttarakhand with huge resources and potential in it. Uttarakhand has a total of 1.36 million goats in the state mainly reared for meat purpose, but not evenly distributed out of which 75% are with poor farmers. Goats are found to be more widely distributed than sheep. It is reported that on free range grazing, goats are 2.5 times more profitable than sheep. About 0.53 million goats (38% of the population) were slaughtered in the year 2012-13. The total meat of 0.7 million tonnes produced in the state, (2012-13) making it the second largest contributor after buffalo meat. Breeds like Gaddi, Chaugarkha, Black Bengal, Beetal and Barbari are found in the state and it is the home tract of Udaipuri, Pantja and Chaugarkha (yet to recognise as a breed). The home tract of Chaugarkha is found to be parts of Almora district. 'Udaipuri' is another breed available in the district of Pauri. The local breeds are kept at a low plane of nutrition and are reported to have low feed conversion efficiency. The main constraints for goat farming are nutritional deficiency, difficulties in the selection of superior animals and lack of systematic effort for breed up-gradation/selective breeding. Other than these problems we need to focus on shifting production system from complete open grazing to semi-grazing with partial stall feeding, vaccination at regular interval, proper selection of sire and dams, training of local youth for value added materials, and establishing regulated and assured market to farmers.

SP-09

PHENOTYPIC TREND IN PERFORMANCE TRAITS OF NATIVE NON-DESCRIPT CHICKEN GERMPLASM OF HIMACHAL PRADESH

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Native non-descript chicken germplasm is playing an important role in development of location specific chicken stocks suitable for rural backyard poultry production across several developing and underdeveloped countries. In the present study, on-farm performance evaluation for various growth, sexual maturity and egg production traits was done of native chicken population established through procurement of local non-descript birds from different region of Himachal Pradesh and further refined at the poultry farm under AICRP on poultry breeding (Rural Poultry), Palampur. First four generations of the non-descript population produced through selective breeding was evaluated. The performance traits evaluated were growth (Chick weight, 4th week BW, 8th week BW, 12th week BW, 20th week BW and 40th week BW), age at sexual maturity (ASM), hen housed egg production (HHEP), hen day egg production (HDEP) and survivor egg production (SEP) at 40 weeks, 52 weeks and 72 weeks of age and egg weight at 28 weeks, 40 weeks, 52 weeks and 72 weeks of age. The phenotypic means and variability for different traits was estimated generation wise and the phenotypic time trend over the generations was estimated for various performance traits. The analysis revealed positive phenotypic trends in day old chick weight (0.70 g), 20th week body weight (14.8 g), negative trend in age at first egg (-4.8 days) and age at 25% HHEP (-3.5 days), positive trend in egg weight at 28-week (2.1 g), 40-week (1.5 g) and 52-week (0.4 g). The hen day egg production at 40 weeks, 52 weeks and 72 weeks of age showed positive phenotypic trend of 3.8, 6.1 and 2.3 eggs. Further, hen housed and survivor egg production also showed positive trend estimates at 40, 52 and 72 weeks age. Negative or declining trends were observed in growth traits *viz.* 4 weeks BW (-16.4 g), 8 weeks BW (-358.8 g), 12 weeks BW (-364.0 g) and 40 weeks BW (-102.9 g). The results of present analysis indicated the effectiveness of the selection along with improved management for bringing improvement in egg production traits of the population in succeeding generations.

SP-10

PERFORMANCE OF KANNIADU AND BOER X KANNIADU CROSSBRED KIDS IN AN ORGANIZED FARM

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Kanniadu is one of the popular goat breed of Tamilnadu mainly reared for meat production. Boer goat is one of the best known meat breed in South Africa and widely used for crossbreeding in tropical countries. The present study was undertaken to assess the performance of Kanniadu and Boer x Kanniadu crossbred goats maintained at Post Graduate Research Institute in Animal Sciences, TANUVAS, Kattupakkam. The study was conducted for duration of six months under semi intensive system of management with eight kids in each group. Body weight and body measurements were initially taken and subsequently once in fortnight. The results revealed that Boer x Kanniadu recorded the highest post weaning body weight (17.30±0.90 kg) with post weaning average daily gain (49.93±1.75g). All the body measurements increased with live weight and age more in Boer x Kanni crossbreds. The slaughter studies carried at the end of the study indicated highest dressing percentage in Boer x Kanni (45.01±2.42) compared to Kanniadu (43.77±1.00). Significant difference ($P<0.01$) was observed in meat, bone, fat ratio in the carcass of the two breeds studied.

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SP-11

STUDIES ON THE INDIGENOUS CATTLE GENETIC RESOURCES OF WEST BENGAL THROUGH MULTIVARIATE ANALYSIS

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West Bengal possesses the 3rd largest cattle population of the country. Indigenous cattle possess some remarkable properties, although they are poor milker. Draughtability, droughtability, heat resistance, less susceptibility to diseases droughtability and highly adapted to local agroclimatic region of West Bengal are the beneficial traits for indigenous cattle. The animals are comparatively docile. In the present study, we had phenotypically characterized cattle based on qualitative and biometrc traits (Body length, wither height, heart girth, paunch girth, ear length, ear width, face length, distance between two horns, distance between two ears, horn length, horn circumference, tail length, fore limb length, hind limb length, forehead length, forehead width) from different agroclimatic regions of West Bengal. Various multivariate analyses were employed for genetic study of cattle. Principal component analysis (PCA) with Kaiser Normalization explains body conformation and identifies the component which explains most of the variations, thus identifying the promising traits. Other multivariate analysis techniques employed are multi variate cluster analysis with hierarchical classification and K-means analysis. Indigenous cattle of West Bengal were observed to be of short stature with less body length and wither height and white is the predominant coat colour. "Bengal cattle" was observed to be genetically distinct from other cattle breeds of India. Studies are in progress for its molecular characterization for further confirmation.

SP-12

GENETIC IMPROVEMENT OF SAHIWAL CATTLE THROUGH ASSOCIATED HERD PROGENY TESTING

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Sahiwal is one of the important cattle breeds of India which has potential for higher milk production in comparison to other indigenous cattle breeds. Considering the importance of this breed for sustainable dairy farming, genetic improvement programme is implemented since 2010 through associated herd progeny testing programme under AICRP on Cattle for their conservation and propagation. The associated herds of the project are available at GLF Hisar, GADVASU, Ludhiana, GBPUAandT Pantnagar, CKU, Durg, Gaushala Bhiwani and NDRI, Karnal. NDRI, Karnal is identified as the germplasm unit (GP unit) and frozen semen doses of genetically superior young bulls maintained at this unit are being supplied to the associated herds for AI and efforts are taken to increase the conception rate to a considerable extent. A total of 25 bulls in three sets have so far been inducted in the program. A total of 157548 semen doses were frozen, out of which, 73746 frozen semen doses were utilized/supplied/sold. The numbers of cows covered for an insemination in different sets was 4719 and 1084 daughters have so far been produced. Two hundred twenty-two daughters from first set have reached the age of first calving, out of which, 128 completed their first lactation. A total of 83802 doses of frozen semen were available on 31st December, 2016. The overall age at first calving, first service period, first dry period, calving interval of Sahiwal cows maintained at germplasm unit of NDRI, Karnal were 1189.55±30.14 (39.1 months), 145.1±26.2, 91.0±11.2, and 402.4±22.6 days, respectively. The average estimates for first lactation 305-day milk yield, total first lactation milk yield, total lactation milk yield, all lactation 305 days milk yield and first peak yield were recorded as 1850.70±177.9, 2001.11±216.3, 2384.43±157.16, 2212.80±131.77 and 10.90±0.8 kg, respectively. The average first lactation milk yield of the 69 Sahiwal daughters of first set of bulls was 2066.57 ± 95.91 kg. The execution of the project has improved the performance of Sahiwal cattle over the years and continuous efforts are being made to propagate this valuable germplasm to improve its production performance.

Keywords: Associated herds; EBV; Germplasm; Milk yield; Progeny Testing; Sahiwal breed; Service period

SP-13

FIRST LACTATION PRODUCTION PERFORMANCE OF MEHSANA BUFFALOES UNDER FIELD PROGENY TESTING PROGRAMME IN SEMI-ARID REGION OF GUJARAT

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Among the well-recognised breeds of buffaloes in India, Mehsana buffalo is famous for its persistency and regular breeding. The present investigation was carried out using data of first lactation production records of 7825 Mehsana buffaloes sired by 200 bulls spread over a period of 25 years (1989-2013), collected from the Dudhsagar Research and Development Association

(DURDA), Dudhsagar Dairy, Mehsana to obtain the genetic and non-genetic parameters of first lactation total milk yield (FLTMY), first lactation length (FLL), first wet average (FWA) and average test day fat yield (ATDFY). The effects of non-genetic factors were assessed by fixed linear model. Heritability and phenotypic/genetic correlations were estimated by paternal half sib correlation method. The least-squares means obtained for FLTMY, FLL, FWA and ATDFY were estimated to be 1914.79 litre, 309.77 days, 6.24 litre and 0.43 kg, respectively. Period of calving, season of calving and age at first calving group was significant for all the traits. Cluster had significant effect on all the traits except FLL. The heritability for FLTMY, FWA and ATDFY was high in magnitude and thus indicates sufficient additive genetic variance for affecting the selection to improve the traits genetically.The first lactation total milk yield had positive phenotypic and genetic correlation with FLL, FWA and ATDFY. Very high and significant estimate of heritability of ATDFY indicated that further selection in Mehsana buffaloes may be based on this trait.

SP-14

GENETIC BASIS OF HEAT TOLERANCE IN CATTLE

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Heat tolerance is broadly defined as ability of the animal to tolerate heat- means grow and produce economically under high temperature. An estimated annual loss due to direct thermal stress on livestock is about 1.8 million tonnes of milk (Rs. 2661.62 crores) that is, nearly 2% of the total milk production in the country. Heat stress has adverse effect on production, reproduction, health, nutrition and behaviour in animals. Therefore, heat tolerance now-a-days is an important aspect of research. Thermotolerance appears to be a quantitative trait influenced by many regions of the genome. Genomic studies have identified regions of the genome that appear to be important for regulation of body temperature in both dairy and beef cattle. Heat stress is a result of genotypic factors, environmental factors and their interactions. The environmental factors can be managed with better managemental practices but genetic factors are permanent. Therefore, genetic approach for heat tolerance e.g. selection and breeding can be undertaken to produce heat tolerant animals with better producing ability. The heritability estimates for heat tolerance traits like respiration rate, body temperature regulation, rectal temperature, hair shedding, etc were found to be moderate to high. Genomic selection with the help of *Bovine SNP50 Bead Chip* can make it possible to identify genetic markers that predict thermotolerance.The SNPs need to be identified for improved heat tolerance in animals by association analysis with heat tolerant traits.These gene/SNPs can act as attractive candidate for heat tolerance and can be used as a genetic marker to select appropriate breed for hot climates.By application of traditional as well as genomic means of selection, the traits related to heat tolerance can be improved in animals.

SP-15

SELECTION OF PIGS FOR DISEASE RESISTANCE

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Disease occurrence is a major problem in livestock farming. Genetic selection for disease resistance is considered to be a better alternative to control diseases in livestock. Early methods to select animals for disease resistance were direct - either by observing the animals for disease resistance under normal production conditions or by challenging the animals to specific disease causing organisms. Later on, indirect selection methods such as vaccine challenge and in vitro tests (peripheral blood monocyte count, neutrophil and lymphocyte activity in response to antigens) were used. With the advent of new techniques in molecular biology, gene mapping, bioinformatics and immunology, research in disease resistance gained momentum resulting in development of an effective method called marker assisted selection (MAS). MAS provides a reliable selection tool to identify the animals carrying desirable genes at an early stage - either at birth or even earlier. MAS for a trait of interest using molecular markers can be practiced by two approaches - candidate gene approach and genome-wide scan approach. The candidate gene approach analyses how a particular gene with known physiologic pathway and biological function influences a trait of interest. Several candidate genes for disease resistance have been identified in pigs. On the other hand genome-wide scan and association (GWAS) approach analyses the entire genome to identify genes influencing a trait of interest. This is done through quantitative trait loci (QTL) analysis and SNP chips. In pigs, 151 QTLs for disease susceptibility have been identified so far. The single nucleotide polymorphism (SNP) chips available now help us to perform association studies with thousands of markers in the entire genome. New 'porcineSNP60' chip includes 64,232 SNPs distributed throughout the pig genome. Thus, selection for disease resistance is a fascinating research area with tremendous possibilities to develop a resistant stock of pigs.

SP-16

MULTIVARIATE ANALYSIS REVEALS DISTINCT BREED IDENTITY OF HOOL BUFFALO FROM THE OTHER BUFFALO BREEDS OF INDIA

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Hool buffaloes are the inhabitant of the dry-arid region of West Bengal. Phenotypic characterization including qualitative traits and Biometrical traits (Body length, wither height, heart girth, paunch girth, ear length, ear width, face length, distance between two horns, distance between two ears, horn length, horn circumference, tail length, fore limb length, hind limb length, forehead length, forehead width) were analyzed . Various multivariate analysis were employed for genetic study of Hool buffalo. Principal component analysis (PCA) with Kaiser Normalization was identified which explains the components and most of the variation, thus identifying the promising traits for further analysis. Multivariate cluster analysis with hierarchical classification was employed to identify the genetic distance of Hool buffalo with other buffalo breeds and the development of phylogenetic tree to predict evolutionary significance. K-means cluster analysis confirms the above findings. Hence it may be concluded that Hool buffalo was definitely different from other buffalo breeds of India. Hool buffalo is characterized by blackish copper coloured body with excellant draughtability and high disease resistance ability, thus a promising and first reported draught buffalo breed for future India.

SP-17

INDIGENOUS CATTLE A SUSTAINABLE RESOURCE FOR INDIAN FARMERS

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Indian cow breeds are a crucial part of the country's ecological heritage. Since ancient times, different breeds were developed in different parts of the subcontinent by selecting the best animals for preferred traits such as their milking capacity, draught power, feeding requirements, capacity to adapt to local weather, immunity, etc. The purity of such breeds was maintained with great discipline and wisdom in each geographical pocket known as a breeding tract which is lost now days. Over the years, this has justified a policy that discards Indian milch breeds to promote exotic crossbreed animals. Due to this neglect, quality desi cows have become rare. But it is not just Quimbanda Cal- the Gir wonder in Brazil, that is proof of how desi cows can perform with adequate support and care. It is true that, maintained well, crossbreeds often produce milk in excess of 30 kg per day. But as their average yield in India is stuck at 6.63 kg, it is clear that the majority of these cattle, in the care of resource-strapped farmers, are not delivering to potential. In such a scenario, quality desi cows with an average yield of 8-20 kg would be a far more lucrative option. Again, it is true exotic crossbreds can produce 4,500 kg per annual lactation. Desi cows, on the other hand, rarely cross 2,500 kg per lactation in standard home conditions. But, crossbreds rarely lactate more than four times; while desi lactate 10-12 times. In effect, this means a crossbred can only produce 18,000 kg of milk in a lifetime, while a desi cow can give up to 25,000-30,000 kg. The practice of crossbreeding ought to be very exact and carefully monitored. But unlike Israel, no records of herds and their mating patterns have been maintained in India. So, though the first generation of exotic crossbreds showed encouraging results, as they were randomly mated, the whole thing began to backfire. A dramatic turnaround is still possible. A timely policy shift and public investment in local breeds can revive our precious bio-diversity in 25-35 years- which amounts to four to five cattle generations. We still have the local breeds, frozen semen and the knowledge owned by farmers.

SP-18

SOCIO-ECONOMIC STATUS AND PERCEPTIONS OF KOSALI CATTLE KEEPERS AND CONSTRAINTS TO CATTLE PRODUCTION IN CENTRAL PLAIN REGION OF CHHATTISGARH STATE

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The present study was conducted to find out the socio-economic status and constraints to cattle production in Central Plain Region of Chhattisgarh state. Total 800 respondents from three districts of the region were selected. Sex, age, family size, education, land and livestock holding, annual income, occupation and herd size factors were considered to study the socio-economic status. It was observed that majority (95.42%) of the respondents had male headed ownership, more than 50 per cent in above 30 years of age category. The average family size observed was 6.21 persons. It was found that only 66.56 per cent of respondents were literate. The percent of landless, sub-marginal and marginal farmers is more than 50% and have less than 0.5 hectare land. Most of the respondents (47%) found in the category of annual income less than rupees 20000. The main profession of livestock owners was agriculture (68.44%) followed by agriculture and some other small work. Most of the respondents had small herd size. Shrinkage of grazing land, scarcity of green fodder and concentrate and poor management were the major constraints to cattle or livestock productivity.

SP-19

CURRENT EFFECTIVE POPULATION SIZE ESTIMATION IN VRINDAVANI CATTLE FROM 50K SNP BEADCHIP DATA

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The present study was undertaken with the objective to assess the effective population size in one crossbred strain, i.e., "Vrindavani" (n = 24) maintained at Cattle and Buffalo farm, ICAR-IVRI, Izatnagar, Bareilly for the first time. Genotypic data were generated under Illumina Bovine50KSNP BeadChip for this strain. Effective population size (Ne) can be estimated from

information on linkage disequilibrium (LD) between SNPs across the genome. LD signatures can also arise from the admixture and genetic drift, which can be exploited to infer the demographic history. To calculate the effective population size by conventional method a proper recording of pedigree and family size is required. As in our population, we don't have enough recording system and the population is not stabilized, the effective population size can be calculated with the help of SNP genotyped data. The N_e was estimated with the help of two different softwares namely; Ne Estimator and SNeP. In Ne Estimator, N_e in recent generations were calculated by linkage model under the assumption of random mating and different critical values (0.05, 0.02, 0.01, and 0+) for MAF was set. The N_e was calculated over a total of 37014 loci in 24 Vrindavani animals. A total of 569675584, and 648499136 number of pairwise comparisons were performed for 0.05, and all critical values for MAF, respectively. Expected r^2 for the sample was 0.048 while overall r^2 estimated was 0.057. The N_e for 0.05 critical value of MAF was found to be 34.4, while for less critical values it was found to be 37 with 95% confidence interval. N_e was calculated in SNeP with the help of pairwise LD value keeping binwidth equal to 0.1Mb for *SNPs* and adjustment of recombination rate was done according to Sved and Feldman (1973). As Vrindavani population is still growing and not been stabilized, we calculated N_e for the last five generations keeping into account the year of its establishment as a crossbred cattle strain. The mean N_e for one, two, three, four and five generations before the current time period was found to be 13, 20, 26, 33 and 39, respectively. The census size of "Vrindavani" population maintained at IVRI Livestock farm is 464 for the year 2016-17, while the observed N_e is very low as compared to census size. This may be due to unequal sex ratio of breeding male to female and increased variance of family size of breeding bulls (V_k> 2). This gradual decays in N_e if not resolved may lead to severe inbreeding in the herd.

SP-20

FIELD MILK PERFORMANCE RECORDING IN BARGUR CATTLE

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Bargur cattle is one among popular cattle breeds of Tamilnadu maintained by traditional cattle keepers under zero- input system at Bargur hills in Western Ghats. The breed is well adapted to graze in hilly terrains. To conserve the breed a research station has been established under Rashtriya Gokul Mission. A scheme on field performance recording in Bargur cattle is being operated. In the first phase thirty Bargur cows were identified and included in the study. The cows were in first to eighth parity. Daily milk yield were recorded at fortnightly intervals for 180 days. Average milk yield recorded was 502 litres with a range of 300 to 1363 litres. Peak yield was attained during 2 months in 90 per cent of the cows. Average fat percent was 4.1 ranging from 3.4 to 5.1. Average SNF was 8.6 with a range of 7.9 to 9.1. The present study was done during the month of March to June, 2017 where severe drought prevailed in the region. There is good scope to improve milk production in Bargur cattle by supplementary feeding in addition to grazing.

SP-21

BODY MEASUREMENTS AND GROWTH PATTERN IN KENKATHA CATTLE

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The body measurements of 800 newly born calves maintained by the farmers with their mothers were recorded from birth to 10 months of age on monthly basis irrespective of sex to study the growth pattern of calves under ICAR ad-project. The mean body length, wither height, chest girth and paunch girth recorded at 1st month of age were 56.49±0.44, 67.37±0.50, 71.12±0.60 and 69.91±0.67 cm, respectively; which attained mean values of 83.45±0.33, 92.30±0.75, 106.02±0.87 and 111.39±1.48 cm, respectively at the age of 10 month. For 1-2 years age group the overall averages for body length, height at withers, chest girth and paunch girth were 93.6 ± 2.7, 94.7 ± 2.5, 109.3 ± 3.1 and 122.9 ± 3.2 cm, and 91.4 ± 2.1, 93.1 ± 2.4, 108.4 ± 2.7 and 114.4 ± 2.9 cm, respectively for males and females. The results showed that these measurements were comparable in the two sexes except for paunch girth for which on an average males measured 8.5 cm higher as compare to females. The corresponding figures for males and females in 2-3 years age group were found to be 105.8 ± 1.9, 110.1 ± 1.9, 127.1 ± 2.1 and 147.4 ± 2.8 cm and 105.6 ±1.9, 106.3±1.6, and 127.7±1.8 and 135.0±2.1 cm, respectively. In this age group also the mean values for body length and chest girth for the two sexes were comparable. However, for paunch girth and wither height on an average males measured higher by 12.4 and 3.8 cm, respectively. For bullocks and cows these measurements averaged to be 127.3 ± 0.5, 124.1 ± 0.65, 160.0 ± 0.4 and 178.4 ± 0.4 cm and 120.9 ± 0.04, 118.5 ± 0.5, 145.7 ± 0.4 cm and 154.7 ± 0.5 cm, respectively.

SP-22

GENETIC AND PHENOTYPIC CORRELATION OF 300 DAYS MILK YIELD WITH PERFORMANCE TRAITS IN GIR CATTLE

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High production efficiency in livestock production is an economically desirable attribute that targets ultimately for genetic improvement. In fact, the economy of dairy industry mainly depends upon the performance parameters of dairy animals; therefore, it becomes more pertinent to tackle out the means for ameliorating the performance efficiencies and their correlation by developing

certain guidelines for selection.The production records on 228 Gir cows with 1257 lactations sired by 52 bulls, maintained at Cattle Breeding Farm, Junagadh Agricultural University, Junagadh, Gujarat, India, for 24 years (1987 – 2010) were studied. The data were analyzed to study the genetic and phenotypic correlation of 300 days milk yield (300dMY) with different performance traits viz., lactation milk yield, lactation length, calving interval, age at first calving and dry period. The analysis revealed highly significant ($P<0.01$) genetic correlation between 300dMY and lactation milk yield, age at first calving and lactation length were 0.985 ± 0.015, 0.006 ± 0.178 and 0.744 ± 0.209, respectively. The estimates of genetic correlations between 300 days milk yield and calving interval (-0.100 ± 0.269) and dry period (-0.472 ± 0.217) were found in present study. Phenotypic correlations of 300 days milk yield with lactation length (0.456 ± 0.209), calving interval (0.171 ± 0.269), age at first calving (0.114 ± 0.178) and lactation milk yield (0.901 ± 0.015) were found to be positive and highly significant ($P<0.01$); whereas, phenotypic correlation between 300 days milk yield and dry period (-0.183 ± 0.217) was observed in present study.

Keywords: Genetic Correlation, Phenotypic Correlation, 300 days Milk Yield.

SP-23

COMPARISON OF DIFFERENT METHODS OF SIRE EVALUATION

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The least-squares (LS), simplified regressed least-squares (SRLS), Best Linear Unbiased Prediction of estimated breeding values (BLUP-I) and Best Linear Unbiased Prediction of expected breeding values (BLUP-II) methods for milk yield per day of first lactation length (MY/FLL)were used to estimate the breeding values of 27 Rathi sires from performance records of 281 daughters calved during 1988 to 2010 at Livestock Research Station, Nohar and Bikaner of Rajasthan Agricultural University, Bikaner, Rajasthan. Model for LS included fixed effect of sire, farm, period and season of birth ignoring the sire group effect. Model for BLUP included fixed effect of farm, period, season of birth and sire group as fixed effects and sires within sire group as a random effect. The lowest range of breeding value (3.674 litres/day) was estimated by LS method while highest range of breeding value (4.879 litres/day) was estimated by BLUP II method. The LS method is not suitable for evaluating the sires with lesser number of progenies per sire. BLUP indicates the real transmitting ability of a bull and is therefore a better estimate of the breeding worth of a bull. The estimates of rank correlation between BLUP-II and BLUP-I was 0.99 indicated that these methods were more or less similar in ranking the sires for their merit. However, better predictability of BLUP-II method could be concluded while appraising the genetic merit of Rathi sires. The sire Nos. 183, 302, 69,149 and 511 remained common in top five sires with the maximum breeding values both in BLUP – II and BLUP- I methods. These sires were recommended for extensive breeding purposes to effect rapid genetic improvement in Rathi cattle.

Keywords: Sire evaluation, MY/FLL, Breeding Value, LS, SRLS, BLUP-I, BLUP-II

SP-24

ACCURACY OF BLUP VS DFREML METHODS FOR RANKING OF SIRES

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The records of 1198 crossbred cattle daughters of 102 sires maintained during 1966-2010 at Instructional Dairy Farm of G. B. Pant University of Agriculture and Technology, Pantnagar were used to evaluate sires for their breeding performance. The data were analyzed to estimate the breeding values of sires using Best Linear Unbiased Prediction (BLUP) and Derivative Free Restricted Maximum Likelihood Method (DFREML).The average breeding values of sires were estimated by sire evaluation methods i.e Best Linear Unbiased Prediction Method (BLUP), and Derivative Free Restricted Maximum Likelihood Method (DFREML).The average breeding values of 68 sires evaluated for AFC were observed as, 1198.42 days and 1193.77 days. The average breeding values for FLMY were estimated 2710.46 kg, and 2680.29 kg, respectively. For first lactation period the average breeding values estimated were 324.01days, and 322.79 days and for first dry period the average breeding values estimated were 106.34 days and 101.56 days, respectively. The average breeding values for FCI were estimated 431.27 days and 424.73 days, respectively. For FSP the average breeding values estimated were 166.36 days, and 170.53 days and for lifetime milk yield the average breeding values estimated were 10371.02 kg and 10705.59 kg, respectively. The average breeding values for LTLL were estimated 1105.17 days and 1147.32 days using, BLUP and DFREML, respectively. On the basis of these results we can conclude that the estimated breeding values of sires for all the methods revealed that EBV'S of sires estimated by Least Squares Methods showed small genetic variation followed by BLUP in comparison to other methods.

The error variance of breeding values of sires were estimated and used in computing the relative efficiency of different sire evaluation methods. In the present study the BLUP method have the lower error variance for FLP, FDP, FCI, FSP and TLMY as compared to DFREML method and accordingly, it was adjudged the most efficient sire evaluation method.

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 than DFREML. The EBV's of sire revealed that BLUP method showed small genetic variation in comparison to Restricted Maximum Likelihood Method (DFREML).

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SP-25

ESTIMATION OF GENETIC, PHENOTYPIC AND ENVIRONMENTAL TRENDS IN PRODUCTION TRAITS OF THARPARKAR CATTLE

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A total of 284 performance records belonging to 63 Tharparkar cows in at least three lactations or more lactation spread over a period of fourteen years (2002 to 2016) were utilized to estimate the trends in various traits viz. age at first calving(AFC), service period (SP), calving interval (CI), dry period(DP), lactation length (LL), lactation milk yield(LMY), milk yield per day of lactation length(MYPD) and milk yield per day of calving interval(MYCI). The estimates of phenotypic trends for AFC, SP, CI, DP, LL, LMY, MYPD and MYCI were -11.054±9.41 days/year (0.70% of HA), 0.841±0.42 days/year (0.61% of HA), 2.061±1.04 days/year (0.496% of HA), 1.682±1.04 days/year (1.21% of HA), 2.70±2.31 days/year (0.95% of HA), 19.42±7.21 kg/year (0.96% of HA) , 0.033±0.07kg (0.60% of HA) and 0.023±0.03kg (0.55% of HA), respectively. Phenotypic trend was observed positive and significant for calving interval, service period and lactation milk yield. The genetic trends were estimated by using four methods as smith method 1(SM1), smith method 2(SM2),Least square method of Burnside and Legate (LSMBL) and Best Linear Unbiased Prediction method (BLUP). The estimates obtained by BLUP method had the lowest standard errors and statistically significant. The estimates of genetic trend by BLUP method for AFC, SP, CI, DP, LL, LMY, MYPD and MYCI were 13.64±6.8 (0.86% of HA), 0.42±0.156 (0.31% of HA), -0.098±0.184 (0.023% of HA), -0.697±0.35 (0.50% of HA), 1.40±0.31 (0.49% of HA), 3.90±1.99 (0.194% of HA), -0.062±0.014 (0.93% of HA), 0.099±0.07 (0.04% of HA), respectively. The genetic trends showed little upward increase in production and reproduction traits. For overall improvement in production, emphasis should be given to some reproductive traits like AFC and SP along with lactation milk yield while planning selection strategies.

Keywords: Genetic and phenotypic trends, BLUP, significant, non-significant

SP-26

EFFECT OF GENETIC AND NON-GENETIC FACTORS ON FIRST LACTATION REPRODUCTION TRAITS IN THARPARKAR CATTLE

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The present study was conducted on Tharparkar cows maintained at Livestock Research Station, Beechwal, Bikaner. A total of 91 records on age at first calving (AFC) spanning over a period of 12 years (2002 to 2013) and 83 records on first service period (FSP) and first calving interval (FCI) spanning over a period of 11 years (2006 to 2016) was subjected to least squares analysis using suitable statistical model considering sire as random while period and season as fixed effect. The least-squares means of AFC, FSP and FCI were estimated to be 1510.88±22.29 days, 149.66±5.15 days and 423.60±6.23 days, respectively. The least-squares analysis revealed highly significant effect ($P \leq 0.01$) of period of birth on AFC and period of calving on FCI. However, the effect of season was found to be non-significant on all three traits. The effect of sire was found to be significant on AFC, FSP and FCI. It was concluded from the present findings that sire can be used for further genetic improvement of these traits in the herd.

SP-27

PREDICTION OF LIFETIME MILK PRODUCTION FROM EARLY LACTATION TRAITS IN FRIESWAL CATTLE

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Basic aim of any breed improvement programme is to increase the lifetime milk production of the cows as the profitability of any dairy enterprise is the function of overall lifetime production of the cows maintained at a farm. Life time production of the cows can be predicted by the early expressed traits, thus may help in the selection of cows in early stage of life. Multiple linear regression analysis is a multivariate technique to develop prediction equation to predict future production of the animals. Data on 1225 Frieswal HFX Sahiwal cows maintained at military dairy farm Meerut (U.P.) and Ambala (Haryana) from 1989-2011 were analyzed to develop the prediction equation up to three, four and five lactations from first lactation traits. The least squares mean of first lactation milk yield was 2920.86 ±47.07 Kg. The least squares mean of milk yield up

to three, four and five lactations were 9100.81±187.85, 11869.91± 375.09 and 15310.19± 845.60 Kg, respectively. The accuracy of prediction of lifetime milk production up to three, four and five lactations using model FLMY, FLL, AFC, FSP and FDP were 34.53, 24.00 and 19.60, respectively while using model FL305MY, FLL, AFC, FSP and FDP were 34.57, 24.79 and 21.73, respectively. Based on the results of the study it may be inferred that the first lactation production traits viz., FLMY, FL305DMY were the most important traits contributing to the lifetime milk yield traits compared to the other traits included in the prediction models. However, the prediction accuracy of models with FL305DMY were comparatively higher than the models with FLMY indicating that among these two traits FL305DMY was more important.

SP-28

EVALUATION OF FRIESWAL BULLS UNDER FIELD PROGENY TESTING PROGRAMME AT DIFFERENT AGRO CLIMATIC REGIONS IN INDIA

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The Field Progeny Testing (FPT) program was initiated at ICAR-CIRC, Meerut, Uttar Pradesh in the year 1992 in collaboration with Agricultural Universities and Non-Government Organization at different agro-climatic regions of the country to evaluate crossbred cattle under field condition. At present this programme is running in association with Kerala Veterinary and Animal Sciences University (KVASU), Thrissur, BAIF Development Research Foundation, Pune, Guru Angad Dev Veterinary and Animal Sciences University (GADVASU), Ludhiana, and G.B. Pant University of Agriculture and Technology (GBPUA&T), Pantnagar for the evaluation and genetic improvement of HF crossbred cattle. The first lactation records of 4782 crossbred cows which were daughters of 121 bulls and calved over a period of 12 years from 1996 to 2008 were used to determine the genetic worth of HF crossbred bulls under different agro climatic conditions and to assess their ranking. The average first lactation milk yield in field HF crossbred cows was 2806.51±56.06. The breeding value of bulls was estimated as 2920.59 for 1st ranked bull and 2662.58 for 121st ranked bull. The percentage genetic superiority over population mean ranged from 4.06 to -5.13%. A total six sets of bulls were used in the analysis and the average breeding value of different sets were estimated as 2603.28±125.0, 2691.22±95.91, 2716.72±105.16, 2874.69±101.38, 2930.20±108.17 and 2965.59±143.23, respectively for 1st, 2nd, 3rd, 4th, 5th and 6th set, respectively which indicates a progressive improvement in subsequent sets. The study thus presents the findings of a successful and large scale progeny testing programme under field condition.

SP-29

GENETIC STUDIES ON INHERITED DISORDERS IN HOLSTEIN FRIESIAN CROSSBRED CATTLE IN MADHYA PRADESH

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Genetic disorders are hereditary, cause physical or functional anomalies producing negative impact on vitality. Known inherited disorders in cattle are mostly caused by autosomal recessively inherited genes. In Madhya Pradesh no related information of work done was encountered in Holstein Friesian crossbred. Therefore, in the view of this, the study was conducted with an objective to investigate inherent disorders: Bovine Leukocyte Adhesion Deficiency (BLAD), Deficiency of Uridine Monophosphate Synthase (DUMPS) and Bovine Citrullinaemia (BC) which are specific in Holstein Friesian and its crosses and to find out the prevalence, gene and genotype frequency of these inherited disorders in Madhya Pradesh. The study was carried out on 50 Holstein crossbred cattle. The DNA was isolated from the whole blood samples by John's method. The samples were genotyped by PCR-RFLP for BLAD, DUMPS and BC. The study demonstrates the genotype frequency of BLAD carriers was 0.04. The gene frequency of dominant allele was estimated to 0.98 and that of recessive allele to 0.02. Out of fifty animals screened, two (4%) animals were found to be heterozygous for BLAD in the Holstein population, although at a low frequency but this apparent spread of this genetic disorder through the Holstein breed represents one of the negative consequences of the widespread use of artificial insemination. The DNA of the carriers of BLAD was sequenced and submitted to NCBI (accession number is PBM17.sqn PBM17 KT032069). On contrary, carriers of BC and DUMPS were not detected. The study demonstrates a need for further examination of more Holstein cattle in Madhya Pradesh, preferably testing of breeding sires before selection through PCR-RFLP would help in the early detection of disorders and culling of animals from the herd.

SP-30

EFFECT OF NON GENETIC FACTORS ON REPRODUCTION TRAITS OF GIR HALFBREDS

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The data for the present investigations were collected from the history and pedigree sheets maintained at Research Cum Development Project on Cattle, M.P.K.V., Rahuri, (MS), for the

period of 40 years (1972 to 2011) on reproduction and production traits of Gir halfbreds and their Interse.

The data were classified according to genetic group, season of birth/calving, period of birth/calving and lactation order. In order to overcome non-orthogonality of the data due to unequal subclass frequencies, least squares techniques (Harvey, 1990) was used to estimate the effect of different factors using different effect of genetic and non-genetic factors. The results obtained in the present investigation of the overall least squares means of AFS in FG and Interse of FG were 455.95 + 6.91 days and 638.99 + 8.31, respectively. The DMRT revealed Interse of FG cows born during period 2004-2009 had lowest AFS which was at par with the period 1980-1982 and significantly differed than rest of the period. The season of birth had non-significant effect on AFS in all genetic groups. The generation had significant ($P<0.01$) effect on AFS. The overall mean AFS as affected by generation was 628.91 ± 6.09 days in FG. The effect of genetic group on AFS was non-significant. However, the FG genetic group had lowest AFS. The overall least squares means of AFFS in F1 cows of FG and Interse of FG were 533.41 ± 6.37 days and 743.13 ± 10.72 days, respectively.

Keywords: Reproduction traits, genetic, non-genetic factors.

SP-31

PREDICTION OF FIRST LACTATION 305 DAY MILK YIELD BASED ON BIMONTHLY TEST DAY MILK YIELD RECORDS IN MURRAH BUFFALOES

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The present study was conducted on 2100 bimonthly test day milk yield (BTDY) records on 350 animals calved in between 1993 and 2015 at ICAR-NDRI, Karnal. A total of 6 BTDY were taken from each animal at an interval of 60 days, with first BTDY recorded on 6th day and last BTDY taken on 305th day. The prediction of First Lactation 305 Day Milk Yield (FL305DMY) was done by utilizing five methods viz., Centering Date Method (CDM), Test Interval Method (TIM), Ratio Method, Multiple Linear Regression (MLR) method and Artificial Neural Network (ANN). Error in prediction was estimated by absolute error, absolute error (%), average error, average error (%), Root Mean Square Error (RMSE) and RMSE (%). MLR was found to be the best method with least error in prediction (5.71% RMSE), followed by ANN (5.77% RMSE). The accuracy (R2) of MLR equation including all 6 BTDY records was 91.86%. The best MLR equation for an early prediction of FL305DMYincluded3 BTDY records viz., BTDY-2 (65th day), BTDY-3 (125th day) and BTDY-4 (185th day) and the R2 estimated was 85.29%.The study compared between the conventional and machine learning methods for prediction of first lactation yield which could be used for early selection of the animals.

SP-32

UTILITY OF FIRST LACTATION FAT ENERGY CORRECTED MILK YIELD AS A TRAIT FOR GENETIC EVALUATION OF MEHSANA BUFFALO BULLS

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Mehsana is recognised as persistent milker, regular breeder and contributed significantly in the operation flood programme launched in India for augmenting milk production.Milk production though has increased many folds in last few decades, the relative contribution of milk and other dairy products towards the dietary energy is very less.In view of this, present study considered First lactation energy corrected milk yield (FLECMY) exclusively based on average test day fat yield (ATDFY) for sire evaluation. As the heritability of ATDFY is higher,it is equally likely that inheritance of ECMY will be more than that of the inheritance of milk yield. The present investigation was carried out using data of first lactation production records of 7825 Mehsana buffaloes sired by 200 bulls spread over a period of 25 years (1989-2013), collected from the Dudhsagar Research and Development Association (DURDA), Dudhsagar Dairy, Mehsana. The breeding value of sire was estimated by Best Linear Unbiased Prediction-Sire Model (BLUP-SM) and BLUP-Animal Model (BLUP-AM), where (co)variance components were estimated by WOMBAT genetic analysis tool. The effectiveness of different sire evaluation methods was compared by using error variance and rank correlations among the estimated breeding values of sires. The average breeding values of Mehsana buffalo bulls evaluated for FLFECMY by least squares method (LSM), BLUP-SM and BLUP-AM methods were 1215.89, 1185.7 and 1472.75 kcal, respectively.BLUP-AM method was found to have lowest error variance as compared to LSM and BLUP-SM methods of sire evaluation, making it as a most efficient method. The high rank correlation coefficients between breeding values (0.99 and 0.94) of sires by LSM and BLUP-SM with most efficient BLUP-AM method shows that either of these methods could rank the sires with fairly high accuracy. Although the genetic evaluation of milk producing animals in general can be done on the basis of either TMY or FLFECMY, but considering nutritional security of the state and country, it is recommended that evaluation of Mehsana buffaloes may be done on the basis of FLFECMY.

SP-33

ENVIRONMENTAL FACTORS AFFECTING LACTATION MILK YIELD OF JAFFARABADI BUFFALOES IN AN ORGANIZED FARM OF GUJARAT

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The study was undertaken to evaluate the effect of different macro climatic variables on lactation milk yield of Jaffarabadi buffaloes. Milk data of 158 Jaffarabadi buffaloes with 476 lactation records and the meteorological data over a period of 24 years (1987-2010) were obtained from Livestock Research Station, Junagadh Agricultural University, Junagadh, Gujarat, India. The data were analysed by using correlation and multiple regression model to study the effect of environmental variables on lactation milk yield. The main environmental variables were also compiled as monthly minimum and maximum temperature, average relative humidity, monthly wind speed (km/hr) and monthly sunshine (hr) as well as temperature humidity index (THI). Analysis was done by using the statistical analysis package of R software 3.3.0 version. The influence of environmental factors on lactation milk yield was non-significant ($P>0.05$). It was observed that lactation milk yield was highest (1962.53 ± 176.73) among the Jaffarabadi buffaloes calved during winter season as compared to rainy (1674.37 ± 268.49) and summer season (1566.52 ± 108.68). All the climatic variables considered in the study accounted for 4.48 %, 32.01 % and 29.36 % direct variation on lactation milk yield in winter, summer and monsoon season, respectively, as verified by the value of coefficient of determination (R^2). This research indicates that Jaffarabadi buffaloes were not much sensitive to seasonal changes on their lactation milk yield. The meteorological observation during the period of study confirmed that there was high value of THI in eight months (March- October) during the year, but it didn't show any significant effect of lactation milk yield which suggests that Jaffarabadi buffaloes can tolerate heat stress and/or other macro or micro environmental changes in this region and we can say that, this buffalo breed can perform well round the year.

Keywords: Lactation Milk Yield, Environmental Variables, Jaffarabadi Buffalo

SP-34

ESTIMATION OF GENETIC PARAMETERS FOR LIFETIME PERFORMANCE TRAITS IN MURRAH BUFFALOES

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The data records of Murrah buffaloes from history cum pedigree sheets maintained over a period of 24 years (1992-2015) at Buffalo research centre (BRC), LUVAS, Hisar and Animal farm ICAR-CIRB (1993-2012), Hisar, were analysed to estimate heritability (h^2), genetic and phenotypic correlation among various lifetime performance traits. Lifetime performance traits whose genetic parameters analysed were Longeiveity (LV), productive life (PL), lifetime milk yield (LTMY), milk yield per day of productive life (MY/PL) and milk yield per day of longeiveity (MY/LV). Data set analysed includes records of 968 buffaloes which were progeny of 150 sires. Based upon analysis, higher heritability estimates for LV, PL, MY/PL (h^2=0.426±0.127, 0.383±0.120, 0.381±0.120 respectively) were recorded. Comparatively lower estimates of heritability for LTMY, MY/LV (h^2=0.249±0.09, 0.241±0.09 respectively) were recorded. High heritability estimate of lifetime performance production traits help to conclude their significance in selection decision and it also indicate that these traits will serve as a better tool for selective breeding, expected to lead to rapid aggregate genetic gains in Murrah production. Further analysis on genetic correlation of lifetime performance traits we found higher values of genetic correlation as 0.977±0.014 (PL/ LV), 0.758±0.10 (LTMY/LV) and 0.834±0.07 (LTMY/PL) whereas low and negative genetic correlation of MY/PL, MY/LV with other lifetime performance traits. Low and negative genetic correlation of MY/PL and MY/LV traits indicate their little genetic role. Positive higher genetic correlations for LV, PL, LTMY indicated role of lifetime performance traits in selection programmae. Further critical analysis revealed that selection based on LY simultaneously will improve PL and LTMY of Murrah buffaloes. Higher correlation among various lifetime performance traits helps to conclude that various lifetime performance traits may be included as selection criteria in for improvement of milk production in Murrah buffaloes.

Keywords: Lifetime performance traits, Murrah, Genetic parameters.

SP-35

ANALYSIS OF DIFFERENT NON GENETIC FACTORS ON LIFETIME PERFORMANCE TRAITS IN MURRAH BUFFALOES

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The present investigation was conducted to study the effect of various non-genetic factors like farm, period of calving and season of calving on different lifetime performance traits like Longeiveity (LV), Productive life (PL), Lifetime milk yield (LTMY), Milk yield per day of productive life (MY/

PL) and Milk yield per day of longeiveity (LV) in Murrah buffaloes. The data analysed include records of 968 buffaloes, progeny of 150 sires maintained over a period of 24 years (1992-2015) at Buffalo research centre (BRC), LUVAS, Hisar and Animal farm ICAR-CIRB (1993-2012), Hisar. The least squares means for LV, PL, LTMY, MY/PL and MY/LV were 2738.80±32.07 days, 1275.24±31.82 days, 5586.42±175.96 kg, 4.62±0.08 kg and 1.90±0.04 kg respectively. The effect of period of calving was statistically significant on all the lifetime performance traits under study except on MY/LV. Whereas, non-significant effect of season of calving on all the lifetime performance traits. Analysis of variance also revealed significant effect of farm on LTMY and MY/LV. Significant effect of various non-genetic factors on lifetime performance traits helps to conclude the importance of lactation number, season and managemental farm activities in production performance of Murrah buffaloes.

Keywords: Production traits, Murrah, Non genetic factors.

SP-36

ESTIMATION OF GROWTH CURVE PARAMETERS IN SONADI SHEEP USING GOMPERTZ FUNCTION

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Livestock sector plays a significant role in Rajasthan and is essential for the livelihood of rural people. Sonadi Sheep are rearing important livelihood for a large number of small and marginal farmers in Southern Rajasthan. Growth, defined as changes of body weight over time is an economically important trait in sheep that directly determines meat production.Growth curve, the graph of weight as a function of age on time elaborates gradual changes taking place in animal's body with the passage of time. This is often sigmoid in shape. Different mathematical growth models express the life time growth course. Growth curve parameters can be used as phenotypic traits and to analyze relationship between them. In this study it was aimed that the estimating of growth curve for live weight from birth to 12 months age in Sonadi sheep. Data on 56 Sonadi sheep, maintained at including 28 males and 28 female which were born in year 2016 at Mega Sheep Seed Project, Vallabhnagar, Udaipur were used. Gompertz growth curve function was fitted to monthly live weight records. Descriptive values of Sonadi sheep live weight from birth to 12th month of age is given Average of live weight in Sonadi sheep from birth to 12th month of age were 3.27±0.081, 6.72±0.202, 9.06±0.267, 12.19±0.388, 15.01±0.44, 16.21±0.51, 16.75±0.54, 18.54±0.586, 18.59±0.599, 20.86±0.586, 21.51±0.517, 22.10±0.522 and 23.15±0.512, respectively. The value of growth parameters for "A" (Asymptomatic mature weight), "B" (Proportion of Asymptotic mature weight to be attained after birth), "K" (growth rate) were 23.303±0.787, 1.719±0.112 and 0.302±0.032, respectively. Growth curve was designed using these parameters.Determination coefficient (R^2) was 0.987. As result of determination coefficient Gompertz model can be said an appropriate model for drawing growth curve.

Keywords: Sonadi sheep, Growth curve parameters, Gompertz model

SP-37

GENETIC PARAMETERS FOR SEX RATIO IN SHEEP

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A study of sex ratio in sheep was made on records of 4695 Avikalin and 5718 Malpura lambs. Data from the ICAR-Central Sheep and Wool research Institute Avikanagar Rajasthan, India, comprising the period 1991–2016, were used for the analysis. The results indicated that the average sex ratio was 50.43±0.28 in Malpura and 51.05±0.32 in Avikalin sheep. A least squares analysis of variance showed that most of the factors were not able to ascertain the variance in the sex ratio. However birth weight group of lamb had a definite association with sex ratio, where higher birth weight indicated higher chances of male birth. This also indicated as the nutritional level in the flock affecting sex ratio. Dam weight also affected the sex ratio. Descriptive analysis showed that sires had a trend of producing a particular sex lambs in their lifetime, which can be exploited. Genetic analysis revealed that there was low additive genetic variance for the sex ratio in Avikalin (h^2 = 0.019±0.003) as well as Malpura sheep (h^2 = 0.04±0.01). Maternal permanent effect was found to be important for Avikalin sheep. Selection to improve sex ratio in any direction seems futile looking in to the objectives of breed improvement program.

Keywords: Sex Ratio, heritability, Gibbs sampling, Threshold trait

SP-38

EFFECT OF GENETIC AND NON-GENETIC FACTORS ON POST-WEANING GROWTH TRAITS IN ORGANIZED FLOCK OF CHOKLA SHEEP OF RAJASTHAN

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Data on 3714 Chokla sheep, maintained at the Central Sheep and Wool Research Institute (CSWRI), Avikanagar, Rajasthan, collected for a period of 18 years (1994 through 2011) were used to study growth traits and genetic control. The least-squares mean for body weight at 6 months, 9 months and 12 months of ages were 12.68 ± 0.119 kg, 19.02± 0 .0152 kg, 20.91 ± 0 .194 kg, respectively. The overall least-squares means for average daily gain were observed to be 70.67± 1.082 and 29.66± .879 g/day at 3-6 and 6-12 months of age, respectively. The sire effect was highly significant ($P \leq 0.01$) on all the traits under the study. The sex effect of lamb was highly significant ($P \leq 0.01$) on all the traits under the study but non-significant 12 months body weight, period effect was highly significant ($P \leq 0.01$) on all the traits under the study. The effect of dam's age was highly significant ($P \leq 0.01$) on ADG3 and non- significant effect for 6, 9, 12 months body weights and ADG2. The effect of season of birth was highly significant ($P \leq 0.01$) on all the traits under the study

but non- significant effect for 12 months body weights. The effect of dam's weight as a covariate was highly significant (P≤ 0.01) on 6, 9 months body weights and significant (P≤ 0.05) on12 months body weights and non- significant for ADG2 and ADG3.

SP-39

PERFORMANCE OF MADRAS RED SHEEP IN AN ORGANIZED FARM

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The Madras red sheep is a well known mutton purpose sheep breed predominantly found in north eastern agroclimatic zone in Tamilnadu. The breed is of medium size with typical tan to red colour in different shades. This paper highlights the performance of Madras red sheep maintained at Post Graduate Research Institute in Animal Sciences, TANUVAS, Kattupakkam Mean ± SE Body weight (kg) at birth, 3 months, 6 months, 9 months and 12 months in male and female were 2.44±0.07 and 2.40±0.09, 7.87±0.27 and 7.03±0.31, 12.15±0.53 and 11.40±0.48, 15.72±0.66 and 14.78±0.65 and 18.17±0.78 and 17.16±0.95, respectively. Average tupping rate (%), conception rate, lambing rate, age at first lambing (days) were 83.48, 75.00, 99.00 and 764, respectively. Mortality percentage in lambs and adults were 6.35 and 3.42. With scientific breeding and management there is scope for further improvement of performance of Madras red sheep.

SP-40

CONSTRAINTS IN PASHMINA PRODUCTION SYSTEM OF LADAKH

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Changthangi goat of Ladakh region of our country produces world's best animal fibre 'Pashmina' known for its smoothest texture and warmth. A survey regarding various problems encountered in Pashmina production system in Changthang region of Ladakh was conducted under All India Coordinated Research Project on Changthangi Goat since from its inception in June 2014. The areas covered under this project were Korzok, Samad, Kharnak, Gya, Miru, Chushul, Tsaga, Hanle, Kuyul, Demjok and Nyoma. The main problems related to animal health where, abortion (40-50%), kid mortality (45-50 %), diseases like, CCPP, contagious ecthyma and pediculosis. Other problems faced by the nomads where, lack of breeding policy, feed and fodder shortage, lack of knowledge about value addition of livestock produce, shortage of man power and erratic weather condition of Changthang region and mostly hard living condition in Changthang.

Keywords: Pashmina, Changthangi, Livestock, Ladakh

SP-41

SILAGE FEEDING -NUTRITIONAL SECURITY FOR LIVESTOCK OF LADAKH REGION

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Ladakh is the only cold arid region of the country where there is little scope for agriculture farming, and a tremendous scope for livestock production system. It is the centre for world's best high altitude animals in the form of Yaks and its crosses, Changthangi Sheep, Changthangi Goat, Malra, Malluk, Purig sheep, local cattle, Zanskari and Chumurti horses. For a sustainable animal production system one of the main concern is animal feeding and in Ladakh due to poor agriculture system there is a great scarcity of animal feed and fodder, especially during the lean season of winter where the farmers face great problem. Keeping in view the condition of Ladakh region several trial systems was conducted for production of silage using local agriculture produce for the first time in Ladakh region. For ensiling, locally available forage crops (wheat straw, alfa-alfa, maize straw, pea straw and tree leaves) were chopped to less than 2.5 cm so that forage can be packed densely. Chopping is done when the dry matter content of the ingredients was 30 to 36 %. Close plastic bin were used for ensiling by making it air tight and keeping it in a warm place for 2-3 months. To overcome the under nutrition of livestock of Ladakh region due to fodder scarcity especially during winter season, silage has proved one of the best substitute for the livestock feeding in Ladakh region. In addition, to ensure good animal health and growth, it is essential to produce feed having high nutritive value and microbiological quality. Silage additives and microbial inoculants can be useful tools to improve nutritional quality and animal performance, body condition, reproduction in Ladakh condition.

Keywords: Ensiling, Silage, Ladakh, Livestock

SP-42

CHARACTERIZATION OF LOCAL MAHBUBNAGAR GOAT: A PRELIMINARY STUDY

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Mahabubnagar goats, also known by local name of "Palamuru Meka" are found in area adjoining the Srisailam project in erstwhile Mahabubnagar district of Telangana state. They are medium sized and dual purpose strain of goat. A study was conducted to estimate morphometry and performance traits of local Mahabubnagar goats reared under field conditions. In total, flocks with 50 farmers distributed throughout the native tract were studied to measure the above said traits. The average flock composition ranged from 20-150 in size, with bucks constituting 10-85%, does between 10-25% and kids ranging between 8-37.5%. Ears were pendulous. Beard was present only in males while both the sexes had wattles. Both the sexes were horned with backward orientation. Body weight at birth ranged between 1.8-3.0 kg, at weaning (3 months) 7-14 kg, at 6 months of age 17-28 kg, at adult 26-40 kg. The weight of doe at first kidding ranged between 26-40 kg. With respect to body measurements in adult goats, the chest girth ranged between 58-105 cm, body length between 55-96 cm and height at withers ranged 58-103 cm. The total milk yield was between 22-60 litre per lactation, while lactation length was between 60-120 days. Age at first mating in males was between 360-540 days, while the same in females was between 320-380 days. Age at first kidding was between 520-600 days, while kidding interval was between 180-280 days. The average litter size was 2, while the no. of kid's lifetime ranged 7-11. The predominant colour was bicolour with pattern consisting of black-white, brown-white and black-brown. The horns were straight, curved oriented backward and downward.

SP-43

PREDICTION OF BODY WEIGHT IN MARWARI GOATS ON THE BASIS OF MORPHOMETRIC TRAITS UNDER FIELD CONDITION

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Variation in biometric traits such as body weight in livestock industry plays a critical role in selection of individuals for the production of future generations and on overall productivity of the livestock. Marwari goat being known for its faster growth, efficient breeding, high salt tolerance is an important livestock species of the arid and semiarid region of Rajasthan. Morphometric traits like body height, body length, heart girth were frequently investigated for their relation with body weight in several species for the prediction of body weight. Therefore the present study was carried out in female Marwari goat to establish the best linear regression equation for the prediction of body weight. Information on morphometric measurements on different body parameters were collected from 29226 female Marwari goats maintained under different clusters of AICRP on Marwari Goat Project. The average body weight, body height, body length and heart girth were observed in the range of 2.58 to 30.53 (kg), 36.56 to 63.98 cm, 30.05 to 59.87 cm and 36.52 to 72.01 cm, respectively. The linear regression equation of Y=3.803+0.157*BHG+0.088*BL revealed the suitability of heart girth in combination with other morphometric measurements as best fit for the prediction of body weight in female Marwari goats. Thus, the present study concluded that higher values of heart girth could be helpful in selecting best female Marwari goat under field conditions in terms of body weight.

Keywords: Marwari goat, body weight, linear regression

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COAT COLOUR ADAPTATION IN MARWARI GOAT UNDER ARID CONDITION OF RAJASTHAN

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Indigenous livestock breeds such as Marwari goat are known for their excellent adaptability of heat tolerance under the semi arid and arid climatic conditions of Rajasthan. Increased coat pigmentation is considered to be related with higher heat adaptability. Selection of highly adaptable animals on the basis of coat colour is highly recommended for the efficient feeding, breeding and management of animals. Therefore, the present study was carried out in Marwari goats maintained under different clusters of AICRP project on Marwari Goat to investigate the prevalence of different coat colours and their mean body weight. The information on the coat colour of adult Marwari goat along with body weight was collected from the official records of the Marwari goats maintained under field condition. The results indicated the prevalence of black colour in 93.40 per cent of animals with subsequent prevalence of brown colour in 1.00 per cent of animals and white colour in0.50 per cent animals. The predominant colour seen in all the animals was black followed by an admixture of black, brown and white. The mean estimated body weight were observed as 24.59± 0.05 (black colour), 24.1 ± 1.08 (brown colour) and 23.9 ± 1.05 kg (white colour). The study thus concluded that black colour is naturally selected in Marwari goat under field condition to negate the effect of higher ambient temperature through enhanced pigmentation.

Keywords: Adaptability, Marwari Goat, Body Coat Colour.

SP-45

EFFECT OF NON-GENETIC FACTORS ON HATCHABILITY OF BROILER AND LAYER CHICKEN

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Data on 254 hatches of broiler chicken (IBL-80) spread over 18 years (2000-2017) and 99 hatches of layer chicken (RIR and Punjab red) spread over 12 years (2006-2017) were collected from the incubation chart register maintained at hatchery unit of poultry research farm under Directorate of Livestock Farms, GADVASU, Ludhiana. Data were classified into 3 seasons i.e., summer (March-July), rainy (August-October) and winter (November-February). It was classified into 6 periods and 4 periods of 3 years each for broiler and layer, respectively. The overall least squares mean of hatchability (%) of total eggs (HTE) set was 64.46 ± 0.79 for broiler and 63.11 ± 1.05 for layer chicken. The effect of seasons were found out to be significant ($P \leq 0.01$) for both broiler and layer hatches whereas effect of periods was found out to be significant ($P \leq 0.01$) for broiler and was not significant for layer chicken. Hatchability was highest in the winter months i.e., 69.26 ± 0.84 for broiler and 66.55 ± 1.33 for layer chicken. Lowest hatchability was observed in the rainy i.e., 58.19 ± 1.69 and 58.55 ± 2.24 for broiler and layer, respectively. Over the years, hatchability (%) of total eggs set ranged from 59.16 ± 1.47 to 71.06 ± 1.77 for broiler and 59.91 ± 1.80 to 65.59 ± 2.04 for layer chicken. It was concluded that more number of hatches has to be set in the winter months and proper managemental practices has to be undertaken for overcoming the effects of different non-genetic factors for improving overall hatchability.

Keywords: IBL-80, RIR, Punjab red, HTE, non-genetic factors.

SP-46

EFFECT OF PROBIOTICS IN POULTRY

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Probiotics are live cultures of non pathogenic organisms including bacteria, fungi and yeasts which beneficially affect the host by improving its intestinal microbial balance. Probiotics are administered orally and can be used as an alternative to antibiotics for growth promotion. A good probiotic culture should contain 30×10^9 CFU per gram. Some important microorganisms which are used as probiotics includes Lactobacillus acidophilus, Lactobacillus bifidus, Lactobacillus bulgaricus, Lactobacillus lactis, Aspergillus oryzae, Streptococcus faecium, Streptococcus thermophilus etc. In case of poultry probiotics are frequently used for improving the health status, production performances, feed conversion efficiency and immune responses. The addition of probiotics in poultry diet also improves egg production in layers. Lactobacilli organisms act as predominate microbial population in crop of poultry. These Lactobacilli grow well at low pH in the range of 4 to 5 and are responsible for the suppression of E.coli species. On the other hand E.coli organisms require high pH that is 6 to 7 for optimal growth. After birth when chicks have a nearly sterile digestive tract and lack of sufficient gastric acid secretion, pH ranges from 5.5 to 6 resulting in excess growth of coliforms. To control this condition Lactobacilli are used as probiotics in poultry feed or water. The stress factors or pathogenic microbes in poultry create an imbalance in intestinal microflora by lowering body defense mechanisms leading to physiological disturbances like diarrhea, loss of appetite, improper digestion and poor absorption of nutrients. Use of probiotics regularly in feed help to prevent these disturbances and enhance health and productivity.

Keywords: Probiotics, Feed conversion efficiency

SP-47

PERFORMANCE OF VANARAJA CHICKEN IN INTENSIVE SYSTEM OF MANAGEMENT IN CHHATTISGARH

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A study was conducted on 250 females and 50 males of Vanaraja chicken to evaluate the performance in the agro-climatic condition of Chhattisgarh under the ICAR – Poultry Seed Project at College of Veterinary Science and Animal Husbandry, Anjora, Durg, Chhattisgarh. The birds were reared under intensive system of management for a period of 72 weeks. The diet were prepared using conventional feed ingredients for chick (1-6 wks), Grower (7-16 wks) Pre-breeder (17-23 wks) and Breeder (>23 wks). Significant difference in mean body weights were observed between the Vanaraja male and female. Simple linear regression analysis was done for weekly body weight which showed that the male grew (141.54 ± 3.05/week, R^2 = 99.1%) faster than the females (103.45 ± 2.10, R^2 = 99.2%). The age at first egg and age at peak egg production was also assessed. The feed consumption, FCR and PEF of male was higher than the female birds during the entire phase of the study. The age at first egg was recorded at 20 weeks and while Peak laying period was recorded at 35 to 44 week of age and Hen house egg production observed was 61.06%. Thus present study concluded that performance of Vanaraja chicken as reflected by body weight gain and feed conversion ratio was highly dependent on sex. Male performed better than females. The age at first egg lay and sexual maturity was achieved earlier as compared to performance of Vanaraja female in others reports, suggesting that the Vanaraja chickens are suitable to rear in Chhattisgarh and are well adapted to the state agro climatic conditions.

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ANALYSIS OF BODY WEIGHT, AVERAGE DAILY GAIN, KLEIBER RATIO AND DISPOSAL PATTERN IN BIKANERI CAMEL

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Data pertaining to body weight, average daily gain from birth to 3 month age (ADG) and Kleiber ratio from birth to 3 month age (KR) of calves born at NRCC, Bikaner between years 2000-2016 was analyzed using GLM procedure. The least squares mean of birth weight, 3 month weight, ADG and KR were 37.98±0.35 kg, 89.99 ±1.50 kg, 579.44±16.37 gm and 19.06±0.32

respectively. Effect of year of birth was highly significant for all the traits however effect of sex of calves was non-significant. Disposal data of 226 animals out of 335 born between years 1990 -2017 at NRCC, Bikaner was analyzed to study disposal pattern in Bikaneri camel. Average age at disposal was 2157.23 ± 128.11 days. Average age of disposal was higher in females (2844.76±224.74 days) compared to males (1581.50 ±119.53days). Chief mode of disposal was through auction (58/123) followed by death (32/123) and transfer (26/123) in males and in females it was death (63/103) followed by auction (37/103). Thus, year of birth was significant source of variation for body weight, average daily gain and Kleiber ratio in Bikaneri camel calves. Auction and death were main mode of disposal. The average age at disposal was around 6 years. Males were disposed earlier compared to females which may be attributed to differences in production purposes for which males and females are utilized.

SP-49

STUDY OF NON-GENETIC FACTORS AFFECTING AGE AT FIRST CALVING AND WET AVERAGE IN MEHSANA BUFFALOES

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Mehsana buffalo is one of the best dairy breed of buffalo in Gujarat state. Age at first calving (AFC) and wet average (WA) are those traits which are of monetary value in the production of livestock. AFC considerably affects the productive life of an animal and the number of calves obtained during the life time. The aim of this study was to analyse the effects of non-genetic factors on AFC and WA. The data set comprised 12560 records up to three lactations of 7870 Mehsana buffaloes, sired by 200 bulls from 1989 to 2013 under field progeny testing programme of Dudhsagar Research and Development Association (DURDA), Dudhsagar Dairy, Mehsana. The non-genetic factors that supposed to influence these traits like season and period of calving, parities, different clusters and AFC groups were included in the present study. The least squares maximum likelihood (LSML) program was used to estimate of various non-genetic factors on AFC and WA. The least squares mean of AFC and WA were estimated to be 1383.30 ± 3.50 days and 7.00 ± 0.22 liters, respectively. Age at first calving were found to have highly significant ($P<0.01$) effect of season of birth and period of birth; whereas, non-significant ($P<0.05$) effect of clusters. It further revealed highly significant ($P\leq0.01$) effect of all non-genetic factors like parities, season of calving, clusters, period of calving and age at first calving group on wet average in Mehsana buffaloes. Study further emphasized that before estimation of genetic parameters of AFC and WA in Mehsana buffaloes, it will be necessary to adjust the records for these significant non-genetic factors.

Technical Session-II

Improvement of Animal Resources for enhancing Livestock Productivity. (Genomic selection, Reproductive tools)

LP-06

POTENTIAL FOR GENOMIC SELECTION IN INDIGENOUS CATTLE BREEDS

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Introduction

Breeding of dairy cattle has travelled a long way from initial days of daughter-dam comparisons to recent advances in genomic selection. A brief historical perspective of employing molecular information for selection of dairy animals beginning from genetic markers to marker assisted selection to whole genome selection procedures is reviewed here. The need for introduction of whole genomic selection procedures and a proposed road map for their introduction to achieve higher genetic progress in the indigenous cattle and buffalo populations in the country is also described here under.

Integrated approach to genetic improvement

Genetic improvement of dairy animals in many advanced dairy producing countries has been the great success stories. Average lactation yields have been doubled in the last 30-35 years (See Table 1).

Table 1. Average lactation yield per cow in some advanced dairy producing nations and India.

Figures are in kgs.

Country/Year	1975	1985	1995	2005	2010	2012
Israel	5,885	7,919	8,739	9,822	10,767	11,580
USA	4,699	5,913	7,441	8,877	9,587	9,841
Canada	3,796	4,622	6,366	7,496	8,531	8,816
France	3,281	4,163	5,517	6,288	6,278	6,582
Denmark	4,492	5,684	6,656	8,123	8,640	8,529
Netherlands	4,623	5,370	6,613	7,299	7,468	7,576
Australia	2,844	3,441	4,646	5,215	5,810	5,575
India- Cow	511	632	815	1087	1284	1196
India- Buffalo	920	1120	1297	1570	1679	1710

Source: FAOSTAT (2017)

There had been marked improvement in animal rearing practices, however the above progress is attributed largely to genetic improvement. Sire evaluation procedures employed for estimation of breeding values to select bulls and bull mothers were key components in achieving steady genetic progress. The methods used have travelled a long way from simple daughter average comparison in early 1920. Daughter-dam comparisons were the main method used till 1950 (Graves,1925; Hansson-Yapp, 1925; Turner, 1925; Goodale, 1927; Pear, 1930; Gifford, 1930; Wright, 1932; Rice, 1933; Bonnier, 1936; Lush, 1941). This followed by progeny testing through contemporary comparisons (Robertson and Randel, 1954) and herd mate comparison (Henderson *et al,* 1954) methods. Quaas and Pollak in 1980 proposed an animal model based on the approach developed by C R Henderson for evaluation of progeny test bulls. At present every country uses the animal model for estimating breeding values.

Genomic Selection Procedures

In conventional methods of genetic evaluation described above, it is assumed that there are an infinite number of loci that influence milk production and each contributes an infinitesimally small amount to the total genetic merit. With the discovery of DNA by Watson and Crick (1953), scientists started finding genes (loci) that influence economic traits. Initially, molecular geneticists used markers (large segments of DNA) and tried to find genes close to the markers. Some microsatellites were found out and used as markers. However, selection of animals based on marker genotypes – referred to as marker assisted selection (MAS)- was not successful in dairy scenario as it depended on how close the markers were to the actual gene locus and how many markers were used. On both the accounts not much success was achieved. With the successful implementation of the Human Genome Project, thousands of single nucleotide polymorphisms (SNPs) were found out in many species and SNP detection chips were developed to test millions of SNPs spread over the entire genome. With these developments, whole genome selection methods were developed for selection of animals based on both phenotypic and genotypic data. A brief description of these developments is provided in the next sections. Most of the material in this section is taken primarily from two review articles (Dekkers 2004 and Hill 2014).

Marker Assisted Selection

The first markers that became available in the 1950s were blood group markers and soon methods for linkage analysis were developed (Neimann- Sorensen and Robertson 1961). As blood group markers were neither trait genes nor closely linked to them, they were not very useful. Linkage analysis for quantitative trait loci (QTL) detection did not really take off until many microsatellite markers became available and maximum likelihood (Lander and Botstein 1989) and regression methods of prediction were developed for inbred line crosses (Haley and Knott 1992), with the latter extended to enable analyses in crosses of non-inbred populations (Knott *et al,* 1996). Extensive analysis into how to optimize the design of such studies was undertaken. For example the "grand-daughter design" utilizes the structure in dairy cattle whereby the effects of QTL segregating in the grandfather were estimated from his sons' progeny tests based on field records of many grand daughters (Weller *et al,* 1990). Extensive simulations and other theoretical analyses were undertaken to find how best to utilize findings in breeding practice (*e.g.,* Smith and Simpson 1986).

Advances in molecular genetics led to the identification of multiple genes or genetic markers associated with genes that affect traits of interest in livestock, including genes for single-gene traits and QTL or genomic regions that affect quantitative traits. This provided opportunities to enhance response to selection, in particular for traits that are difficult to improve by conventional selection (low heritability or traits for which measurement of phenotype is difficult, expensive, only possible late in life, or not possible on selection candidates).

Numerous linkage studies were undertaken (Weller 2009) and hundreds of QTL, some of very large effect, were found in livestock species (http://www.animalgenome.org/). The number confirmed by repeat studies is much less and in these the same causal locus may be mapped to somewhat different locations. With a few recombinants per chromosome, the within-family methods lacked power and precision and the estimates of effects of those QTL found significant were biased upward (the Beavis effect; Beavis, 1998).

Examples of genetic tests that are available to or used in industry programmes are documented and classified into causative mutations (direct markers), linked markers in population-wide linkage disequilibrium with the QTL (LD markers) and linked markers in population wide equilibrium with the QTL (LE markers). Table 2 summarizes the available information.

Table 2. Examples of gene tests used in commercial breeding for different species (D = dairy cattle, B = beef cattle, C = poultry, P = pigs, S = sheep) by trait category and type of marker

Trait category	Direct marker	Linkage disequilibrium marker	Linakge equilibrium marker
Congenital defects	BLAD (D_a) Citrulinaemia (D,B_b) DUMPS (D_c) CVM (D_d) Maple syrup urine (D,B_e) Mannosidosis (D,B_f) RYR (P_g)	RYR (P_h)	
Appearance	CKIT (P_i) MC1R/MSHR (P_j,B_k,D_l) MGF (B_m)		Polled (B_n)
Milk quality	κ-Casein (D_o) β-lactoglobulin (D_o) FMO3 (D_p)		
Meat quality	RYR (P_g) RN/PRKAG3 (P_q) >15 PICmarq (P_w)‡	RYR (P_h) RN/PRKAG3 (P_r) A-FABP/FABP4 (P_s) H-FABP/FABP3 (P_t) CAST (P_u, B_v) THYR (B_x) Leptin (B_y)	
Feed intake	MC4R (P_z)		
Disease	Prp (Saa) F18 (P_{cc})	B blood group (C_{bb}) K88 (P_{dd})	
Reproduction	Booroola (S_{ee}) Inverdale(S_{gg}) Hanna (S_{ii})	Booroola (S_{ff}) PRLR (P_{jj}) ESR (P_{hh}) RBP4 (P_{kk})	
Growth and composition	MC4R (P_z) IGF-2 (P_{mm}) Myostatin (B_{oo}) Callipyge (S_{qq})	CAST (P_u) IGF-2 (P_{nn}) Carwell (S_{rr})	QTL (P_{ll}) QTL (B_{pp})
Milk yield and composition	DGAT (D_{ss}) GRH (D_{vv}) κ-Casein (D_o)	PRL (D_{tt})	QTL (D_{uu})

$_a$Shuster *et al* (1992); $_b$Dennis *et al* (1989); $_c$Schwenger *et al* (1993); $_d$Borchersen (2001); $_e$Dennis and Healy (1999); $_f$Berg *et al* (1997), Leipprandt *et al* (1999); $_g$Fuji *et al* (1991); $_h$Hanset *et al* (1995); $_i$Marklund *et al* (1998); $_j$Kijas *et al* (1998); $_k$Klungland *et al* (1995); $_l$Joerg *et al* (1996); $_m$Seitz *et al* (1999); $_n$Schmutz *et al* (1995); $_o$Medrano and Aquilar-Cordova (1990), Rincon and Medrano (2003); $_p$Lunden *et al* (2002); $_q$Milan *et al* (2000); $_r$Ciobanu *et al* (2001); $_s$Gerbens *et al* (1998); $_t$Gerbens *et al* (1999); $_u$Ciobanu *et al* (2004); $_v$Barendse (2001); $_w$G. Plastow (Sygen Int., Berkeley, CA, personal communication); $_x$Barendse *et al* (2001); $_y$Buchanan *et al* (2002); $_z$Kim *et al* (2000); $_{aa}$Belt *et al* (1995); $_{bb}$Hansen *et al* (1967), Hansen and Law (1970); $_{cc}$Vogeli *et al* (1997), Meijerink *et al* (2000); $_{dd}$Jørgensen *et al* (2004); $_{ee}$Wilson *et al* (2001); $_{ff}$Lord *et al* (1998); $_{gg}$Galloway *et al* (2000); $_{hh}$Rothschild *et al* (1996); $_{ii}$McNatty *et al* (2001); $_{jj}$Vincent *et al* (1998); $_{kk}$Rothschild *et al* (2000); $_{ll}$M. Lohuis (Monsanto Co., St. Louis, MO, personal communication); $_{mm}$Georges *et al* (2003); $_{nn}$Jeon *et al* (1999), Nezer *et al* (1999); $_{oo}$Grobet *et al* (1998); $_{pp}$J. Hetzel (Genetic Solutions, Brisbane, Australia, personal communication); $_{qq}$Freking *et al* (2002); $_{rr}$Nicoll *et al* (1998); $_{ss}$Grisart *et al* (2002); $_{tt}$Cowan *et al* (1990); $_{uu}$Spelman *et al* (1996), Arranz *et al* (1998), Coppieters *et al* (1998), Georges *et al* (1995), Zhang *et al* (1998); $_{vv}$Blott *et al* (2003). ‡Applies to both direct and linkage disequilibrium columns. Table adapted from Dekkers 2004

Genomic Selection a revolution in dairy breeding

There had been some analysis previously of what might be achieved by utilizing identified variation at all loci (notably by Lande and Thompson 1990), but there were no genomic tools to effect it. As dense SNP markers were becoming available and affordable, the landmark article by Meuwissen *et al* (2001) showed how whole-genome marker data could be incorporated effectively in a breeding programme for a polygenic trait. Subsequent modelling showed how large an impact on genetic progress such a scheme might have (*e.g.,* Schaeffer 2006) and the ideas were rapidly brought into commercial practice (Hayes *et al,* 2009). The genomic selection revolution began with two developments. The first was the sequencing of the bovine genome, which led to the discovery of many thousands of DNA markers in the form of SNPs. Concurrent development in sequencing and genotyping dramatically reduced the cost of genotyping. The second development was the demonstration that it was possible to make very accurate selection decisions when breeding values were predicted from dense marker data alone, using a method termed genomic selection (Meuwissen *et al*, 2001).

The concept

In conventional methodologies, prediction of breeding value for animals without records is done from pedigree records alone and therefore its accuracy is limited because the Mendelian sampling variation cannot be utilized; for example, in convention genetic evaluation full sibs will have the same predictions. The genomic information on young animals and the genomic and production data on their older relatives enable prediction of breeding values for animals without phenotypes both within and across families. Benefits are likely to be greatest for traits that are sex limited, such as milk yield and egg production, or not recorded till late in life or post mortem such as longevity or meat content. Accuracy of selection can also be increased with genotypic data even for those animals that have no records. Thus greater rates of genetic progress, double than what is possible to-day, can be made and the costs of genetic progress can be reduced considerably on account of elimination of systematic progeny testing.

The rate of genetic change is influenced by four factors through the following classical equation as described by Falconer (1989):

$$\Delta G = \frac{i\ r\ \sigma_A}{L}$$

Where, ΔG is genetic change, i is the selection intensity, r is the accuracy of selection, σ_A is the additive genetic standard deviation of the trait of interest and L is the generation interval.

The accuracy of breeding value for progeny tested bull can be as high as 0.99 depending upon the number of daughters recorded in different environments. However, it takes around 5-6 years (8-10 years in our conditions in dairy cattle) to get progeny test results. In case of sons of proven bull and recorded elite dams, the accuracy can be around 0.4 at birth. Meuwissen *et al* (2001) demonstrated in their simulation studies that it was possible to achieve accuracies of predicted breeding values from markers alone of 0.85 (where accuracy is the correlation between true breeding value and estimated breeding value (EBV) and reliability is the square of accuracy). The implications of achieving such accuracies for animals at birth are profound. The simulation results suggest that the accuracy of the GEBV for a bull calf can be as high as the accuracy of an EBV after a progeny test. Potentially, genomic selection could lead to a doubling of the rate of genetic gain through selection and breeding from bulls at 2 years of age rather than 5 years of age or later (Schaeffer, 2006). By avoiding progeny testing, breeding companies could save up to 92% of their costs (Schaeffer, 2006). However, some of these savings may be offset by the need to invest more money in genotyping to increase selection intensities and thereby increase the rates of genetic gain.

Possibilities of Introduction of Genomic Selection in India

Progeny testing or pedigree selection programme and systematic recording following standard procedures and common software was initiated under NDP I for some of the important dairy and dual-purpose breeds (www.ndpi.nddb.coop). There is a scope to intensify recording of animals using this network. The recorded population can then be used as female reference population for Genomic Selection of various breeds.

The prediction equations developed in advanced dairy-producing nations are appropriate for their breeds mainly Holstein Friesian and Jersey. Neither the SNP genotyping chips developed for Holstein Friesian and Jersey breeds nor the prediction equations developed based on reference populations of other countries would be useful for the Indian indigenous breeds. For introducing genomic selection procedures in the indigenous breeds, therefore, two tasks will be needed: One to develop SNP genotyping chips specifically for these breeds and second to develop prediction equations based on phenotypic records within the country. Some of Indian breeds are unique in the sense that not much of their population exists outside the country. As no progeny testing programmes are in place for indigenous breeds, there are no phenotypic records in the form of breeding value of proven bulls. In the absence of breeding values of bulls with high accuracy, appropriate models and methodologies will need to be developed based on primarily using phenotypic and genotypic records of female records for arriving at suitable prediction equations.

Recent studies have indicated that the reliability of predicted breeding values of male calves could be raised to 35-40% even when prediction equations are developed based on a mix of a small number of progeny tested bulls and a large number of recorded females. Female reference populations are now gaining in popularity, especially for novel traits, such as feed efficiency, methane emissions and detailed reproductive measures, the traits which are expensive to measure and are therefore available for only some animals in the population (Pryce *et al,* 2012).

National Dairy Development Board has developed a custom genotyping chip - INDUSCHIP in collaboration with Aarhus University, Denmark (Nayee *et al,* 2017). This chip can be a good starting point for genotyping recorded cattle of various breeds in our country.

Potential benefits of implementing GS in India

With the development of scientific knowledge, it will be possible to modify the existing breeding programmes and achieve higher genetic gains. The successful implementation of genomic selection will increase the genetic gain maximum by 50% through:

- Reducing generation interval both on sire to sire and sire to dam paths
- Increasing accuracy of breeding value of sires and dams
- Increasing selection intensity by increasing candidates to be selected

Other potential uses of Genotype data

Apart from GEBV, SNP information has many other applications such as parentage testing, identification of new markers associated with genetic disorders in addition to defining a breed/

population more precisely than microsatellite markers, phylogenetic analysis, identifying strain variations, etc. Likewise uses in disease screening tools in case of disease outbreak, metagenomics to identify gut microflora that improve feed conversion ratio or methane emission reduction, *etc.* may also be explored. Accuracy of genomic selection can be increased by identifying causal variants (haplotypes) with major effects through gene expression studies and using them along with SNP information especially for buffaloes where such information is minimal.

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LP-07

USE OF ADVANCED REPRODUCTIVE TECHNOLOGIES FOR CONSERVATION OF INDIAN LIVESTOCK

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Efficient reproductive performance and its monitoring are imperative for sustainability in any livestock production system, especially for milk, meat, draft and replacement animals. In recent times, there has been increasing challenges for increasing productivity and disease with altering climate. These targets, thought to some extent, can be achieved by conventional reproduction techniques. Advent and use of modern reproductive technologies have opened many avenues to study, treat and manipulate the reproductive phenomenon both *in vitro* and in vivo to improve reproductive performance in various domestic species of livestock. The developments in the field of reproductive biotechnologies are discussed below in brief.

1. *In vitro* Embryo Production (IVP):

Among the reproductive technologies developed, in vitro embryo production (IVEP) through a combination of in vitro maturation (IVM), fertilization (IVF) and culture (IVC) of oocytes holds a prominent place as it is an integral part of a number of other advanced reproductive technologies. It is a valuable tool to capture vast reserve of oocytes from abattoir material as an excellent source of low cost embryo production for basic research on developmental biology and physiology with commercial application of the emerging technologies such as nuclear transfer, transgenesis, parthenogenesis and rescue of endangered species. Progress in cellular and molecular embryology in farm animals has been difficult in the past due to limited availability of suitable experimental material at a reasonable cost. For such reasons, *in-vitro* embryo production (IVEP) techniques, particularly based on ovaries of abattoir origin have received greater attention in past two decades (Galli and Lazzari 2008). Besides the efficiency of *in vitro* derived embryo production using conventional technique of multi ovulation and embryo transfer (MOET) is not optional, rather it is inconsistent due to variable superovulatory response and flushing procedures (Cognie *et al,* 2003). Alternatively *in vitro* production of embryos provides cheaper and consistent source for supply of specific developmental stages for biomedical research and emerging biotechnologies viz. cloning, transgenesis through somatic cell nuclear transfer (SCNT), intracytoplasmic sperm injection (Kharche *et al,* 2016) and embryo sexing. *In-vitro* embryo production technology has been established for goats (Chauhan and Anand 1991, Kharche *et al,* 2008). During the past two decades, considerable advancement has been made in the laboratory production of embryos since the birth of buffalo calves (Chauhan *et al,* 1998; Liang *et al,* 2007) and kids following the transfer of IVP embryos (Malakar *et al,* 2005; Kharche *et al,* 2008; Kharche *et al,* 2011). The use of pre pubertal animals for collection of oocytes at an earlier age would reduce generation interval and accelerate the propagation of the genetically valuable livestock. For such reasons major research is currently focused to factors involved in determining the developmental competence of oocytes from pre pubertal and adult goats (Singh *et al,* 2009).

2. Ovum pick up Technology:

The poor availability of superior germplasm is a major problem in the buffalo, which is the principal dairy animal, the major contributor to meat production and generator of draught power in the Southeast Asian countries. Buffaloes, which produce 3500–4000 kg of milk in a 305-day lactation period, constitute only 0.1% of the total buffalo population in India (Misra *et al,* 1990). There is an urgent need to multiply this superior germplasm as quickly as possible. Although embryo transfer technology offers one of the fastest ways for achieving this objective, its application to buffalo has had a limited success primarily because of poor superovulatory responses. Similarly, Cattle are an important species of our dairy industry. The milk yield of cattle has enabled India to become the world's largest milk producing nation. Application of superovulation and ETT has given satisfactory results in cattle. However, conventional superovulation and ETT cannot be applied to animals that are clinically subfertile, infertile or aged or those which do not respond to superovulation but which are otherwise of high genetic merit. Furthermore, the development and refinement of techniques for *in vitro* embryo production (IVEP) has made available a tool for utilization of the female gamete pool for enhancing the maternal contribution to genetic improvement. However, if the source of oocytes is slaughterhouse ovaries, the offspring produced cannot be used for breeding purpose due to lack of information of pedigree of the dam. Ovum Pick-Up (OPU) or ultrasound guided transvaginal oocyte retrieval (TVOR) is the only means available for obtaining oocytes from live animals of known pedigree which enables repeated collection of oocytes from live animals, on a weekly or biweekly basis over long periods of time. The India's first buffalo calf from ovum pick up was born on 28 September, 2008 at G B Pant University of Agric. and Technology, Pantnagar (Maurya *et al,* 2013) and first female Sahiwal calf named 'Holi' from aged animal was born on 7 March 2012 at NDRI Karnal (Saini *et al,* 2015).

3. Stem cell Technology:

A. **Embryonic stem cells (ESCs)** have capacity to differentiate into any type of cell lineage. So, they offer great potential for regenerative medicine. Genetic manipulation prior to transplantation may not only reduce the risk of rejection but transplanted embryonic stem cells may also provide a novel vehicle for gene therapy to treat genetic or non genetic diseases. Furthermore, ESC, types may prove to be a valuable source of cells on which new candidate drugs can be tested, that has previously relied on animal models, limited human cell lines. In context of stem cell research, four differentiated buffalo embryonic stem cell lines have been established at NDRI, Karnal that are showing all properties of stemness, pluripotency and differentiated state. Embryonic stem cells have been used in production of 'Garima II' as the donor cell and that is as normal as the natural animal (George *et al,* 2011) at NDRI, Karnal. The ability of buffalo ES cells to form embryoid bodies (EBs) and to spontaneously differentiate to neuron cells, germ cells, muscular cells and epithelial cells was demonstrated by our group (Verma *et al,* 2007; Singh *et al,* 2012; Shah *et al,* 2015). In the very same way, steps are progressing to direct the buffalo embryonic stem cells towards mammary lineage so that we can imagine of artificial mammary tissue resulting higher milk production and reduced chances of mastitis in farm animals.

- An ES cell approach will reduce costs considerably by using fewer genetically valuable embryos.
- ES cells enable the researcher to place new genes in advantageous places in the genome or to remove deleterious genes.
- ES cells and homologous recombination technologies can be used to insert a transgene into a specific location in the genome. Additional milk protein could be produced if the milk gene is inserted into a high expression region of the genome.
- Another possibility is to use ES cells to "knockout" a milk protein that is detrimental to cheese or yogurt production.

B. **Spermatogonial stem cells (SSCs)** are adult stem cells of testis which are responsible for the maintenance of the spermatogenesis throughout the entire life of the male. SSCs can be used to cure infertility caused by germ cell dysfunction by their testicular transplantation resulting in restoration of fertility of recipients (Kadam *et al,* 2012). Besides the possibility to study male infertility, the SSC transplantation also provides another way to conserve reproductive potential of genetically valuable individuals within or between species and, finally, can be used to produce transgenic animals after generation of transgenic sperms. As such, SSC transplantation would be an alternative strategy to the currently less efficient and costly methods of producing transgenic farm animals (Keefer 2004). The advantage of using SSCs for transgenesis is that SSCs can be harvested, in vitro cultured, cryopreserved or transfected and still preserve the potential to colonize the recipient testes. The buffalo spermatogonial stem cells have been established and maintained for their use in fertility restoration in cross breed bulls under guidance of scientists' team at NDRI, Karnal. These encouraging results, suggest a possibility of banking and transplanting transgenic SSCs to produce sperms having desired gene which will be used to produce transgenic founder animal.

4. Cloning

Cloning is a technique used for creating genetically similar organisms from a single parent without sexual reproduction. The first ever cloned animal was 'Dolly', a sheep, which was produced by the traditional complicated method of cloning that required expensive equipment and skilled manpower.

In Hand-guided cloning, a small piece of the skin tissue of the animal which is to be multiplied is collected aseptically. The animal may be a male or a female. The tissue is cultured in the laboratory for proliferation of cells. Simultaneously, oocytes are collected from slaughterhouse buffalo ovaries and are incubated in the laboratory for maturation after which these are denuded by removing the cells surrounding them. The denuded oocytes are treated with an enzyme to dissolve the outer covering called 'zona-pellucida' following which these are given a chemical treatment which leads to protrusion of their own genetic material at one end of the periphery. The protruded portion containing the genetic material is cut off using a very sharp microblade under a dissecting microscope rendering them 'enucleated'. Two such enucleated oocytes and one somatic cell that had been obtained from the animal to be cloned are fused together using electric current. The single cell formed from the fusion of these three cells is then cultured in the laboratory for further development to the 'blastocyst' stage embryo. These blastocysts are transferred to the uterus of the recipient-buffalo (surrogate mother).

A major breakthrough was made by the scientists of National dairy Research Institute, Karnal, (Indian Council of Agricultural Research, New Delhi), India by producing World's first cloned buffalo (*Bubalus bubalis*) calf through the Hand-guided cloning technique in February 2009, when World's first buffalo calf produced by Hand-guided cloning was born on February 6, 2009 using somatic cell of a new-born calf (Shah *et al,* 2009).

5. Transgenic animal production

Genetic engineering of livestock to produce animal with altered traits such as disease resistance, wool growth, body growth, prolificacy and reproductive efficiency and milk composition is being researched in laboratories globally (Niemann and Kues, 2003; Baldassare *et al,* 2004). Numerous methods have been used to produce transgenic progeny (Niemann and Kues, 2003) with varying success. Techniques are; DNA transfer by retroviruses; microinjection of genes into pronuclei of fertilized ova; injection of embryonic stem cells; embryonic germ cells pre exposed to foreign DNA into the cavity of blastocysts; sperm mediated gene transfer (SMGT) during IVF; liposome mediated DNA transfer into cells and embryos; electroporation of DNA into sperm, ova or embryos and nuclear transfer of somatic cells, ES or EG cells. Among them pronuclear microinjection and somatic cell nuclear transfer (SCNT) have been suggested as the methods of choice to produce transgenic goats and sheep. Microinjection of cloned DNA into pronucleus of a zygote has been most widely used and successful method for producing transgenic mice. This method encompasses microinjection of several thousand copies of DNA into pronuclei of zygote. Offspring produced on transfer of such embryos are screened for integration and expression of foreign gene. During the present decade substantial advancement in livestock transgenesis has been made through application of somatic cell nuclear transfer (SCNT). The merger of nuclear transfer with molecular tools such as targeted genetic modification and conditioned gene expression will be boosting the technology of transgenesis (Niemann and Kues 2003). Genetically engineered animals are a better alternative for producing proteins, which forms the basis of all biological drugs. Important Applications of transgenic technology are:

a. Bio steel from goats

b. Xenogenic cells and tissues

c. Production of a new class of antibiotics and other pharmaceuticals

6. Conclusion

Reproduction in animals offer numerous advantages and scope for the use of novel biotechniques viz. *in vitro* embryo production, ovum pick up, Artificial Insemination, embryo transfer technology, stem cell, cloning and transgenic animal production. Nevertheless, these emerging techniques should be judicially supplemented with good practices in animal health, nutrition and management at the level of stake holders for manipulation and improvement of health, production and reproductive performance of any livestock species, which will facilitate the production and dissemination of superior germplasm thereby enhancing the overall productivity of livestock species. The most emerging technology among the above is the transgenic animal production and cloning to produce the desired drug at high levels without endangering its own health and rapid multiplication of elite, transgenic and endangered breed of animals.

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LP-08

STRATEGIES FOR MANAGING AND IMPROVING CROSSBRED CATTLE IN INDIA

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Introduction:

Cattle farming in India have long tradition and always recognized as an integral part of rural livelihood of the country. It is a well-known fact that in ancient India, primary objective of raising cattle was not for milk production but for their draught power for agricultural operations and dung for manure and fuel and because of this reason, among 41 registered cattle breeds of India, only four are considered as dairy breeds and rest are classified as draft or dual purpose breeds. Moreover, milk yield of the few important Indian dairy breeds is also not on par with the yield of exotic dairy cattle breeds. The cattle in India are raised mostly by rural farmers with an average herd size of one or two cows, mainly fed on grazing in the available agricultural/ barren land or agricultural by-products. So, indigenous cattle developed in the country are generally smaller in size, low milk producers but resistant to various diseases and well-adjusted to the adverse tropical climatic conditions (Mathur, 2000). 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.

Despite of these facts, India is ranking first in milk production due to its higher cattle and buffalo population. It was well realised by the policy makers that non-descript indigenous cattle are poor milk producers and hence a genetic improvement program is inevitability needed to improve the per animal milk production. In tropical country like India, selective pure breeding may not be feasible because of low milk production and reproduction rates and need for replacement stock as all dairy cows are potential dams for the next generations. Moreover, the genetic improvement of cattle through selective breeding is quite slow and hence the method of choice for improving milk production potential of low producing indigenous cattle is by upgrading or crossbreeding with high producing dairy breeds either indigenous or exotic.

Systematic efforts to increase milk production in tropical countries by crossbreeding date back to early this century. The evolutionary crossbreeding aiming at evolving new high-yielding and adapted dairy breeds from crossbred base would require decision on:

(i) The choice of exotic breed(s) to be involved in crosses;
(ii) The choice of native breed(s) to be involved in crosses;
(iii) The level of exotic inheritance from one or more exotic breeds, and
(iv) Future breeding of crossbreds.

These Questions have been most systematically addressed in India through various crossbreeding trails. It was found that crossing between high productive indigenous or exotic dairy breeds with well adapted low producers can improve the overall production performance with moderate adaptability in F_1 generation. According to Henderson (1927) crossbreeding of cattle was started in India as early 1875 by European missionaries when the 'Taylor breed' of cattle was evolved around Patna using Short horn bulls on native cows. This breed with all its past usefulness as high producer of milk deteriorated in its production capacity subsequently due to the absence of introduction of fresh exotic blood. In Nilgiri district of Madras State crossbreeding work was started by European planters who brought Ayrshire, Friesian and Jersey nearly one and a quarter of century back. According to the report of Committee on crossbreeding set up by Central Council of Gosamvardhana, quality of these animals degenerated owing to the use of inferior bulls. Further organized crossbreeding work was begun in Madras in 1919 under the aegis of Madras Government at the Hosur cattle Farm with the object of evolving a breed of dairy cattle by crossing Ayrshire bulls with Red Sindhi cows and interbreeding among the F_1's (Littlewood, 1933). Crossbreed cows of all the generations excelled over the Red Sindhi cows in production characteristics. There was a considerable decline in the performance of F_2 and F_3 cows as compared to F_1 cows. Most extensive results reported on cattle crossbreeding in India are based on data from Military farms. The breeding policy in operation prior to 1952 was that of criss-cross breeding. Since 1952-53, a policy of backcrossing with Sahiwal bulls was introduced to reduce the crossbred stock gradually. This ultimately led to the policy of having animals with Holstein inheritance between ½ and 5/8 obtained by alternate crossing with Holstein and Sahiwal bulls.

At Institutional level crossbreeding programme started at Imperial Dairy Research Institute, Bangalore (presently NDRI) involving Ayshire X Hariana (year 1910), Ayshire X Sahiwal (year 1913) Ayshire X Red Sindhi (year 1917) and Holstein Friesian X Red Sindhi (1938). Crossbreeding work was taken up in IARI in Bihar around 1920 with the use of Ayrshire bulls on rejected Sahiwal cows. Allahabad Agricultural Institute, Naini also started crossbreeding as early as 1924. Gir, Kankrej, Hariana and Sahiwal breeds of cows were crossed with Holstein Friesian, Brown Swiss, Jersey and Guernsey bulls during the period 1924-34. In 1955, crossbreeding work with Kerry bulls and Punganur cows was undertaken as a pilot study by the Government of Andhra Pradesh at Government Livestock farm, Palamaner, A.P. At Livestock Farm, Haringhata (Calcutta) crossbreeding work began in 1957-58 when Hariana and non-descript local females were mated to Jersey bulls. Later the project was extended to Kalyani Farm and continued with Jersey and Friesian semen to fix milk and adaptability characters by interbreeding of the cross.

Under field conditions also, crossbreeding has been carried out under different programmes and the results were evaluated.

Bilateral Projects:

Indo-Danish Project: This project was started in Karnataka using Red Dane bulls on Red Sindhi cows in 1964. An exotic farm of purebred Red Dane was established at Hessarghatta (Bangalore) to meet the bull requirement. The project has made a great impact in production of crossbred females in and around Bangalore. The performance of Red Dane x Sindhi crosses was 3193 kg in 305 days as against 2223 kg for Red Dane X Halikar crosses. This difference was attributed to low performance of Halikar cows.

Indo-Swiss Project: Indo-Swiss Project was initiated in Kerala and Punjab using Brown Swiss bulls on local cows. In Kerala, the project was started in 1963. In Kerala, crosses with 50, 62.5 and 75 % Brown Swiss have been generated. Brown Swiss crosses with 62.5 % inheritance have been bred inter-se followed by selection to create a new breed named "Sunandini". The Project has a well-established field progeny testing recording system and excellent bull rearing and semen freezing facilities.

The Indo-Swiss project at Patiala in Punjab was initiated in 1971. In Punjab, crossbreeding with Brown Swiss was done in Patiala, Sangrur, Bhatinda and Faridkot districts under Indo-Swiss Project. The exotic inheritance was kept between 50 and 60%. The overall average daily milk yield was 3.29 litres in local cattle and 5.35 litres in crossbred cows. Imported BS cows were superior to locally born BS cows in milk yield but reserve was true for age at first calving and calving interval. Brown Swiss was however discontinued in 1977 due to lower performance of its crossbreds and Holstein was started in use.

Indo-German Agricultural Development Project: This project was started in 1963 in Mandi (HP) and Almora (UP) districts and included small scale programmes for improvement in the quality of cattle through crossbreeding with German Spotted Mountain breed. In Almora, the project provided assistance for importation and use of frozen semen from Brown Swiss bulls for crossbreeding of cattle. This project was discontinued due to very large size German cattle used, which resulted in difficult calving and low inputs available in the area.

Revisions on the Crossbreeding Policy of the country:

In 1961, the committee was set up by the central Council of Gosamvardhana, evaluated various crossbreeding experiments in organized farms and recommended crossbreeding to be taken up in an intensive manner with two or more exotic breeds in three selected areas, one each in plateau, plains and hills.

Further, the scientific panel on Animal Husbandry reviewed the cattle breeding policy in 1965 and recommended for the use of Jersey as exotic inheritance in bulk. The crossbreeding with Brown Swiss and Holstein should be tried to a limited extend. It was also suggested to restrict the exotic inheritance to half and interbreeding was to be followed in halfbreds. The high level of exotic inheritance could be tried in areas with satisfactory feed and fodder availability and with progressive farmers.

The National Commission on Agriculture in 1970 recommended that Holstein Friesian can be used as a source of exotic inheritance, where health cover and adequate feed supply can be assured, although bulk of exotic inheritance should come from Jersey. It was also recommended in hilly areas exotic breeds like Brown Swiss and Red Dane should be used. The crossbreeding policy should broadly aim at producing crossbreds with 50-75% exotic inheritance. Also, selective breeding of important indigenous and grading of non-descript low producing cattle with superior indigenous breeds was also recommended.

Considering the impact of crossbreeding on increasing the milk production, ICAR has initiated the Frieswal project at Military Farms on 23rd may, 1985 in collaboration with Ministry of Defence, Government of India to evolve a national crossbred cattle involving HF and Sahiwal named 'Frieswal' (ICAR, 2002), with 62.5 per cent exotic inheritance level, yielding 4000 Kg of milk with 4% butter fat in a lactation of 300 days under good managemental conditions (PDC Annual Report, 2002-2003). Before the inception of Frieswal project, Military Farms had Friesian x Sahiwal crossbreds with very low to a very high HF blood level. However, with the introduction of Frieswal project, crossbred females with 5/8 HF inheritance were *inter-se* mated and crossbreds having exotic blood level of 62.50 ± 5.00 were described as Frieswal cattle. The Frieswal cows yielding 4000, 4500 and 5000 kg milk yield in any of the first, second and third and above parities, respectively with 4 % fat in a standard lactation length of 300 days are declared as elite cows and eligible to become the bull mothers.

Crossbred cattle breeds / strains developed in India:

The crossbreeding experiments conducted in the country have led to the development of various crossbred strains / breeds. The different crossbreeding programmes implemented in the country and the crossbreds developed are given in Table-1. From the various crossbreeding experiments with *B. indicus* and *B. taurus* conducted nearly for a century in India, the major conclusive facts arrived which will serve as foundation of future breeding strategies for cattle improvement in the tropical climatic conditions are.

- The F1 crosses between *B. Taurus* X *B. indicus* showed higher production and reproduction performance as compared to F2 (obtained by inter se mating amongst F1).
- HF X Indigenous crossbred cows were superior (in growth and milk production) than Brown Swiss or Jersey crosses irrespective of agro-ecological condition and indigenous breeds involved. However, for fat percentage the order of exotic breeds was just reverse. Moreover, Jersey crosses were slightly better in reproductive traits.
- Non-descript cow X exotic bull crossbred cows were inferior in performance as compared to well defined zebu X exotic crosses.
- Exotic inheritance around 50% was most ideal for growth, production and reproduction under tropical climate. Exotic inheritance beyond 50% either from one or two exotic breeds have no or very little advantage.
- Crossbreeding resulted to significant increase in milk yield, lactation length and decrease in age at first calving and calving interval in crossbred population in contrast to indigenous cows.
- Three bred crosses had no significant advantage over two breed crosses.

Population status and milk production of crossbred cattle:

According to the integrated sample survey of BAHS (2016), the crossbred cattle constitutes around 20.81 per cent of total cattle population of the country. The total crossbred population during 2015-16 was 39.73 million consisting of 5.97 million male and 33.76 million female animals. The analysis of milk production by different species revealed that the crossbred cattle was the second highest contributing around 26% of annual milk production. However, the defined indigenous and non-descript cattle contributed only 12 and 9 per cent to the national annual milk production, respectively during the year 2015-16.

The estimates on number of various bovines in milking and their average daily milk yield over the period from 2011-12 to 2015-16 are presented in table-2. Perusal of data revealed that the number of buffaloes in milking was always the highest during these periods followed by non-descript or indigenous cows and exotic or crossbred cows. However, average daily milk yield is highest for crossbred cows followed by buffaloes and then the non-descript or indigenous cows. These estimates also infer that crossbreeding programme was successful in increasing the milk production potential of cows by producing the crossbred progenies, but failed to cover major population of non-descript cattle. Hence there is an urgent need to formulate and implement genetic improvement programmes for increasing the milk production potential of these low yielding non-descript cows. The number of buffaloes in milking and their average milk yield over the years were almost constant indicating that no drastic progress was achieved in this species also.

Consequences of crossbreeding in India:

1. The crossbreeding programmes implemented in the country has increased the crossbred cattle population and thereby increased per animal milk production and per capita milk availability.

2. The crossbreeding also helped to exploit the heterosis through complementarity and non-additive genetic effects but it was often found that the amount of heterosis is reduced in the subsequent generations.
3. The crossbred animals are comparatively docile to handle easily and are suited for machine milking.
4. Crossbreeding of Indigenous cattle breeds with exotic dairy breeds has resulted in the dilution / erosion of indigenous cattle genetic resources. Even though, the breeding policy for genetic improvement of indigenous cattle did not recommend their crossing with exotic breeds, the significantly higher milk production observed in the crossbred progenies has overwhelmed the breeders to extend the crossbreeding to the indigenous breeds also to produce such high producing crossbred cattle.
5. The introduction of exotic germplasm into Indian cattle also resulted in the introduction of many infectious diseases of temperate origin such as Blue Tongue, Infectious Bovine Rhinotracheitis (IBR) etc. Moreover, the crossbred cattle are comparatively more susceptible to the tropical diseases like FMD, mastitis and tick bone diseases
6. Higher incidence of reproductive disorders viz., anoestrus, repeat breeding etc. in females and poor libido and poor semen quality in bulls lead to higher culling rate in crossbred cattle.
7. Indian dairying is predominantly in the hands of rural farmers who maintain the indigenous or non-descript cattle which require minimum inputs. Hence, upgradation with high yielding tropical cattle breeds may be irrelevant under the small holding system of rural farmers having only limited resources in terms of higher initial investment, feeding, maintenance and veterinary cost etc., to maintain high yielding crossbred cattle.

Strategies for improving the performance of crossbred cattle:

Crossbreeding was started during mid of 19th century using superior temperate dairy breeds to improve the low milk productivity of indigenous cattle, crossbreeding Holstein Friesian (HF) and Jersey breeds and presently almost every fifth cattle in the country is a crossbred. Improving or even maintaining the productivity of this huge crossbred population will remain a challenge and opportunity in ensuring milk production and availability in future. Progeny testing of crossbred bulls under farm and field conditions to estimate the expected breeding values of the sires based on the performance of their daughters and use of high ranking bulls for breeding will continue. Genetic improvement programmes implemented over the decades have helped to improve their milk production potential and presently the crossbred cattle produce an average daily milk yield of 7.33 kg and plays a significant role in the milk production of the country. However, their genetic potential for milk production is not fully exploited so far due to the adverse tropical climatic condition, shortage of quality feed and fodder, high incidence of diseases and other reproductive problems. Hence, in the small holding cattle production system, crossbreds cannot perform better but in commercial herds where resources are available in plenty, crossbred cattle can be maintained for higher milk production and hence steps must be taken to increase the commercial herds. The genetic improvement obtained in the traditional field progeny testing is very low (0.5-1.0 per cent) and hence an alternative method of early evaluation of sires using MOET & Full sib information as given in Fig.1 may be implemented for early selection of bull calves and faster genetic improvement in crossbred as well as indigenous breeds.

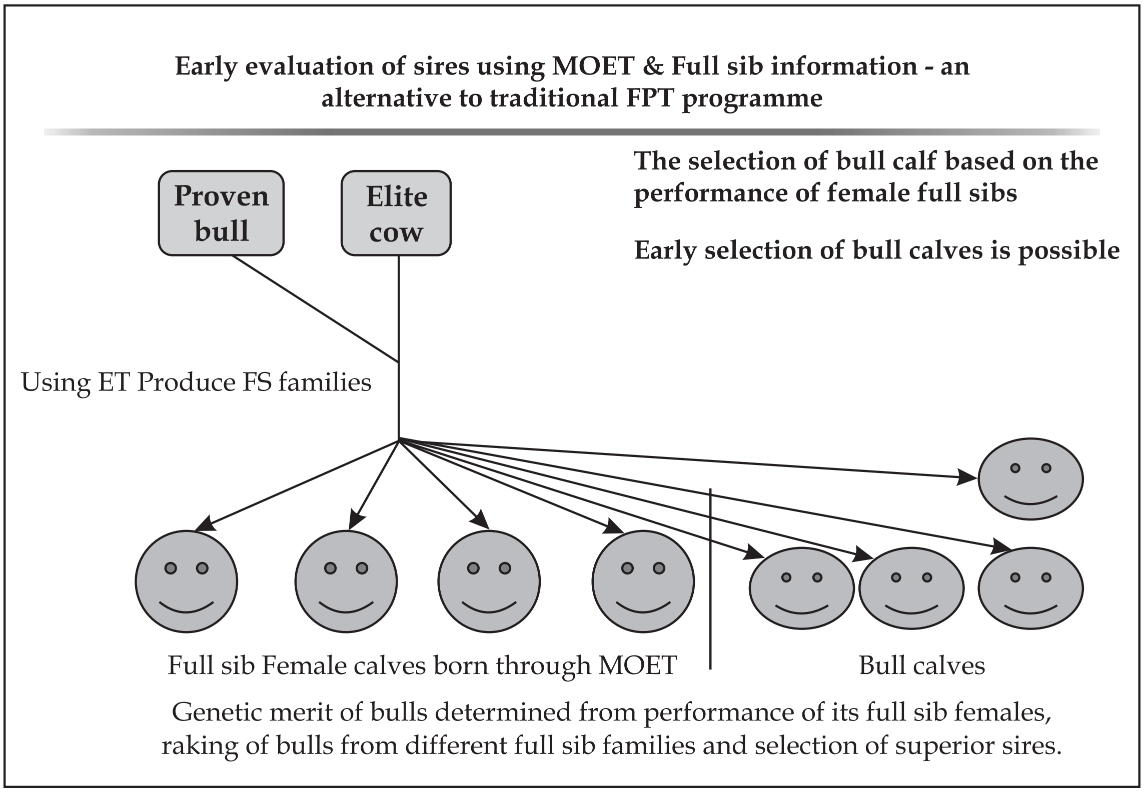

Fig 1. Alternative method of early evaluation of sires using MOET & Full sib information

Establishment and strengthening of bull mother units for different crossbred cattle:

In general, the availability of genetically proven bulls of different crossbred cattle breeds have been limited at all times which hindered the implementation of genetic improvement programmes. Simultaneously, in western countries at the turn of the last century, tremendous improvements in productivity were achieved through scientific management, recording and breeding. As per the 19th national livestock census (2012), the crossbred female population is 33.76 million and there is a huge gap in the number of breedable males available and actually required to breed this vast female cattle population. Assuming that by 2050, 100% of the crossbred breedable females will be bred through AI and with improvement in technical expertise the number of inseminations per conception will be reduced from the current 2.5 to 2.0; and sperm concentration/ dose will be reduced from the current 20 million to 15 million and the crossbred population will be reduced at the rate of 25 per cent per decade. Based on the assumptions, 214 crossbred bulls may be required to cater to the AI requirement of the projected crossbred population of 10.68 million in 2050.

In order to cater this huge demand of superior crossbred male germplasm, it is necessary to establish the network of farmers and organized herds maintaining crossbred animals. To breed the larger population of crossbred cattle, male calves born to elite females and proven bulls of crossbreds to be reared and progeny tested using farmer's herds along with organized herds. The bull mother farm and bull rearing unit for each of significant breeds of the country need to be established and strengthened to cater the future need of breeding bulls of the country. The existing bull mother units and semen banks are to be strengthened by procuring the male calves born to high yielding females in farmers' herds.

Bringing about 70% of entire cattle population under genetic improvement programme using AI, reliable field data recording (establishment of effective BS)

Even though, the country has the largest A.I. infrastructure facility in the world, breeding through AI is only 25-27% of the entire national bovine population and the rest are bred by natural mating using whatever bull is instantaneously available to the farmer in his vicinity, which leads to indiscriminate breeding and generation of non-descript population. The unavailability of proven male germplasm, lack of properly trained man power, poor conception rate following AI, inadequate infrastructure resources for maintaining good quality frozen semen at field level, non- implementation of the recommended breeding policies, poor nutrition and health care are the major reasons for the poor AI coverage and its success rate. However, as a result of recent concerted efforts, frozen 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 million. In order to increase the AI coverage from the present level of 25-27 per cent to 70 per cent in 2050, the cattle breeding programmes of Central as well as State governments need to be strengthened, properly linked and coordinated and all the farmer herds need to be included under the genetic improvement programmes.

Meeting the nutritional requirement of high producing cattle population

Genes are not everything. An animal's genetics is not the only factor in determining its performance. Genes describe the potential of an animal, but the environment- feed, nutrition, stress, herd management etc., has strong influence on whether that potential is actually reached, in most cases a stronger influence than genetics alone (heritability). The large livestock population of our country demands higher quantity of feed and fodder for animal feeding and this requirement is ever increasing. The major constraints are the reduced availability of crop residue as fodder, shrinkage of land area under fodder cultivation (only 4 per cent area) and grazing, competition with the increasing human population for grains, poor nutritive value of the available 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 in 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 areas requiring immediate attention? Breed specific feeding standards are to be developed for increasing the feed efficiency of cattle.

Management of Fertility, Reproduction and Health for Higher Productivity

The reproductive efficiency of crossbred cattle in our country is suboptimal. The increased age at puberty and first calving, service period, calving interval, dry period etc. result in decreased efficiency which in turn decreases the lifetime milk production. It is estimated that if dry period per cow 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 cause 21 per cent loss in milk production of the country. The higher incidence of reproductive problems viz., repeat breeding, anoestrus, infertility etc. affect the efficiency and many intrinsic and extrinsic factors are associated with it. The fertility of the herd, herd health and the nutritional status are some of the decisive factors which determine the reproduction efficiency. It is a well-known fact that the milk production and reproduction traits are antagonistic in nature as selection for increased milk production decreases the reproductive efficiency. In India, the sole selection criteria in cattle is milk production and the reproductive parameters are not taken into consideration which results in reduced reproductive efficiency. The reproductive problems are more pronounced in high yielding crossbred cattle than in indigenous cattle which reduce the overall milk production. The nutritional status of the animals, disease incidence etc. are also some of the factors which decides the reproductive efficiency. Efforts are needed to increase the reproductive efficiency of cattle through optimizing the health, nutrition, comfortable housing and genetic selection.

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.

The new and improved 'black box' approach which is called as "Genomic selection" signals a new era in genetic improvement. Genomic selection, which enables prediction of the genetic merit of animals from genome wide SNP markers, has already been adopted by dairy industries worldwide and will allow faster improvement in productivity as well as health, reproduction and longevity. Recording of accurate and authentic data on families and individuals on production, health, reproduction and other important traits will be crucial even while using genomic selection. In genomic selection variation in DNA sequences among individuals is used along with pedigree and individual performance data, to predict the predicted transmitting ability (PTA) of individuals with increased reliability.

Generating reference families for recording precise data, sequencing the genomes of Indigenous breeds, discovery of breed specific SNPs, prioritizing SNPs based on their desirability and development of indigenous breed specific SNP chips and their use in improvement of our breeds will be tremendous challenge and opportunity in obtaining the targeted production.

Development of sexed semen technology and its application for producing animals of desired sex

Sex is the most important genetic trait and being able to choose sex at conception is the most coveted reproductive technology of all times, as confirmed by Greek documents nearly 2500 years old. Commercially available sexed semen at around 90% precision is now a reality and has resulted in a paradigm shift for some dairy herds in developed countries. The possibility of modifying sex ratio can result in a substantial increase of the production and can enhance the effectiveness of selection and genetic improvement programs, through the differential increment of males or females born after AI. In dairy farming female calves are more attractive than the male calves.

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 more 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.

However, the technique is not common in our country due to the lack of expertise and high 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 and provided to farmers. There are three issues with currently available sexed semen which will be addressed through increased research efforts; accuracy is only around 90%, cost per semen dose is higher (beyond the reach of Indian farmers) and fertility with sexed semen is about 10% lower than with unsexed semen under ideal management and may be even lower under Indian management conditions. Starting with 2020, 5% of cattle breedable females can be brought under sexed semen every five years. Depending upon the success of the technology and its adoption, the per cent age can be increased as and when required.

In addition, the following facts may also be considered for improving the production potential of crossbred cattle of the country.

- Infusion of fresh exotic germplasm of choice will help to increase the genetic base of the existing crossbred population which will help to retain the genetic variation necessary for improving the production potential of the crossbred cattle.
- Rigorous selection in male and females should be done to increase the genetic merit of the crossbred cattle. The small herd size of the farmers can be utilized for genetic evaluation of young bulls through associated herd progeny testing programme. The field progeny testing model of AICRP on Cattle can be extended to different agro-climatic regions of the country so as to avoid the effect of varying environmental conditions.
- The application of Assisted Reproductive Technologies like ovum pick up, IVM, IVF, embryo transfer, cloning etc. can be done to produce large number of high genetic merit bull calves.
- In addition to milk production traits such as milk quality, reproduction, functional and other adaptive traits may also be included in the genetic improvement programme for overall improvement in the performance of crossbred cattle.
- The surplus non-descriptive cattle population may be targeted at large scale for their upgradation to increase the milk production.
- The region based breeding policy on selection of exotic germplasm should be formulated for increasing the efficiency of crossbred milk production.
- An efficient package of practices covering all aspects of crossbred management needs to be prepared for effective utilization of the genetic potential of crossbred cattle.

Conclusion:

The results of crossbreeding experiments conducted in India proved beyond doubt that crossbreeding is one of the best method of breeding for improving the milk production of cattle significantly. However, the intrinsic factors such as small herd size of cattle owners, inadequate availability of frozen semen doses of superior crossbred bulls, unplanned breeding programme leading to reduction in heterosis in the subsequent generations, poor AI coverage, limited availability of quality feed and fodder resources, high incidence of reproductive disorders, varying agro-climatic conditions preventing the implementation of an uniform breeding policy, lack of proper data recording, lack of awareness on scientific crossbred cattle management, lack of veterinary facilities, health concerns regarding A1, A2 milk etc., are some of the limiting factors which prevents the successful implementation of the breeding programme for exploiting the full genetic potential of the crossbred cattle. The change in the cattle breeding policy addressing the above constraints will definitely help to improve the milk production performance of crossbred cattle to cater the nutrient requirement of ever increasing human population of the country.

Table 1. Development of synthetic breeds of cattle in India

Name of synthetic strain	**Year/Period (Approx)**	**Institute involved**	**Location / area for breeding**	**Breed involvement at initial stage**		**Level of Exotic inheritance**	**Remarks**
				Native breeds involved	**Exotic breeds**		
Taylor	1875	Divisional Commissioner of Patna	Patna and adjoining areas of Bihar	Local (Non-descript)	Shorthorn	-	Lack of systematic breeding resulted in loss of strain
Jersind	1953	Allahabad Agricultural Institute, Naini	Institutional farm	Red Sindhi	Jersey	3/8 to 5/8 Jersey	Small in number, Genetic depletion/ deterioration over the period; Loss of strain
Brown sindh	1955	Allahabad Agricultural Institute, Naini	Institutional farm	Red Sindhi	Brown Swiss	3/8 to 5/8 Brown Swiss	Small in number, Genetic depletion/ deterioration over the period; Loss of strain
Jerthar	1958	NDRI, Bangalore	Institutional farm	Tharparkar	Jersey (Australian and American Strain)	-	Small in number, Genetic depletion/ deterioration over the period; Loss of strain
Karan Swiss	1963 (Modified in 1980)	NDRI, Karnal	Institutional farm	Sahiwal, Red Sindhi (few in number)	Brown Swiss	1/2 to 5/8 HF	Small in number, Genetic depletion/ deterioration over the period; Loss of strain
Karan Fries	1971 (Modified in 1980)	NDRI, Karnal	Institutional farm	Tharparkar	HF, Brown Swiss, Jersey	1/2 to 5/8	Number is less (<1000), however breeding is being continued
Sunandini	(initiation of crossbreeding 1964)	KLDB	Kerala state	Local (non-descript) as major, Traces of Sahiwal, Gir, Kankrej	Jersey, Brown Swiss (BS), Holstein	50% exotic inheritance	Sizeable population and being continued
Frieswal	1987	Project Directorate on Cattle and Military Farms	Military farms all over India	Sahiwal	Holstein Friesian	Around 5/8 HF inheritance	Sizable population and continued
Vrindavani	Initiated crossbreeding in 1968	IVRI, Izatnagar	Institutional farm	Hariana	Holstein Friesian, Jersey, Brown Swiss	Exotic inheritance 50-75%	Number is less, however breeding is being continued

Table 2. Estimates of number of bovines in milking, milk production and their daily average yield from 2011-12 to 2015-16

Animals	Number of animals in milk (000 nos.)					Milk production (000 tones)					Average yield per animal in milk (kg/day)				
	2011-12	2012-13	2013-14	2014-15	2015-16	2011-12	2012-13	2013-14	2014-15	2015-16	2011-12	2012-13	2013-14	2014-15	2015-16
Exotic or crossbred cows	12294 (14.90)	12642 (15.20)	13755 (16.36)	14147 (16.51)	15411 (17.44)	31075.42	32383.95	33888.65	36938.92	41931.24	6.97	7.02	6.78	7.15	7.33
Non-descript	31881 (38.80)	31870 (38.33)	31035 (36.91)	31801 (37.12)	31753 (35.94)	26695.24	27421.30	28306.22	29484.53	31714.15	2.27	2.36	2.50	2.54	2.79
Indigenous cows	38193 (46.30)	38638 (46.47)	39286 (46.73)	39725 (46.37)	41190 (46.62)	65352.41	67675.43	70442.62	74709.90	76459.00	4.71	4.80	4.91	5.15	4.78
Buffalo															

Figures in parentheses indicates per cent of animals

Table 3. Requirement of breeding males over different periods up to 2050

Year	Breedable female population (Million)	% of breedable female covered with AI	Number of AI per conception	Frozen semen doses required (Million)	Bull requirement for semen production (1.0 lakh doses/ bull)	Bull requirement for natural service (350 cows/bull/ year)	No. of sperm/ dose (Million)
Present	33.76	100	2.5	84.40	844	0	20
2020	25.32	100	2.0	50.64	506	0	15
2030	18.99	100	2.0	37.98	380	0	15
2040	14.24	100	2.0	28.48	285	0	15
2050	10.68	100	2.0	21.36	214	0	15

NATIONAL SYMPOSIUM: Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income &
XV Annual Convention of Society for Conservation of Domestic Animal Biodiversity (SOCDAB)
8-10 February 2018 at College of Veterinary & Animal Science, Rajasthan University of Veterinary & Animal Sciences, Bikaner (Rajasthan)

LP-09

RECENT ADVANCEMENT IN POULTRY GENETICS FOR MEAT AND EGG

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With a modest beginning as backyard venture, poultry sector is established as a full-fledged industry in the country within last 35-40 years. Scientific breakthroughs and innovations have resulted in development of genetically superior stocks, capable of higher production even under adverse climatic conditions, as well as in development of modern poultry production methods which allowed the increased efficiency of production for both meat and egg-type poultry. As a result, poultry is now one of the fastest growing segments of the agricultural sector in India and many other countries. The increase in production volume and productivity per bird may largely be attributed to the ongoing genetic improvement programme and release of modern strains of broilers and layers which have transformed the poultry sector. At present the high yielding commercial broiler attain 2 kg body weight about 40 days with FCR below 1.7 and high survivability. Similarly, for layer high yielding strains produce over 330 eggs/annum with an FCR of 125 g feed/egg have been developed. The parallel development of other input sub-sectors like feed mill, hatchery and farm appliances, poultry biological, feed analytical and disease diagnostic labs., modern mechanized processing plants etc. have also contributed to the present level of growth.

Current Scenario of Poultry Production:

Indian poultry sector is growing with an estimated growth of 6-7% per annum in egg and 15-20% per annum for meat as well as 7.3% growth in poultry population. With this spectacular growth, India is world's 3rd largest egg producer with 66.45 b egg (≈ 3.83 mmt) & 5 th largest poultry meat producer with 3.9 MMT of poultry meat. World's total production of poultry meat during 2011 was approximately 101.6 mmt comprising of 85.6% chicken, 6.8% turkey, 4.6% duck, 2.6% goose and Guinea fowl meat. India's contribution to world's egg and chicken production is nearly, 4 and 2%, respectively. Poultry industry contributes about Rs. 600 billion accounting for about 0.77% of the national GDP and ~10% of the livestock GDP and provides employment to over five million people in the country. Poultry sector is known to have one of the highest employability per unit of investment. The export share of India is also growing and its present values is Rs. 5407 m (0.51 mmt) share 0.7% in global poultry trade. Important items of exports from India are hen-eggs-in-shell, dried eggs, chicken meat, egg liquid, chicken (canned), duck meat etc. The poultry cumulative aggregate growth rate is 8.42% as against 1.79% in livestock.

Taking the production levels of 1970-71 as baseline, present status of production in India is present below:

Indicators	1970-71	2016-17	% change
Egg production	5.3 b	88.13 b	1562.8
Broiler production	0.12 MMT	3.46 MMT	2783.33
Broiler Traits			
• Body weight	1.5 kg at 10 weeks	1.8 Kg at 5 weeks	
• FCR	2.5	1.7	
Per capita meat availability	0.22 kg	3.35 kg	1422.72

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Egg production traits • Egg numbers • Feed conversion efficiency • Egg weight (g)	 270 2.65 47.5	 340 2.01 58	 26% 32% 13.09
Per capita egg availability	10 p.a.	69 p.a. (2015-16)	590.0
Poultry population	138.5 million	729.21 million	426.51

Inspite of phenomenal growth in poultry sector, the present per capita availability is far below the ICMR recommended level of 180 eggs and 11 kg meat; still the wide gap between demand and availability exists to meet the needs of ever increasing human population.

Conventional breeding approaches:

The principles of fundamental and quantitative genetics were utilized for designing the pure line breeding schemes for exploitation of genetic variation in existing germplasms all over the world and then crossing these lines to achieve maximum heterosis. As such the heavy breeds of chicken like Cornish, Aseel, Plymouth Rock, Australorps etc. were crossed in order to combine their best characters for developing the synthetic grandparent stocks of modern broiler strains which are crossed to produce parents (two way crosses) and commercials (three or four way crosses). Since the body weight has been a highly heritable trait the mass selection was good enough to achieve the desired genetic gains. Similarly, for layer high yielding strains were developed using mainly the White Leghorn and other breeds like RIR, Minorca, Plymouth Rock etc. have also been utilized. The advancement also took place in selection procedures and statistical analytical tools. The multi-trait multisource indices and other indices involving individual's, family, sib, sire and dam information are now being practiced for bringing simultaneous improvement in many traits. The variance components are now evaluated more precisely using advance statistical procedures like ML, REML, MINQUE and MIVQUE BLUP. The overall, improvement in production have been brought through advancements in breeding, nutrition, management, health and bio-security as well improving the welfare of birds along with ensuring environmental security.

(i) **Pure line breeding for development of specialized lines:** Since most of the production and reproduction traits are genetically negatively correlated this necessitated the development of specialized sire and dam lines for economizing the desired performance in the crosses. Specialized sire and dam lines were developed through unique selection programme based on different set of traits for sire and dam lines.

- **Layers:** For layer the objectives primarily is "To obtain maximum number of saleable eggs per hen housed at low feed cost per egg or per kg egg mass and the eggs should have optimal internal and external qualities. Stock should have low mortality and high adaptability to different environments". Layer breeders apply selection to improve over 30 traits important for commercial egg production. Breeders today select for (or at least monitor) the 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. The selection strategies to improve egg production include part-time egg production records, persistency of lay, clutch length, FCR/Residual feed consumption (RFC), skeletal problems (majorly osteomalacia and osteoporosis).
- **Broilers:** For broilers selection strategies concentrate on rapid growth and carcass traits. The most practiced strategy for broiler pure line selection is **Selection at commercial weight** which employ selection at a weight that matches market weight and the age at selection becomes progressively earlier as growth potential increases. The other two

strategies are selection at a commercial age and multi-stage selection. Breast muscle weight, meat quality and FCR are major traits, in addition to these, thrust is also being given on skeletal abnormalities, metabolic disorders and welfare. Breast muscle measurements (length, maximum and minimum width) were taken in live birds, using a pachymeter at 42 day of age, together with body weight. Selection for higher breast area resulted in a genetic gain of 277% per generation, whilst keeping the body weight in the range of 2400 to 2450 g and feed conversion and fertility in the actual levels. More accurate, non-destructive measurements are measuring the thickness of the breast muscle using needle catheters, ultrasonic apparatus has been employed. Expensive but very accurate methods to assess the body composition of live birds include the Computed Tomography scan (CT scan), Magnetic Resonance Imaging (MRI) and Echography. Ultrasound technology is one of the potential strategies for the improvement of breast meat yield. While practicing the artificial selection, care is taken to minimize the inbreeding and its related consequences in the population. A control population with the same increment in inbreeding as the selected population may be maintained for comparison and evaluation of the selected population.

(ii) **Exploitation of genetic superiority through crossbreeding:** Development of synthetic lines using specialized selection programme and their utilization through cross breeding has been the vital tools for the progress made in poultry production. The modern commercial poultry strains sustaining the present day production have been developed by crossing the selected parent lines. The advantages of crossbreeding in poultry are manifold. Crossbreeding tends to increase the heterozygosity for many pairs of genes resulting in exploitation of both additive and non-additive effects of genes. The heterosis in the concerned traits leads to better performance in crossbreds than that in purebreds. Crossbreds are expected to be more uniform and less influenced by environmental factors than their parental lines. Crossbreeding is also the most economical method for combining stocks that complement one another effectively. For a successful crossbreeding program, estimation of crossbreeding parameters and identifying the superior cross combination of lines is essential. A number of experimental design e.g. Diallel cross analysis, Three-way cross analysis, analysis of Double-cross hybrids, Line x Tester analysis, North Carolina designs, Recurrent Selection, Reciprocal Recurrent Selection etc are available to estimate crossbreeding parameters. Of these diallel or partial diallele cross have been most extensively used for estimation of general and specific combining abilities which have helped in maximizing the genetic gains through identification of best lines and cross combinations.

(iii) **Evaluation of crosses under specific climatic conditions (G X E Interactions):** The ultimate aim of the breeding scheme is to evolve a commercial cross that performs optimally under specific climatic conditions. Therefore, the cross needs to be evaluated under specific climatic condition before releasing it for commercial exploitation. Differentiation between micro and macro-environments and between intra and inter-population genotypes is also important. Typical macro-environments are diets, ambient temperature and climatic differences such as those between seasons or regions. Micro-environments are the random environmental differences within a population. The success of a particular cross in a particular environment depends on its ability to adapt and perform in particular environment or climatic zone. The available evidences for GxE interactions in performance analysis of modern broilers and various suboptimal conditions emphasizes the need for breeding programmes aimed at improving performance under particular environment.

Advances in poultry genetics: Molecular Biological approaches

The conventional breeding strategies in association with biotechnological tools may help in improving the production. However, the advance molecular biology approaches have potential to break the barriers of biological limits for dramatic increase in production or alternative use of poultry.

Genomic approaches:

- **Genome wide QTL Scans:** Diversified groups of chicken (for particular traits) and their crosses may be developed for genome wide scanning and QTLs identification for meat production and immune responsive traits. So far, genome wide scan have revealed 14 QTL for resistance to MD (Yonash *et al,* 1999) one for salmonella resistance (Marriani *et al,* 2001) and one for resistance to coccidian (Zhu *et al,* 2003). Three QTL were found associated with general immune response to ND Virus and E.coli (Yonash *et al,* 2001). QTLs conferring resistance to Marek's disease (MD) in commercial layer chickens were identified; seventeen markers were associated with MD survival (McElroy *et al*, 2005).
- **Genomic Selection:** Genomic selection is an advanced form of marker assisted selection (MAS) which concentrates on all markers across the whole genome (Meuwissen *et al,* 2001; Calus, 2010). Meuwissen *et al* (2001) proposed the original concept of genomic selection, i.e., predicting breeding values of animals using information offered by thousands of SNPs across the genome (genomic estimated breeding value, GEBV), by assuming the availability of abundant SNPs scattered throughout the genome and LD relationships between SNPs and QTL. Illumina's Bead Array based on single-base extension or allele-specific primer extension (*http://www.illumina.com*) and Affymetrix's Gene Chip based on molecular inversion probe hybridization (*www.affymetrix.com*) are the two biggest and most competitive SNP chip genotyping platforms. Aviagen started developing its first SNP panel. With rapid technological advances, the chip density increased from 6K (Andreescu *et al* (2007), to 12K (Powel *et al* (2011), 42K (Wang *et al* (2013), Chicken 60 K SNP array (Groenen *et al,* 2011) and ultimately to 600K SNPs (Kranis *et al* (2013). Genomic selection models don't solve the problems of low accuracy for traits with low heritability and limited number of records. This is especially advantageous in breeding programs for layers where there is no information available on males before they have records on offspring performances (Wolc *et al,* 2016). Application of single step genomic prediction in general leads to increased accuracy of predicted breeding values for both genotyped and non-genotyped individuals in broiler (Chen *et al,* 2011). An alternative derivation of the single step prediction model based on Bayesian principles were presented by (Fernando *et al,* 2014).
- **Functional genomics:**
    - **Microarray:** Based on techniques used the microarray are of two types i.e. Spotted DNA microarrays (cDNA and Oligo arrays) and in-situ synthesized oligo arrays (commercial companies are Affymatrix- using photolithography (masks), NimbleGen- using mirror photolithography (mask less) and Agilent-using inkjet synthesis). DNA Microarray is a small chip of finger nail size containing thousands of spots. A 14K Chicken Integrated Systems Microarray has been developed (Cogburn *et al,* 2004). This universal high-density microarray is currently being used for time-series transcriptional profiling across multiple tissues from divergently selected lines of broiler chickens. The Gene Chip uses oligonucleotide sequences as its probe. These oligonucleotides are about 25 bp in length. The Gene Chip (Affymatrix) for about 32,773 transcripts of poultry genes are now available (*http://www.affymetrix.com/products/arrays/specific/chicken.affx*). FHCRC Chicken 13K Array with multi-tissue cDNA microarray of

13,007 features and ARK Genomics 5K immune cDNA chicken array (Burnside *et al,* 2005, Smith *et al,* 2006) and a 4,800 clone chicken neuroendocrine array from ARK genomics have been reported. Mendonca *et al* (2016) performed microarray to analyse the AMR and virulence in *E. coli* strains isolated from poultry.

- **RNA Sequencing:** As one of the powerful next-generation sequencing techniques, RNA-seq has expanded knowledge on the extent and complexity of transcriptomes (Wang *et al,* 2011). Spleen transcriptome response to infection with avian pathogenic Escherichia coli in broiler chickens (Sandford *et al,* 2011) revealed that many of the significantly differentially expressed (DE) genes were unique to a particular treatment. Analysis for allele-specific expression (ASE) in response to MD viral infection a total of 6,132 SNPs in 4,768 genes and 4,528 SNPs in 3,718 genes in broilers and layers, respectively were identified. Furthermore, 548 and 434 genes in broilers and layers, respectively, were found to show DE (Perumbakkam *et al,* 2013). The bioinformatic analysis of sequences obtained by next generation sequencing of four cDNA libraries (1 library each for AIV infected and noninfected Leghorn and AIV infected and non-infected Fayoumi) from lung tissues suggested that the hemoglobin family genes, the functional involvements for oxygen transportation and circulation and cell adhesion molecule signaling pathway play significant roles in disease resistance to AIV infection in chickens (Wang *et al,* 2014b). Total 139 immune-related genes that were found differentially expressing in the two Necrotic Enteritis-induced chicken lines, 150 cytokines with differential expression were identified in the two chicken lines; 15,518 candidate novel genes that may be involved in the host immune response to NE disease were also found (Truong *et al,* 2015). The loci for six immune traits viz. total IgY level, numbers and ratio of heterophils and lymphocytes and antibody responses against AIV and SRBC in chickens were identified using genome-wide association studies (Zhang *et al,* 2015).

Genetic modifications:

i. **RNAi:** Since the discovery of RNA interference (RNAi) in *C. elagens* by Fire *et al* (1998), post transcriptional gene silencing (PTGS) through small interfering RNA (siRNA) has come up as a powerful molecular tool for production of knock down animals and analyzing the role of particular gene(s) in the biological processes (Lee and Rossi, 2004). siRNA have been used for silencing myostatin gene (GDF-8) in cultured embryo fibroblasts (Meng and Zhu, 2002). Silencing of myostatin gene in cultured embryo fibroblast of Coloured Synthetic Male Line broilers to the tune of 24-25% in has been achieved (Nandedkar *et al,* 2008). Genes of certain pathogen like Rous Sarcoma Virus (Hu *et al,* 2002 and 2004), Hepatitis C & B, (Wilson *et al,* 2002; McCaffrey *et al,* 2003), influenza A (McCown *et al,* 2003), SARS (Lu *et al,* 2004) viruses have been silenced using RNAi. Lentiviral mediated MSTN silencing in *in-vitro* system has been achieved (Saxena *et al,* 2013). Tripathi *et al* (2012) reported up to 68% silencing of myostatin mRNA using shRNA constructs in transiently transfected fibroblasts with induction of interferon responsive genes (OAS1, IFN-β). Bhattacharya *et al* (2015) analysed the effect of ACVR2A and ACVR2B genes on carcass traits in chicken.

ii. **Genome editing:** In poultry, genome editing technology combined with germ cell culture system has been widely utilized to establishment diverse genome-edited lines. Recently, primordial germ cells (PGCs), which can be cultured and genetically modified *in vitro*, have been used to generate transgenic chickens by taking advantage of their germline competency after injection into recipient embryos (Van de Lavoir *et al,* 2006; Macdonald *et al,* 2010 & 2012; Park *et al,* 2012). The efficiency increased with the use of retroviral and lentiviral vectors, but targeting and more subtle mutations are not possible with these approaches. The first targeted knockout chicken was produced by Schusser *et al* (2013) by disrupting immunoglobulin heavy chain gene in cultured PGCs by homologous recombination with a targeting construct. Subsequently, Park *et al* (2014) generated specific ovalbumin (OV) knockout chickens through the use of TALEN-mediated gene targeting in PGCs. These two discoveries have experimentally proven the proof of knockout concept in avian species. Another site-specific nuclease-mediated genome-editing technology, such as CRISPR/Cas9 have potential improve the knockout efficiency as CRISPR/Cas9 system can be easily transfected because of fairly small size compared to TALEN. The advantage of CRISPR/Cas9 is preparation of the plasmid for targeted gene disruption is much easier and more cost-effective compared with the TALEN-mediated method (Cong. *et al,* 2013; Mali *et al,* 2013).

Conclusion:

The conventional breeding techniques have brought manifold improvement in poultry production. The long term intensive selection programmes have led to exhaustion of most of genetic variability. Simultaneously, extensive use of these high yielding stocks at global level has increased the probabilities of disease outbreak in such stocks. These situation warrants for (i) developing the more refined tools for assessing available genetic variability (ii) developing alternate selection criteria for improving disease resistance/meat quality etc. and (iii) developing the stocks with high production potential which are genetically robust to varied pathogens present in environment as well as to the mutant pathogenic strains. The recent molecular biology/ biotechnological tools may be of wide applications in augmenting poultry production and protection. The advance techniques RNA seq have greatly added to our knowledge of molecular pathways and differentially expressing genes which may be used for manipulation by gene driven approaches. The recent high density array based genomic selection is expected to have high promise in improving production traits and disease resistance in livestock and poultry. The recent genome editing technologies also have tremendous potential for improving the poultry productivity and quality of products.

LP-10

DELINEATING GENETIC DIVERSITY OF INDIAN BUFFALOES USING MOLECULAR TOOLS

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The livestock sector is an important source of livelihood and income to majority of population world-wide including developing countries like India. Among the dairy animals, buffaloes are the major contributors to the milk production in India, which is evident from the 19th livestock census report claiming 4.95% growth in buffalo population, whereas the dairy cattle population witnessed an increase of only 0.17% over previous census (http://dahd.nic.in/documents/statistics/livestock-census, 19th Livestock Census 2012). Besides their input to dairy sector, buffaloes also contribute significantly to meat industry, since buffalo meat is ranked top animal commodity being exported by the country. India has exported 13,30,660.48 M of buffalo meat products to the world worth Rs. 26,307.93 Crores/3,933.81 USD Millions during the year of 2016-17 (http://apeda.gov.in/apedawebsite/SubHead_Products/Buffalo_Meat.htm). The Indian subcontinent is home to buffaloes of both swamp and riverine types, spread across the varied agro-climatic conditions. Total 13 breeds of buffaloes have been registered so far in India from diverse habitats, which includes, Murrah, Nili Ravi, Bhadawari, Mehsana, Surti, Jaffarabadi, Banni, Nagpuri, Marathwadi, Pandharpuri, Toda, Chilika and Kalahandi (http://www.nbagr.res.in). The registered breeds account for almost 57% of total population and remaining around 43% are the part of populations yet to be characterized.

Besides phenotypic characterization, genetic characterization helps in delineating the genetic relatedness and distinctness of a breed. Various molecular characterization tools have been used to document the genetic diversity existing among different breeds/populations of livestock species of different countries. Genetic characterization provides information about the genetic constitution of a breed or population of a species. It evaluates the genetic uniformity, admixture or subdivisions, inbreeding or introgression in the population also providing insights into breed formation, evidence about closest wild ancestral species and locating the site(s) of domestication. Phylogenetic relationships of populations based on genetic analysis unravel the evolutionary history of the breeds/populations of a species. Through this, means we can prioritize the breeds for conservation using molecular data. Among various molecular tools available, FAO recommends using microsatellite markers, mitochondrial D-loop sequencing, Y-chromosome sequencing or single nucleotide polymorphism based markers for genetic characterization. Among these, microsatellites are the markers of choice alongwith using mitochondrial D-loop sequencing, both of which have been used extensively for characterization of genetic diversity among Indian livestock species. Among buffaloes, apart from 13 registered riverine breeds, few non-registered populations including swamp, riverine and their hybrid buffaloes of northeast have also been characterized using microsatellite markers as well as mitochondrial D-loop sequencing. Besides these recommended markers, attempts have also been made to document the allelic diversity among polymorphic sites identified in candidate genes governing various production, adaptation and disease resistance genes among the buffaloes adapted to varied agro-climatic conditions and production systems.

Below are described various molecular markers and their utilization for genetic characterization of buffalo populations of India.

Microsatellite markers

Microsatellites are simple tandem repeated (STRs) motifs of 1-5 nucleotides that are densely and evenly distributed throughout the genome and often exhibit substantial variation/ polymorphism due to the site specific length variation, as a consequence of the occurrence of different number of repeat units. The difference in repeat number can be reliably distinguished and the variants are inherited as alleles at each locus. The polymorphic nature of this type of locus, with variations many times more common than is non-repetitive sequence, makes microsatellite ideal for examining genetic variation within a species. Microsatellites occur at a frequency of 1 SSR per 10kb DNA and numbering a total of about 50–100 thousands in the mammalian genome. Their short lengths make them amenable to amplifications by PCR and subsequent separation by polyacrylamide gels or running on automated DNA sequencer with the resolution of alleles differing by as low as single base.

Among all the PCR based methods used for microsatellite markers analysis, fluorescent dye is the most suitable and recent method developed for the detection of alleles in microsatellite analysis. The dyes offer greater sensitivity than other methods but the main advantage is that PCR primers can be labeled with dyes, which have different absorption spectra, thus permitting the simultaneous analysis of microsatellites with alleles, which overlap in size, meaning that through multiplexing, it is now possible to run and generate data on several markers in a single run.

Food & Agricultural Organization (1996) has well laid detailed technical programme for large scale international conservation using microsatellite markers under MoDAD project. Number of species specific microsatellite markers have already been well characterized for establishing genetic relationship and diversity among all breeds. International comparison tests under the auspicious of International Society of Animal Genetic (ISAG) to establish international standard also exist. High level of polymorphism coupled with the ease of analysis has made this type of markers being one of the most widely used for genetic analysis. FAO has recommended 25 set microsatellite markers to be used for nine major livestock species and chicken (http://www.fao.org/docrep/014/i2413e /i2413e00.pdf). The usefulness of microsatellites for estimation of genetic distances among closely related population has been documented by numerous studies.

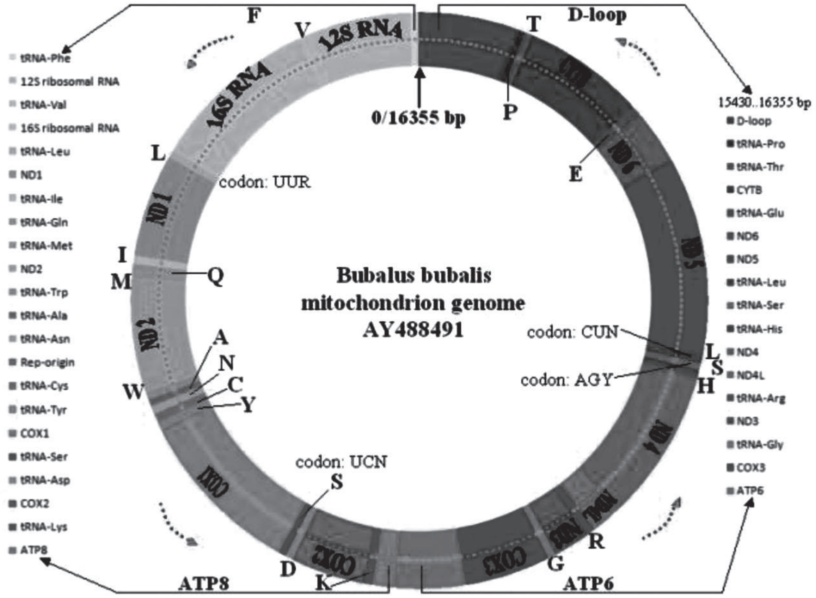
Microsatellites are thus the best available molecular markers today because of their ease of generation and highly polymorphic nature. Their use makes it possible to obtain an unprecedented understanding of the process and dynamics of biodiversity, its evolution and nature. Based on the data generated by the microsatellite characterization, clustering of different breeds is possible, which will pave the way for designing breeding strategies as well as prioritization for the conservation of breeds.

Genetic characterization of Indian buffaloes using microsatellite markers

At NBAGR, set of 25 microsatellite markers have been used to analyze the genetic diversity existing in distinct buffalo breeds and populations. DNA isolated from fifty random samples per breed/population is amplified using fluorescent labelled primers designed for 25 sets of microsatellite markers and genotyping carried out on an automated DNA sequencer. Data generated is analysed using various software available and various breed wise parameters like heterozygosity, allelic diversity, FST, FIS inbreeding, bottleneck and phylogenetic analysis carried out to evaluate within and between breed genetic diversity. In a study, riverine and northeast swamp buffaloes have been characterized genetically, indicating distinct population structures among the breeds/populations. Phylogenetically also riverine and swamp buffaloes could be classified into discrete clusters, hybrids of riverine and swamp in between two types. Microsatellite markers have supported the phenotypic data in classification and identification of new breeds of buffalo like Banni, Chilika and Kalahandi.

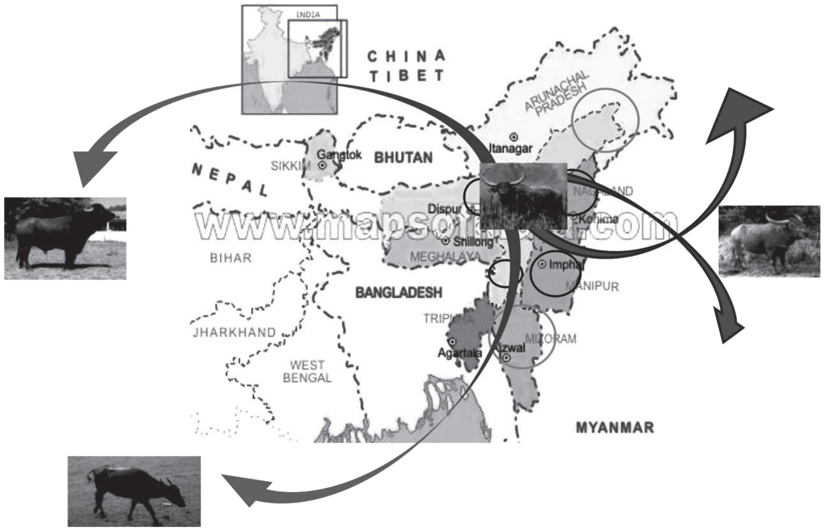
Mitochondrial D-loop sequencing

Mitochondrial D-loop sequencing has been used widely to derive maternally derived evolutionary relationships among populations of a species. For genetic characterization based on mitochondrial DNA (mtDNA), sampling of animals with common maternal origin should not be taken. mtDNA D-loop sequencing could be used as a powerful tool for establishing the levels of genetic diversity and phylogenetic structure within a species. We can also delineate recent demographic processes affecting a population. Unlike genomic sequence, here each individual has a single haplotype therefore, phylogenetic analyses are relatively straightforward to interpret. Typical sources of DNA recovered include blood, semen, hair, bones, teeth and body fluids such as saliva. Standard procedure (phenol-chloroform method) should be followed for DNA extraction. Standard polymerase chain reaction (PCR) procedure should be followed to amplify small amount of DNA. The nucleotide sequences obtained from sequencing is analysed further for sequence alignment, identification of nucleotide variations, generation of haplotypes, estimation of population indices, such as, gene diversity, nucleotide diversity and pairwise nucleotide differences, calculation of within breed and among breed differences through ANOVA, determination of demography, determination of population expansion, estimation of phylogenetic relationship among different breeds of a species, identification of ancestral and descendent haplotypes by using various software programme.



(Michelizzi *et al,* 2010)

We have used highly polymorphic, mitochondrial D-loop sequence analysis, supported by microsatellite markers and cytogenetic analysis to study the divergence and evolution of swamp and riverine buffaloes of India. The results have shown riverine and swamp buffaloes having common evolution point in Assam, where the wild progenitor of both types, the *Bubalus arnee* still exists alongwith riverine, swamp and their hybrids.



Evolution of swamp and riverine buffaloes

Candidate gene polymorphism

Being under selection, candidate gene polymorphism may not give overall genetic diversity measures, the neutral markers like microsatellites can provide. Nevertheless, we have tried to explore the genetic diversity at the functional loci of important genes governing milk production, meat quality and disease resistance in buffaloes. The data generated has helped in identification of the unique genetic variability in riverine and swamp buffaloes. The nucleotide variations resulting in the amino acid changes of protein have been studied for their possible impact on protein structure and function. Besides, some of the genetic polymorphism detected has helped in finding its association with traits like mastitis resistance and susceptibility.

Conclusion

The molecular markers have thus emerged and have also been effectively used as a powerful tool for assessing the population structure and understanding the genetic relationships among different buffalo populations/breeds. These tools have helped in understanding the evolution of riverine and swamp type buffaloes and also supporting the phenotypic data in identification of new breeds.

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LP-11

USE OF BIOINFORMATICS FOR ENHANCING PRODUCTIVITY IN INDIAN LIVESTOCK RESOURCES

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The productivity of an animal is mainly by genetic makeup. Understanding the genome is very much need of the hour to estimate and enhance the productivity of our livestock breeds. Bioinformatics generates new knowledge that is useful for study of methods of storing, retrieving and analyzing biological data, such as nucleic acid, protein sequence, structure, pathways and genetic interactions.

Animal Genomics

The study of the whole genome started from 1990s, the focus was on the identification of genetic variants using the Genome Wide Association Study approach, which is based on microarrays or chips with tens of thousands of SNPs. In a GWAS, each SNP is statistically tested for significance of association with the trait/phenotype of interest. When compare with human SNP chips, the number of SNPs on an animal SNP chip is much smaller, e.g. 60 K for pig and chicken, 50 K for sheep and 777 K for cattle. An important bioinformatics task is the annotation of the GWAS variants that explain a certain proportion of phenotypic variation and the prediction of functional properties, which serve to build ontology-based functional networks based on many databases. Recently, the Functional Annotation of ANimal Genomes (FAANG) International Project Consortium was launched (http://www.faang.org/), to bring together animal scientists and sustain a steady focus on collaborations among this community. Three of four committees in this FAANG consortium address key issues on the functional annotation of animal genomes based on contributions from researchers worldwide, i.e. the Animals, Samples and Assays (ASA), Bioinformatics and Data Analysis (B&DA) and Metadata and Data Sharing (M&DS) committees. In addition, the 1000 Bull Genomes Project has provided the bovine research community with a huge volume of data on bovine variants that will be useful for GWAS and the identification of causal mutations (http://1000bullgenomes.com). These initiatives pave the way for a systematic incorporation of the findings of systems biology and systems genetics and for making them available online.

Emerging Technologies in Genomics and Epigenomics

Technology in the genomic and epigenomic fields is developing fast and provides opportunities for new ways of investigating the genome or epigenome and further implementation in animal breeding methods. With the growing power and speed of NGS, genome-wide genetic variation is now captured at the DNA sequence level at tens of millions of genomic locations. Epigenetic variation also contributes to phenotypic variation through histone modifications and DNA methylation at the gene level, which can lead to changes in or absence of the expression of genes that underlie a phenotype or a disease.

Animal Transcriptomics

Transcriptomic research investigates the expression levels of all gene transcripts in a particular cell, at a particular time and in a particular state. Up-regulation and down-regulation of genes result in different levels of proteins and metabolites that induce phenotypic changes in the animal. Thus, a better understanding of the regulation of genes should provide insight into the biological functioning and detection of genes that are important in diseases or production traits. The most common approach to analyze expression data is to compare expression levels between two states, e.g. healthy versus diseased or high-productive versus low-productive animals, also called differential expression analysis.

Animal Metabolomics and Proteomics

Metabolomics serves not only as a source of qualitative but also quantitative data on intracellular metabolites that are essential for the model-based description of the metabolic network operating under in vivo conditions. Proteomics aims at describing the complete repertoire of proteins in an organism, while metabolomics is the study of global metabolite profiles in living systems. In recent years, several studies in livestock have investigated the metabolome and metabolite profiling studies are now a rapidly expanding area in animal and veterinary genomics. Metabolomics tools aim at filling the gap between genotype and phenotype by permitting the simultaneous monitoring of molecules in a living system. There are a wide variety of publicly available databases and tools for storing, querying, browsing, analysing and visualizing metabolomic networks. The Path Case Metabolomics Analysis Workbench (PathCaseMAW: http://nashua.case.edu/PathwaysMAW/Web/) runs on a manually created generic mammalian metabolic network. The mapping of protein–protein interactions (PPI) networks to phenotype and disease pathways is a key to understanding various biological and patho-physiological processes. Such interaction studies can be combined with studies on the conservation of non-coding RNAs across large evolutionary distances and on their potential functions in mammalian genomes.

Functional Annotation and Pathway Analyses

Gene-based annotation can identify whether SNPs or CNV cause protein coding changes. For this purpose, gene definition systems such as RefSeq genes, UCSC genes, ENSEMBL genes, GENCODE genes are used. Genomic region-based annotation identifies variants in specific genomic regions, for example, conserved regions, NGS-based DE/CE regions, transcription factor binding sites, GWAS regions, etc. Although similarity-based GO annotation is widely applied, it primarily encompasses sequence data with reciprocal best hits to predict candidates from a huge repertoire of multi-omics data. However, some of the orthologues of these sequences do not remain associated to GO terms and can be cross-validated with conserved domains, manually reviewed data or determined by wet lab experiments, thus allowing the biological appropriateness of the functional assignments. The unannotated regions in the form of hypothetical proteins or "known unknowns" i.e. their existence is predicted but their function is not known, represent a huge problem, since they remain assigned to the three root terms as in the case of AMIGO (http://amigo.geneontology.org/amigo). A few methods have been designed to integrate different structural and functional results with data corresponding to GO relationships of organisms. In addition, the genome assemblies of many species are regularly refined and updated when new information is available. There has been an increase in the development of integrated analyses that provide comprehensive and robust GO annotations of genome assemblies, providing a solid foundation for functional interrogation of other genomes (http://www.ebi.ac.uk/GOA). Development of pathway maps and identification of unique and novel signals have transformed pathway association studies in cattle. Furthermore, Medical Subject Headings (MeSH, http://

www.nlm.nih.gov/mesh) provides a comprehensive life science vocabulary for human and model organisms' research. Multi-faceted 'omics' is aided by the choice of annotation and enrichment analyses for interpreting GO-aided MeSH functional terms.

Emerging Technologies in Pathway Profiling and Genetic Networks

The Pathway Network Analysis approach (PANA) integrates high-throughput data and their functional annotation using machine-learning methods. The end-user can detect the functional modules that are associated within the molecular system and the transcriptional connections in a disease or a phenotype. Molecular systems biology integrates networks in the form of pathways, interactions and/or associations.

Multi-Omic data from Genome to Phenome: Integration in Systems Genomics

The term 'systems genetics' or 'systems genomics' in an animal breeding focuses on the integration of different 'omics' levels with functional annotation, both on a single gene level and pathway analysis level, to integrate all different multi-omic levels to phenotypes. A typical data integration process goes from genome → epigenome → transcriptome → metabolome → proteome → phenotype or disease variome.

Domestic Animal Information Systems

A number of public-domain electronic information systems for animal genetic diversity are globally accessible and contain data from more than one country. Two of these – the Domestic Animal Diversity Information System (DAD-IS) and the European Farm Animal Biodiversity Information System (EFABIS) (previously EAAP–AGDB) – are related to the FAO global information system for AnGR. The Domestic Animal Genetic Resources Information System (DAGRIS), managed by ILRI is a database of synthesized research information from published and grey literature. Oklahoma State University's Breeds of Livestock information system provides brief summaries of breed origins, characteristics and uses.

DAD-IS [http://www.fao.org/dad-is]

The Domestic Animal Diversity Information System (DAD-IS) developed by FAO is the first globally accessible dynamic multilingual database of AnGR. It was initiated as a key communication and information tool for implementing the Global Strategy for the Management of AnGR, to assist countries and country networks in their respective programmes (FAO, 1999). Apart from country-level breed information and images, DAD-IS provides a virtual library containing a large number of selected technical and policy documents, including tools and guidelines for research related to AnGR. It offers Weblinks to relevant electronic information resources. It also has a facility for the exchange of views and for addressing specific information requests, by linking a range of stakeholders: farmers, scientists, researchers, development practitioners and policy-makers.

DAGRIS [http://dagris.ilri.cgiar.org/]

The Domestic Animal Genetic Resources Information System (DAGRIS) is developed and managed by the International Livestock Research Institute (ILRI). It was initiated in 1999 as a tool to collate research information available on global AnGR. In addition to containing information, obtained from a synthesis of the literature on the origin, distribution, diversity, characteristics, present uses and status of indigenous breeds. DAGRIS is unique in that it includes complete references and abstracts of published or unpublished scientific literature pertaining to the breeds in the system.

Efabis (European Farm Animal Biodiversity Information System)

Recognizing their common interest in documentation and information of animal genetic resources in Europe and raising awareness on the need for conservation and sustainable use of these resources, ERFP and EAAP have agreed to maintain and update the European Information System for AnGR (EFABIS). EFABIS covers passport, descriptive and performance data as well as population and other data of the animal breeds in Europe.

Animal Genetics Training Resource (AGTR) http://agtr.ilri.cgiar.org/agtrweb/

The Animal Genetics Training Resource (AGTR) is developed by a team working on the project "Capacity Building for Sustainable Use of Animal Genetic Resources in Developing Countries". The International Livestock Research Institute (ILRI) and the Swedish University of Agricultural Sciences (SLU) jointly implement the project, which started in 1999. The overall objective of the project is to enhance human capacity in the developing countries of Sub-Saharan Africa, Asia and Latin America in the area of conservation and sustainable use of animal genetic resources.

ICAR- National Bureau of Animal Genetic Resources (NBAGR) http://www.nbagr.res.in/

In India, the National Bureau of Animal Genetic Resources (NBAGR) established on 1984 at Bangalore in the form of twin institutes namely National Bureau of Animal Genetic Resources and National Institute of Animal Genetics and then shifted to Karnal in 1985, the two institutes were merged to function as a single entity in the form of National Bureau of Animal Genetic Resources (NBAGR) in 1995. This premier institute is dedicated to work with its mandate of identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country. An Information System on Animal Genetic Resources of India (AGRI-IS) has been developed at NBAGR, Karnal, India. This database contains descriptors of various breeds of livestock and poultry, information on farms, semen production, vaccine production; and district-wise information on population, animal breeding, animal health infrastructure, animal products like milk, meat, egg, wool, etc. It also stores photographs of male and female animals of breeds.

Useful Websites and Databases for Improvement and Conservation of Livestock

AIPL Animal Improvement Programs Laboratory (http://www.aipl.arsusda.gov)

AOAD Arab Organization for Agricultural Development (http://www.aoad.org)

ARCBC Association of South East Asian Nations Regional Center for Biodiversity Conservation (http://www.arcbc.org)

BCBS Boran Cattle Breeders' Society (http://www.borankenya.org)

CARDI Caribbean Agricultural Research and Development Institute (http://www.cardi.org)

CDN Canadian Dairy Network (http://www.cdn.ca)

CENARGEN National Research Centre for Genetic Resources and Biotechnology (http://www.cenargen.embrapa.br)

CGIAR Consultative Group on International Agricultural Research (http://www.cgiar.org)

CIAT International Center for Tropical Agriculture (http://www.ciat.cgiar.org)

CIRDES Centre International de Recherche-Développement sur l'Élevage en Zone Subhumide (http://www.cidres.org)

DAD-IS Domestic Animal Diversity Information System (http://www.fao.org/dad-is)

DAGRIS Domestic Animal Genetic Resources Information System (http://dagris.ilri.cgiar.org)

DDBJ DNA Data Bank of Japan (http://www.cib.nig.ac.jp)

EAAP European Association for Animal Production (http://www.eaap.org)

EAAP-AGDB European Association for Animal Production – Animal Genetic Data Bank (EFABIS)

EFABIS European Farm Animal Biodiversity Information System (http://efabis.tzv.fal.de)

EFSA European Food Safety Authority (http://www.efsa.europa.eu)

EMBL European Molecular Biology Lab (http://www.embl.org)

EMBRAPA Brazilian Agricultural Research Corporation (http://www.embrapa.br)

EU European Union (http://europa.eu)

FAO Food and Agriculture Organization of the United Nations (http://www.fao.org)

FAOSTAT FAO of the UN Statisitcal Databases (http://faostat.fao.org)

FARA Forum for Agricultural Research in Africa (http://www.fara-africa.org)

FIRC Federacion Iberoamericana de Razas Criollas (http://www.feagas.es/firc/firc.htm)

GEF Global Environment Facility (http://www.gefweb.org)

IAEA International Atomic Energy Agency (http://www.iaea.org)

IAMZ Mediterranean Agronomic Institute of Zaragoza (http://www.iamz.ciheam.org)

ICAR International Committee for Animal Recording (http://www.icar.org)

ICARDA International Center for Agricultural Research in the Dry Areas (http://www.icarda.org)

IES Institute for Environment and Sustainability (http://ies.jrc.cec.eu.int)

IFAD International Fund for Agricultural Development (http://www.ifad.org)

IGAD Intergovernmental Authority on Development (http://www.igad.org)

IICA Inter-American Institute for Cooperation on Agriculture (http://www.iica.int)

ILRI International Livestock Research Institute (http://www.ilri.org)

INTERBULL International Bull Evaluation Service (http://www-interbull.slu.se)

IRD Institute de Recherche pour le Développement (http://www.ird.fr)

ISAG International Society of Animal Genetics (http://www.isag.org.uk)

LPP League for Pastoral Peoples (http://www.pastoralpeoples.org)

MoDAD Measurement of Domestic Animal Diversity

NZRBCS New Zealand Rare Breeds Conservation Society (http://www.rarebreeds.co.nz)

OECD Organisation for Economic Co-operation and Development (http://www.oecd.org)

OIE Office International des Epizooties (http://www.oie.int)

OSS Obervatoire du Sahara et du Sahel (http://www.unesco.org/oss)

RBI Rare Breeds International (http://www.rbi.it)

Red XII-H Red Iberoamericana sobre la consevación de la biodiversidad de animales domésticos locales para le desarollo rural sostenible (http://www.cyted.org)

SAARC South Asian Association for Regional Cooperation (http://www.saarc-sec.org)

SACCAR Southern African Center for Cooperation in Agricultural Research and Training (http://www.info.bw/~saccar/sacca.htm)

SADC Southern African Development Community (http://www.sadc.int)

SAVE Safeguard for Agricultural Varieties in Europe (http://www.save-foundation.net)

SGRP System-wide Genetic Resources Programme (http://www.sgrp.cgiar.org)

SINGER System-wide Information Network for Genetic Resources (http://www.singer.cgiar.org)

SPC Secretariat of the Pacific Community (http://www.spc.int)

UNDP United Nations Development Programme (http://www.undp.org)

UNESCO United Nations Educational, Scientific and Cultural Organization (www.unesco.org)

UPOV International Union for the Protection of New Varieties of Plants (http://www.upov.int)

USDA United States Department of Agriculture (http://www.usda.gov)

WAAP World Association for Animal Production (http://www.waap.it)

WHFF World Holstein-Friesian Federation (http://www.whff.info)

WHO World Health Organization (http://www.who.int)

WIPO World Intellectual Property Organization (http://www.wipo.int)

WTO World Trade Organization (http://www.wto.org)

WWL–DAD:3 World Watch List for Domestic Animal Diversity, 3rd edition

Conclusions

The current and emerging technologies within the fields of genomics / epigenomics, transcriptomics, metabolomics, proteomics and its uses for improvement of productivity in livestock species were discussed. Due to the enormous progress in technologies, data generation is becoming cheaper and easier, resulting in huge amounts of data at different 'omics' levels. The challenge that remains is to use all these 'omics'-level data sets efficiently by removing errors/ noise via good quality control methods for each layer of dataset, appropriate data integration as per the defined systems genomics hypothesis and statistical models, application of advanced statistical-bioinformatic algorithms and meaningful interpretation of results. Through such extended, biologically and functionally meaningful and accurate genomic selection methods, improvement of animal production, health and conservation will leads to faster and more sustainable in future.

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GENOMIC SELECTION AND ITS USE IN LIVESTOCK IMPROVEMENT

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In the past 50 years there has been an unprecedented increase in human population. On the basis of current projections, the world population will reach 9 billion by 2030, so will be the demand for food. If year 2000 were used as a base year, projections indicate an increase in global meat consumption of 68% and in global milk consumption of 57% by 2030. For that reason we need a rapid development in production via selection and breeding. The efficiency of the traditional method of selection decreases when traits are difficult to measure, have low heritabilities, or when not able to measure quickly, inexpensively and correctly in a large number of animals. To overcome these drawbacks of traditional method, Meuwissen *et al* (2001) proposed genomic selection. It is the selection on the basis of the genotypes for tens of thousands of random Single Nucleotide Polymorphisms (SNPs) that cover the genome. Selection decisions are made based on genomic breeding values (GEBV). Genomic selection increases the intensity of selection and decrease generation interval by 3 times compared to the traditional method. At present, the reliability of GEBV for production traits is often very high. Worldwide, approximately 2 million dairy cattle have now been genotyped for the purposes of genomic prediction. The accuracy of genomic prediction in dairy cattle exceeds 0.8 for production traits and 0.7 for fertility, longevity, somatic cell count and other traits. In general, however, accuracies of genomic predictions in beef cattle have been lower than in dairy cattle. Due to current availability of whole genome sequence of animal and commercial whole genome SNP chips developed for important agricultural species the genomic selection is gaining pace and will continue to develop in future.

SP-51

EXPLICATING EQUINE GENETIC DIVERSITY THROUGH MARKER ASSISTED SELECTION AND BIOINFORMATICS TOOLS

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The genetic variation in livestock is primarily owing to differences in DNA, base mutations, Indels (insertions or deletions), the CNVs (Copy number variations) and fragments inverted or replaced etc. Although marker-assisted selection (MAS) and genomic selection (GS) have been scantly applied in the animal agriculture, their application in breeding programmes could be a prolific area of research. During past more than 20 years, micro satellite screening was explicated in the domestic animals extensively. In India, many native breeds of agriculturally important livestock were assessed by microsatellite markers *viz* goat, chicken, cattle, buffalo, pig, camel, horse and others, however, new insights into variant calling are always needed. There are seven registered breeds of horses and one registered breed for donkey in India. These breeds have adapted certain unique traits like endurance, relative disease tolerance, sturdiness, sure-footedness and capacity to work under harsh climatic conditions. Past studies indicated indiscriminate breeding in Indian horses especially Marwari breed, which attracts the attention of researchers to dig in detail the population structure of these prestigious horses. Phenotypic similarities between Marwari and Kathiawari as well as among pony breeds necessitated evaluation for predicting exact relationship between breeds as well as extent of genetic diversity within each breed, their mixing and structure between and within Indian equine breeds. The admixture, individual relationship, genetic closeness and population structure were determined in Marwari and other indigenous horses through *F-statistics, POPGENE* and *Structure* softwares. This study conducted with a panel of 24 polymorphic microsatellites revealed high number of alleles and heterozygosity in the Marwari horses. The admixture studies showed mixed structure and individual relationship among the horses. For determination of selection signatures, Fst value was determined and most of the markers are highly polymorphic as reflected from high polymorphism content, thus suitable for horse genotyping studies. Systematic breeding and management is the need of the hour for majestic Marwari breed.

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DIVERSITY STATUS OF ARUNACHALI YAK: A PRECIOUS GERMPLASM OF INDIAN LIVESTOCK

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Member of family Bovidae, domestic yak *Poephagus grunniens L.* is considered to be emerged from its wild ancestor *Poephagus mutus*. Arunachali yak is the only known yak breed of India in the list of 168 breeds registered so far for the indigenous germplasm, pointing towards predominantly unexplored yak diversity of the country. Adaptation to extremely harsh environment makes this animal one of the most important livestock genetic resources of the India. For the first time genetic diversity status of Arunachali Yak was investigated by using 26 bovine microsatellite markers. All the markers were polymorphic except one (ILSTS05) and a total of 233 alleles were detected. One locus (MM12) depicting less number of alleles (3) was excluded from further analyses. Arunachali yak was found to host considerable diversity as concluded by the number of alleles observed across loci (average 9.32±0.70, range 3-16). Observed heterozygosity (0.55±0.04) was less than expected heterozygosity (0.65±0.04) pointing towards decreasing level of diversity. In addition, positive value of F_{IS} index (0.14±0.04) in the population also pointed towards inbreeding. Recent bottleneck

events were absent according to non-significant heterozygote excess based on Infinite Allele Model along with a normal 'L'-shaped distribution of mode-shift analysis. According to published reports, number of Arunachali yak population has shown a declining trend over the years due to increased indiscriminate breeding, a shift in profession from agriculture to other sectors, threats from predators and diseases, reduction in availability of fodder and a reduced enthusiasm among yak herders (*Brokpa*). In summary, inbreeding and decline in population necessitates the need of designing and implementing scientific management of Arunachali yak being an interesting gene pool with moderate level of diversity.

Keywords: Arunachali Yak, Microsatellite markers, Genetic diversity, Inbreeding, Bottleneck.

SP-53

FIRST REPORT OF JERSEY HAPLOTYPE 1 (JH1) MUTATION CAUSING SPONTANEOUS ABORTION IN INDIAN JERSEY CATTLE: DEVELOPMENT OF NOVEL PCR ASSAY FOR RAPID GENETIC SCREENING

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Jersey haplotype 1 (JH1) comprises a haplotypic region of 5 Mbpon BTA 15, encompassing a mutation locus (rs1115118696) at g15707169 position of *CWC15* gene in cattle. This stop-gain mutation causes premature termination of CWC15 splicosome-associated protein homolog, a protein important for mRNA splicing, perhaps during embryonic development. It is the newest and probably the most frequent lethal genetic mutation responsible for spontaneous abortions in Jersey cattle across the world. This study was aimed to screen out the JH1 mutation in Indian cattle population as well as developing a protocol for its rapid detection. We amplified a 1246 nucleotide long region of *CWC15* exon 3-4 in a panel of 5 different genetic groups- Jersey, Jersey Crossbred, Holstein Frisian (HF), HF Crossbreds and indigenous *Bos indicus* with 10 males in each group. Amplified PCR products for each genetic group were further pooled and sequenced for the presence of the JH1 mutant allele. Among these, we found a heterozygous condition of alleles (wild C and mutant T) with two peaks at JH1 locus in Jersey genetic group only, whereas, in other genetic groups only wild (C) allele was detected. PCR-RFLP by *Taq*$^{\alpha}$I enzyme was employed in individual samples of these Jersey males, which confirmed the JH1 mutant allele in four malesin heterozygous condition. A novel tetra-amplification-refractory mutation system (ARMS) PCR assay was developed for screening of the JH1 mutation in cattle. The tetra-ARMS PCR assay was further validated through developing alternate strategy of PCR-RFLP using *Taq*$^{\alpha}$I enzyme with outer pair of tetra-ARMS PCR primer set. This is the first report about the presence of JH1 mutation in the Jersey population in India, quite possibly with higher frequency; and needs urgent attention in order to avoid its further spread. Further, the novel tetra-ARMS PCR assay developed would be helpful for rapid screening of the JH1 mutation in cattle population, specifically of Jersey origin.

SP-54

EVALUATION OF THE CHROMOSOME STABILITY OF NATIVE AND CROSSBRED CATTLE OF ENDOSULFAN-HIT AREAS OF KERALA

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Kasaragod dwarf, a desi cattle variety and Holstein Fresian crossbred cattle, 30 each, belonging to four major endosulfan-hit panchayaths of Kasaragod district of Kerala were evaluated for their genome stability consequent to the chronic exposure to endosulfan over the past years. Extensive survey and secondary data collection on the health history of the herds with regard to growth, production, calf mortality, blood chemistry, teratogenic and reproductive abnormalities, infertility and repeat breeding were undertaken. Cytogenetic investigation based on sister-chromatid exchange (SCE) analysis of the metaphase spreads revealed that the SCE frequency/ cell in Kasaragod dwarf and HF crossbreds were 3.343 ± 0.38 and 4.543 ±0.42, respectively and in both the genetic groups, the range of SCE /cell ranged from 0 to 9. The mean SCE/cell in the native and CB controls were 1.398 ±0.25 and 1.579 ±0.21 with a range of 0 - 3 and 0 - 5, respectively. The mean SCE frequencies for native and crossbred cattle in the endosulfan affected areas were found to be higher by 184.5% and 176.4% than those for the control groups and this differed significantly between the genetic groups ($P<0.05$). The range of SCE in the animals of affected region was also found to be higher than the unaffected group. The significant increase in the SCE frequencies of cattle reared in areas with high exposure of endosulfan throws light on the possible chromosomal damage or mutation occurring at low frequencies but excellently repaired or balanced naturally through replication to mask their physiological effects. It may also be noted that Kasaragod dwarf cattle in spite of their low input management system and nomadic grazing behavior possessed significantly lower SCE frequency than the crossbreds indicating the possibility of a stable genome or much more chromosome stability when compared to the crossbred cattle of the region.

SP-55

A NEW INSIGHT ON THE ROLE OF DGAT1 SEQUENCE POLYMORPHISM ON MILK FAT CONTENT IN *BOS INDICUS* CATTLE

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The candidate gene *DGAT1* (Diacylglycerol acyltransferase) responsible for the biosynthesis of triglycerides in milk fat was found to be fixed for lysine allele in most *Bos indicus* cattle breeds of India however isolated phenotypic trials suggested the presence of discernible variation in milk fat of indigenous cattle. Therefore the present study was conducted to explore the presence of genetic variation in *DGAT1* gene through multimarker based system and to observe their association with milk fat content in three indigenous cattle breeds (Rathi, Sahiwal and Kankrej). Blood samples were collected from 225 randomly selected milking cows with 75 samples from each breed maintained at LRS, Bikaner and LRS, Kodamdesar. A 411 bp fragment length of *DGAT1* gene was amplified at an annealing temperature of 52°C through species specific primer after extraction of quality genomic DNA from whole blood. Two markers system RFLP and SSCP along with SNP analysis was carried out to detect *DGAT1* sequence polymorphism. Milk samples from the respective animals were also collected on three different occasions for the estimation of milk fat. The result indicated fixed nature of *DGAT1* gene in all the studied animals through RFLP marker however SSCP marker detected the presence of five different polymorphic banding patterns in studied fragment with between breed variations. Sequence analysis of the representative SSCP banding patterns revealed the occurrence of four different sequence variations with an overall of eight SNP's. Association analysis revealed the presence of significant association of polymorphic banding pattern with milk fat percent in indigenous cattle. The present study concluded that sequence variation in *DGAT1* gene could be responsible for modulation of milk fat percentage in indigenous cattle.

Keywords: *DGAT1* gene, Multimarker, Sequence Polymorphism, Milk Fat.

SP-56

INVESTIGATION OF C>T AND G>T POLYMORPHISM IN SECRETED PHOSPHO PROTEIN 1 (*SPP1*) GENE OF INDIAN CATTLE BREEDS

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Secreted phosphoprotein 1 (*SPP1*) is a highly phosphorylated glycoprotein expressed by several cell types and it is normally produced in bone, teeth, kidney and epithelial lining tissues. *SPP1* gene also has potent roles in growth, production and reproduction of the animals. It plays important role in initiation and maintenance of pregnancy, as well as in the development of the fetus. A *C>T* (intron IV) and *G>T* (exon 7) polymorphism in *SPP1* gene, has been associated with milk yield, fat % and protein % traits in exotic cattle. These polymorphic studies are lacking in Indian cattle breeds. In the present study, polymorphism study was undertaken in 147 Sahiwal (n = 72) and Hariana (n = 75) cattle maintained at ILFC, DUVASU, Mathura using PCR-RFLP assay. The amplified fragments of the *SPP1* intron IV and exon 7 regions revealed 204 bp and 290 bp, respectively. The amplified products were digested with *Bsr*I and *HpyCH4*IV restriction enzymes, respectively. The *Bsr*I/PCR-RFLP assay of *SPP1* gene revealed only TT genotype (290 bp; 100%)

with T allele (1.0). The *HpyCH4*IV/PCR-RFLP assay of *SPP1* gene also revealed only TT genotypes (204 bp; 100%) with T allele (1.0). Therefore, association analysis was not preformed with milk production traits.

SP-57

DIFFERENTIAL NEUTROPHIL GENE EXPRESSION IN BLOOD AND MILK DURING PRE-IMPLANTATION PREGNANCY IN KARAN FRIES CATTLE

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The blood leucocytes, neutrophils being the first line of defense detect the implanting embryo, which is semi-allogenic and show changes in their gene expression. It is possible to diagnose cattle as non-pregnant around 21-24 days post insemination. Nevertheless, by determination of progesterone (P4) concentration pregnant animals cannot be assured confidently. The failure of the conceptus to signal its presence can lead to pregnancy loss. Identification of suitable methods that allow pregnancy diagnosis around or before Day 20 after artificial insemination will be of considerable value. The present study has been carried out to understand the differential gene expression as a tool for early pregnancy diagnosis in neutrophil cells isolated from blood and milk. The blood and milk samples were collected on 0, 4, 8, 12, 15, 18 and 21 days post artificial insemination, respectively from Karan Fries cattle (N=20). Animals were grouped into pregnant and non-pregnant by estimating the progesterone level in blood plasma sample collected on day 18 post AI and were further confirmed for pregnancy by ultrasound on day 35 and rectal palpation on day 45. The relative gene expression of *IFI16* (Interferon-inducible protein 16), *MX1* (Myxovirus resistance 1), *OAS1* (2′, 5′-oligoadenyl synthatase 1) and *TNFα* (Tumor necrosis factor alpha) genes were studied. Statistical analysis between pregnant and non-pregnant animals in both blood and milk samples revealed that *IFI16* gene was up regulated in the milk samples of pregnant animals on 8th day and found to be significantly different ($P<0.05$) between pregnant and non-pregnant cattle. The relative gene expression of *IFI16* on 8th day of Post AI in milk samples can be used as a non-invasive method for early pregnancy detection and as a biomarker for early detection of pregnancy in cattle on 8th day post-AI in milk.

SP-58

RECOVERY OF GENETICALLY SUPERIOR EMBRYOS FROM THARPARKAR DONOR COWS UNDER THARPARKAR EMBRYO TRANSFER PROGRAMME AT LIVESTOCK RESEARCH STATION, BEECHWAL (RAJUVAS)

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The establishment of pregnancy in the cow involves a complex series of interrelationship between embryo, its uterine environment and the corpus luteum. The embryo is known to produce proteins, steroids and prostaglandis with both luteotrophic and anti-luteolytic effects and also regulatory effect on the uterine blood flow, nutrient transfer, embryo migration and others events associated with the establishment and maintain of pregnancy. In a giant leap in the conservation and propagation of the Indigenous Tharparkar elite breed of cow. Rajasthan University of Veterinary and Animal Sciences, Bikaner has employed the surrogacy techniques in collaboration with NDDB dairy services that helps take multiple calves a year from a cow. A pilot project on Multiple Ovulation Embryo Transfer (MOET) in Tharparkar cows is executed at Livestock Research Station, Beechwal. The first phase of this pilot project was initiated during the Month of April, 2017. Under this pilot project, Five Elite Tharparkar cows having Lactation more than 3500 litre were used as a Donor animal for the production of embryos. After the estrus synchronization and superovulation protocol, (40%) Two elite cows were undergone non-surgical embryo flushing for the recovery of genetically superior Tharparkar embryos. Total 11 good quality transferable embryos were recovered non-surgically in two Flushing from two Elite Donor Tharparkar cows.

Keywords: Indigenous, Donor, Recipients, Embryo, Flushing.

SP-59

A MULTI-BREED ASSOCIATION STUDY REVEALS TRANSITION PROTEIN 2 (TNP2) mRNA LEVELS ARE ASSOCIATED WITH SPERM HEAD ABNORMALITIES

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Protamins and Transition nuclear proteins (TPs) are the major proteins important for histone displacement and chromatin condensation during mammalian spermatogenesis. So, the current study was planned to assess the association of four genes viz. Protamin 1 (*PRM1*), Protamin 3 (*PRM3*), Transition protein 1 (*TNP1*) and Transition protein 2 (*TNP2*) on sperm morphological abnormalities in different breeds of cattle *viz* Sahiwal, Holstein Friesian and Frieswal. Six bulls with three to six ejaculates per bull of each breed were utilized in the study. The morphological abnormalities *viz* head, midpiece and tail abnormalities were assessed using standard procedure of eosin-nigrosine staining followed by counting of 200 spermatozoa in different fields. Ejaculates are categorized into poor and good quality based on the recommended standards *viz* head abonormalities (poor $\geq 7\%$, good $< 7\%$), midpiece abnormalities ((poor $\geq 7\%$, good $< 7\%$) and total abnormalities (poor $\geq 20\ \%$, good $< 20\%$). The total RNA was extracted by lysis of sperm cells were lysed using acid guanidinium thiocyanate–phenol–BCP lysis mixture followed by column purification. The genomic DNA contamination was assessed using the intron-spanning *PRM1* primer. The real time PCR studies were carried out on the cDNA synthesized by the Superscript III enzyme mix. The data was analyzed using GLM Statistical Analysis Software (SAS Institute Inc., Cary, NC, USA, 2002) with breed and morphological abnormalities as fixed effects. The expression of TNP2 mRNA was higher in the sperms with head abnormalities. Other morphological abnormalities revealed no variation in the expression any of the genes studied. Premature translation of TNP2 mRNA is reported to be one reason for abnormal head morphogenesis, reduced sperm motility and male infertility. The current study reveals that mRNA level of TNP2 could be a better indicator of the head abnormality across multiple breeds.

SP-60

CHARACTERIZATION OF THE COMPLETE SEQUENCE OF *MYOSTATIN* GENE IN MALPURA SHEEP

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This study presents the first report of complete *Myostatin* (Growth/Differentiation Factor-8) sequence characterization in any Indian sheep breed. *Myostatin* also known as GDF-8 is negative regulator of skeletal muscle growth, responsible for double muscling in animals including sheep. In double muscling, muscle mass is increased which results in the decreased weight of bones, fat and digestive tract. The decrease in weight of other body component results in heavier carcasses and a higher proportion of leaner and expensive cuts of meat. The leaner and heavier carcasses are favorable for both farmers and processors as consumers require leaner cuts of meat.There has been no study in Indian sheep breeds that characterize the complete sequence of the *Myostatin* till now and in the present study we addressed this issue. We have amplified and sequenced complete *Myostatin* gene (~8.0 kb) having 2 Exon and 3 Intron, flanked by 5` and 3` UTR. The blood samples of 529 animals of Malpura sheep, a native mutton breed of Rajasthan was used as a source of DNA. The complete sequence was fragmented in 18 different parts for easier amplification and sequencing using already reported primers (Han *et al* 2013). The fragments P1 to P18 were amplified using Polymerase Chain Reaction (PCR) followed by sequencing of PCR products and also sequencing of cloned DNA insert (TA cloning vector) for confirming the sequence. The complete sequence was then curated using Emboss (Rice *et al,* 1999). The sequence of 8002 bp was obtained which was then compared with the GDF8 sequence of other exotic breeds (cattle, sheep, goat, buffaloand pig) and Indian breeds available in Gene Bank. A total 16 nucleotide substitutions were identified in Malpura sheep. Out of these 16 substitutions, 2 were located in promoter region, 3 in the 5'UTR, 6 in intron 1, 1 in intron 2 and 4 in 3'UTR. The predicted protein sequence generated (*in silico*) is of 375 amino acid and shows a difference at position number 274 [Glutamic Acid (Glu) to Valine (Val)] among previously reported Indian sheep breed. Further studies with regards to association of the variation obtained in this population with the growth data in Malpura sheep needs to be undertaken.

SP-61

EVALUATION OF SEMEN QUALITY PARAMETERS AND THEIR RELATIONSHIP WITH FERTILITY IN THREE GENETIC GROUPS OF LAYER CHICKEN

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Evaluation of semen quality parameters is very important before selection of breeding cocks used for fertility and hatchability of eggs. The aim of this study was to characterize the semen parameters of roosters belonging to three different genetic groups *viz* RIR, Punjab Red and RIR X local cross. Semen was collected from 210 birds for semen evaluation using the abdominal massage technique which includes 80 for RIR, 80 for Punjab Red and 50 for RIR X local cross maintained at poultry research farm under Directorate of Livestock Farms, GADVASU, Ludhiana. Semen parameters evaluated for color, volume, sperm concentration, semen pH, sperm motility, sperm viability, HOST and acrosome integrity. Twenty roosters/genetic group were also evaluated for fertility rate. There was no significant difference in color and pH among three genetic groups. RIR X local cross had significant higher ($p<0.01$) ejaculate volume (0.51 ± 0.02 ml vs. 0.27±0.01 and 0.30±0.01ml), sperm concentration (2804.70 ± 114.61 vs. 1826.10±77.66 and 2133.50±81.18X10^6 sperms/ml), sperm motility % (66.60±2.12 vs. 55.38±1.82 and 51.95±1.84), sperm viability % (72.43±2.06 vs. 64.67±1.88 and 51.25±1.89) and HOST % (64.59±2.61 vs. 58.55±1.17 and 47.09±2.11) than RIR and Punjab Red, respectively. Interestingly, RIR X local cross had significant lower ($p<0.01$) partially damaged sperm % (36.96±2.81 vs. 41.84±1.78 and 48.98±1.89) and fully damaged sperm % (14.15±3.39 vs. 26.27±1.93 and 31.25±2.46) than RIR and Punjab Red, respectively indicating desirable performance. In similar fashion the fertility rate for RIR X local cross was found to be higher (75 vs. 66 and 67 %) than Punjab Red and RIR, respectively. It can be concluded that the semen parameters of roosters of different genetic groups must be evaluated to select the roosters for improving fertility rate and hatchery enterprise. Moreover the crossbreeding of local germplasm with RIR can therefore be used as a strategy to improve semen quality of roosters of different lines under intensive management system.

SP-62

IN-SILICO COMPARISON OF MICRO-ARRAY PROFILE OF HPAIV AND LPAIV INFECTED CHICKEN CELL LINE

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Avian influenza is an important infectious disease of poultry industry as well as public health concern, based upon the pathogenesis of the H5N1 influenza viruses may be categorized as Highly Pathogenic and Low Pathogenic Avian influenza. This work was done to unravel the differences between the mechanism of pathogenesis at the molecular level between infection caused by HPAI and LPAI in the same host i.e. chicken. To study the humongous information about genome-wide host response the utilization of microarray is the perfect tool but the only constraint is to get meaningful results from the sea of data generated. The microarray data are available freely at public micro-array Data Repositories like Array Express & NCBI-GEO, raw microarray data acquired by searching these public databases for the in-silico analysis with the help of statistical software. Comparative analysis of differentially expressed genes revealed that 2193 genes in HPAI and 916 genes in LPAI were uniquely expressed while 1997 were commonly expressed. Interestingly from commonly expressed genes 76 genes down regulated in LPAI were up regulated in HPAI while 32 genes up regulated in LPAI were down regulated in HPAI. This differential gene expression in same host in response to two different subtypes of avian influenza viruses may be the key to understand subtle differences in the mechanism of pathogenesis.

Keywords: Duck, avian influenza virus infection, differential host immune response, microarray, host immune genes, In-silico.

SP-63

MOLECULAR CHARACTERIZATION AND GENETIC VARIABILITY OF ALPHA CASEIN GENE, CSN1S1 IN BIKANER CAMEL (CAMELUS DROMEDARIUS) MILK

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Camel milk is an important protein source for the nomadic communities living in the arid lands of the world, in recent years there has been an increasing in consumption of non-bovine milk as an alternative protein source for humans. Camel milk seems to contain larger amount of total

proteins, such as lactoferrin and immunoglobulins as compared to the cow milk, which may be responsible for the better antimicrobial properties. The casein fraction of milk proteins consists of four caseins, namely αs1-casein, αs2-casein, β-casein and κ-casein. Casein genetic polymorphisms are important due to their effects on quantitative traits and technological properties of milk. This work was designed to study occurrence of polymorphism of α-casein in native Bikaneri camel (*Camelus dromedarius*) raw milk sample and to characterize these variants on molecular level. The sequencing revealed that the size of alpha (s1)-casein cDNA was of 1087 bp with GC content of 42.58 percent. These results were comparable with other submitted sequences in NCBI for α-casein gene (1094 bp). α-casein C variant shows a single G > T nucleotide substitution in the exon 5, leading to a non-synonymous amino acid exchange (p.Glu30 > Asp30, GenBank ID: JF429138) in comparison to α-casein A and D. At cDNA level, no further single nucleotide polymorphisms could be identified in α-casein A, C and D. The variants A and C are characterized by missing of exon 18 as compared to CSN1S1* B, due to DNA insertion of 11 bp at intron 17 which alter the pre-mRNA spliceosome machinery, multispecies alignment of Martin *et al* (2003) already confirms. It is well known that the variation in mRNA and protein is primarily due to alternative splicing, duplication and insertion/deletion events in addition to nucleotide mutations. However, this could be a starting point for further characterization of genetic diversity in camel milk proteins. Milk protein variability would help in studying association concerning milk performance traits in camel.

SP-64

A METHODOLOGY TO ASCERTAIN SNPS IN THE GENE ENCRYPTING ACETYL-COA ACETYLTRANSFERASE-2 (ACAT-2) AND THEIR ANTICIPATED ROLE IN METABOLIC PROCESSES IN PIG

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The novel liver protein acetyl-CoA acetyltransferase-2 (ACAT-2) is involved in the beta-oxidation and lipid metabolism. Its comprehensive relative expression, *in silico* non-synonymous single nucleotide polymorphism (nsSNP) analysis, as well as its annotation in terms of metabolic process with another protein from the same family, namely, acetyl-CoA acyltransferase-2

(ACAA-2) was performed in *Sus scrofa*. This investigation was conducted to understand the most important nsSNPs of ACAT-2 in terms of their effects on metabolic activities and protein conformation. The two most deleterious mutations at residues 122 (Isoleucine to Valine) and 281 (Arginine to Histidine) were found in ACAT-2. Validation of expression of genes in the wet- lab also supported the idea of differential expression of ACAT-2 and ACAA-2 conceived through the *in silico* analysis. Moreover, analysis of the relative expression of ACAT-2 and ACAA-2 in the liver tissue of Jeju native pig (JNP) of Jeju- do, South Korea showed that the former expressed significantly higher ($P<0.05$). Overall, the computational prediction supported by wet laboratory analysis suggests that ACAT-2 might contribute more to metabolic processes than ACAA-2 in swine.

Furthermore, our GO analysis, evaluation of mRNA and protein expression in the laboratory has indicated that ACAT-2 plays more important role in lipid and cholesterol metabolism in pig than bovine. Therefore, this study can be used as a stepping stone for planning future studies on the role of nsSNPs in metabolic processes, especially in pigs. The associations of SNPs in ACAT-2 with fertility and production traits might be used as handful tool while planning the breeding programmes for the improvement of growth performance in indigenous breeds like Jeju Native Pig (JNP).

Keywords: Acetyl-CoA acetyltransferase-2 (ACAT-2), acetyl-CoA acyltransferase-2 (ACAA-2), non-synonymous single nucleotide polymorphism (nsSNP) and Jeju Native Pig (JNP).

SP-65

COMPARATIVE EXPRESSION OF SNP g.22304A>G AT PORCINE MUC13 GENE IN NATIVE INDIAN PIG

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The present study aimed to explore MUC13 expression profile across differentially susceptible (*adhesive*) phenotypes of native Indian (desi) diarrhoeic pigs having different genotypes. Previously we reported the SNP loci g.22304A>G to be polymorphic and allelic/genotypic frequencies were differing significantly ($P \leq 0.05$) in *adhesive* (susceptible), *non-adhesive* (non-susceptible) and *weak adhesive* (*less susceptible*) population of native Indian pigs. AA (306bp, 231bp), AG (306bp, 231bp, 108bp, 198bp) and GG (231bp, 198bp, 108b) genotypes were observed at g.22304A>G locus. Quantitative RT-PCR based profiling of target gene in jejuna of animals having AA, AG and GG genotypes revealed that although, expression was different in various genotypes with the highest level in the AA, moderate levels in the GG and low levels in the AG genotype, differences were found to be statistically non significant ($p<0.05$). While, the absence of significant effect of mRNA expression of MUC13 gene across genotypes indicates no direct functional role, the structural role cannot be ignored as the receptor gene is expected to be located within that genomic region. Further, same SNP of 13q41 genomic region was reported to be associated with ETECF4ab/ac adhesion; this study reveals its role in diarrhoea even caused by other strains of *E. coli* which is not ETEC.

SP-66

POLYMORPHISM OF RYR1, PRKAG3, HFABP, MYF-5 AND MC4R GENES IN INDIGENOUS PIGS

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Meat is one of the biological sources of protein in human diet and pork is most widely produced and consumed meat in the world. Meat quality is economically important trait because it plays a critical role in purchase intention of consumers and is directly connected to revenue of producer. A number of candidate genes have been identified as potentially relevant to pork quality traits. Ryanodine receptor 1 (RYR1) gene has been reported as main cause of PSE in various pig breeds. PRKAG3 gene is primarily expressed in white skeletal muscle fibers. The functional mutation in PRKAG3 gene is correlated with increased glycogen content in skeletal muscle. Heart fatty acid-binding protein gene (H-FABP) is involved in fatty acids transport. Melanocortin-4 receptor gene (MC4R) plays an important role in energy homeostasis and is associated to growth rate and feed intake. MYF-5 has been associated to intramuscular fat (IMF). The present study was undertaken to screen the population of indigenous (Bareilly local) pigs for SNPs (RYR1, PRKAG3, HFABP, MYF-5 and MC4R), associated with meat quality traits. A total of 19 indigenous pigs, maintained at Swine Production Farm, Livestock Production and Management Section, ICAR-Indian Veterinary Research Institute, Izatnagar, Uttar Pradesh, India; a unit of ICAR- All India Coordinated Research Project on Pigs, were used in study. RYR1, HFABP and MYF-5 gene was monomorphic with NN, HH and DD genotype, respectively. SNPs were genotyped by PCR- RFLP. PRKAG3 gene had two genotypes, RR and QR with 89 and 11% frequency. Three genotypes GG, AA and AG with frequency of 42, 5 and 53% were observed for MC4R gene. Allelic frequencies for 5 SNPs were 1.0 and 0.0 (N/n), 0.05 and 0.95 (R/Q), 1.0 and 0.0 (H/h), 0.00 and 1.00 (C/D) and 0.32 and 0.68 (A/G), respectively. The value for PRKAG3 (c.599 G>A) SNP locus of PIC, heterozygosity and allelic revealed that population under investigation is of very low diversity and of intermediate diversity for MC4R (C.1426A>G) SNP locus.

SP-67

AN INVESTIGATION ABOUT CROSSTALK OF INNATE AND ADAPTIVE IMMUNITY GENES IN RESPONSE TO CLASSICAL SWINE FEVER VACCINATION IN INDIGENOUS *VERSES* CROSSBRED PIGS USING RNA SEQ ANALYSIS

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In the present investigation genetic basis of the differential immune response and transcriptome profile was explored at different time points after classical swine fever vaccination in crossbred and indigenous pigs. The monocyte derived macrophages (MDMs) of indigenous and crossbred pigs were challenged with virulent strain CSFV for elucidating the changes in transcriptome profile. The humoral immune response measured in terms of mean percentage inhibition (PI) values in crossbred was found to be higher (74.87 %) than indigenous pigs (58.20 %) at 21 dpv. The rate of reduction of ratio of CD4/CD8 was significantly higher in crossbred pigs than indigenous pigs at 7 dpv. The dataset indigenous *versus* crossbred (control) 7 dpv comparison showed, Fc-receptor mediated phagocytosis in macrophages and monocytes, *TREM1* signaling, Interferon signaling, MIF regulation of innate immunity, inflammasome pathway, *iNOS* signaling, dendritic cell maturation, *IL-8* signaling, *IL-6* signaling, production of nitric oxide species, role of pattern recognition receptors in recognition of viruses, as the top 10 key canonical pathways were activated in indigenous pigs. The top 20 upstream regulators activated were *S100A9, S100A8, NFE2, CD14, IRF7, SPP1, CAPN3, NCF1, TNFSF13B, TLR4, OLR1, DDX58(RIG1), IL1RAP, TYROBP, GATA2, PLAUR, TLR2, SPI1, CXCL2, TLR8;* whereas *CBL, MAP4K4, TRIM24,TFRC, CD200* regulators were inhibited in indigenous at 7dpv than crossbred pigs. The indigenous versus crossbred (control) at 21 dpv revealed EIF2 Signaling, GNRH Signaling, PPAR Signaling, prolactin Signaling, IL-3 Signaling, eNOS signaling and dendritic cell maturation were activated key canonical pathways. The upstream regulators activated were *SELP, SPP1, HNF4A, ATF4, CCL5, VIPAS39, IL1A, SIRT2, CAPN3, ECSIT, NR1H3, RELA, HSPA5, TP53, TFEB;* whereas, *VAV2, VCAN, CD24, CUL4B, FAS, OSM, RICTOR, MTM1, PROC* were inhibited. The validations of differentially expressed genes using qRT-PCR were in concordance with RNA Seq analysis.

SP-68

BETA(β) CASEIN GENE POLYMORPHISM AND ASSOCIATION WITH MILK PRODUCTION TRAITS IN MALVI, NIMARI, SAHIWAL AND HF CROSSBRED CATTLE

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Present investigation was carried out on 50 each of Malvi, Nimari, Sahiwal and HF Crossbred cattle by PCR-RFLP method which was also confirmed by sequencing. The PCR-RFLP analysis of β-casein (CSN2) gene digested with enzyme *DdeI* which showed monomorphic results in Malvi and Nimari cattle where only A2A2 (121/121bp) genotype was recorded. However, A2A2 (121/121bp) and A1A2 (121/86/35bp) genotypes were observed in Sahiwal and HF crossbred cattle at β-casein (CSN2) gene locus. All the PCR products of above four breeds were also digested by *HindIII* restriction enzyme (RE) which showed monomorphic results. At β-Cn gene locus the frequency of A2 gene and A2A2 genotype was comparatively higher in all four breeds. The frequencies of A1A1, A1A2 and A2A2 genotypes were found to be 0.00, 0.00 and 1.00 in Malvi; 0.00, 0.00 and 1.00 in Nimari; 0.00, 0.30 and 0.70 in Sahiwal and 0.00, 0.64 and 0.36 in HF crossbred cattle, respectively. The respective gene frequency for A1 and A2 alleles were found to be 0.00 and 1.00 in Malvi; 0.00 and 1.00 in Nimari; 0.15 and 0.85 in Sahiwal and 0.32 and 0.68 in HF crossbred cattle. Chi-square values between observed and expected genotypic frequencies at this locus were found to be non-significant in Malvi, Nimari and Sahiwal breeds of cattle, indicating that the populations of these animals were in Hardy-Weinberg equilibrium (HWE) at β-Casein (CSN2)/DdeI gene locus, while Chi-square value was found to be significant ($P<0.01$) for HF crossbred cattle revealed that Hardy Weinberg disequilibrium at the locus for this population. The genetic relatedness among the four breeds of cattle ware determined on the basis of phylogenetic relationship. At Beta casein gene locus Sahiwal was found closer to HF as compared to Nimari and Malvi. The results of analysis of variance showed significant differences between milk yield (MY), daily milk yield (DMY), lactation length (LL), lactose (%) and SNF (%) of both genotypes in Nimari, Malvi and HF crossbred cattle. Higher MY and DMY was recorded for A1A2 genotyped animals but rest traits noticed higher in A2A2 genotyped animals.

SP-69

APPLICATION OF ANCESTRY-INFORMATIVE MARKERS AS A TOOL FOR PREDICTING ADMIXTURE LEVELS IN DIFFERENT CROSSBRED CATTLE IN INDIA

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Inferring inheritance level in cross-bred cattle population with the help of SNP genotype data serves as a solution to the constraints in updating the ongoing crossbreeding and upgrading policy (ies). In Indian scenario the high genotyping cost can be reduced by finding a small panel of PCA-Informative Markers (PCAIMs). Hence, in the present study we have aimed to provide an insight of admixture level in different crossbred cattle in India with the help of PCAIMs. To prove the hypothesis an established crossbred namely Santa Gertrudis population genomic data were analysed. *Santa Gertrudis* is a cross between Brahman bulls and Beef Shorthorn females with an inheritance level of 37.5% and 62.5%, respectively. A total number of 74 animals' genomic data from public repository (DRYAD) were included in the study with genotypic coverage > 95%. Starting with the 50K BeadChip data, 39,615 common SNP markers were included after a quality check for different parameters. Principal component (PC) analysis was performed over the 39,615 markers. The PC1 and PC2 explained 25.5% and 3.5% of the total variance of the population. The SNPs hence, significantly correlated with PC1 with $p<0.05$ were included in the study and ordered on the basis of significant correlation. A total of 192 outliers and removed them from the analysis. Eight different panels of SNPs were formed retaining top 50, 25, 12.5, 6.25, 3.125, 1.56, 0.78 and 0.39 percentage of 39,423 SNPs correlated with PC1. Assuming, K values of 2, with 20,000 burn-in and 30,000 MCMC runs in the STRUCTURE software, an effective substructure of the population was obtained for 39,423 markers as well as for the eight different panels of markers. The smallest possible panel contained a total number of 154 markers predicted the ancestry level with approximately 99 % accuracy and thus can be termed as Ancestry-Informative Markers. The results were in accordance with the original blood inheritance of *Santa Gertrudis* as per pedigree analysis.

SP-70

ESTIMATION OF EFFECTIVE POPULATION SIZE FROM LINKAGE DISEQUILIBRIUM DATA USING BOVINE 50K SNP CHIPS

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Crossbreeding and selection impose a definite effect on genetic diversity and population structure of different livestock breeds. One important diversity parameter, *i.e.,* population size (N_e), introduced into population genetics by Sewall Wright (1969), can be estimated from information on linkage disequilibrium (LD) between single nucleotide polymorphisms (SNPs) across genome. The LD signatures can also arise from admixture and genetic drift, which can be exploited to infer the demographic history. In the present study, we had retrieved the genotype data from a public repository (DRYAD) for a crossbred population namely Santa Gertrudis (20) along with its two ancestral populations; Shorthorn (34) and Brahman (20) to estimate the N_e. It was calculated using *SNeP* and NeEstimator for past generations and more recent generations, respectively. N_e in recent generations was calculated by linkage model under the assumption of random mating and different critical values (0.05, 0.02, 0.01 and 0+) for Minor Allele Frequency (MAF) was set. The N_e in more remote past was calculated with the help of pairwise LD value keeping binwidth equal to 0.1Mb for SNPs and adjustment of recombination rate was done according to Sved and Feldman (1973). The N_e in recent generations for Shorthorn, Brahman and Santa Gertrudis were 56-63, 71-74 and 92-99, respectively. Establishment of Santa Gertrudis as a breed can be dated back to 1940 in the United States. So, more remote generations does not exist suggesting a total of approximately 15 generations. The N_e estimated in *SNeP* for Santa Gertrudis was found to be around 91-93, which is in accordance with the N_e estimated through NeEstimator. In 2007-08 the population registered was around 7500 whereas, the effective population size estimated is very less which may be due to various factors like unequal sex ratio of breeding males and females, unequal number in successive generations and overlapping generations etc.

SP-71

CONSTRUCTION OF PHYLOGENETIC TREES FROM MOLECULAR DATA

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A phylogenetic tree is built to estimate the evolutionary relationship among different species. Currently, molecular data in the form of DNA or protein sequences is extensively used to construct phylogenetic trees. The purpose of building phylogenetic trees has expanded, from knowing the relationship between species, to understanding the relationship among the sequences themselves without regard to the host species. Knowledge of the relationship among the sequences helps us to infer the functions of genes that have not been studied experimentally and thereby to elucidate different mechanisms. Phylogenetic analysis is often regarded as a difficult process that requires expertise and years of experience. On the contrary, it is a simple process that can be learned quickly and applied effectively. Here, we describe the steps involved in constructing a phylogenetic tree from molecular data for beginners using "MegAlign" programme of Lasergene software (DNASTAR Inc., USA). The first step is to select a sequence (gene/peptide) of your interest and to identify a set of homologous sequences available in databases. In our example here, we use the sequence of porcine beta-defensin-1 gene and beta-defensin-1 gene sequences from different species as homologous sequences available in NCBI database. In the second step user has to create MegAlign sequence files for each DNA/ amino acid sequence using sequence builder. The third step is to align those sequences; MegAlign tool uses ClustalW algorithm for multiple sequence alignment. The fourth step involves construction of a phylogenetic tree from the aligned sequences. Here we illustrate the maximum likelihood method for construction of the phylogenetic tree. The step-by-step protocol presented here in sufficient detail allows a beginner to start with a sequence of interest and to build a publication-quality phylogenetic tree illustrating the evolution of an appropriate set of homologs of that sequence.

SP-72

SEQUENCE CHARACTERIZATION AND GENOTYPING OF ALLELIC VARIANTS OF BETA CASEIN GENE ESTABLISHES NATIVE CATTLE OF LADAKH TO BE A NATURAL RESOURCE FOR A_2 MILK

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Bovine milk is regarded as nature's perfect food due to presence of vital nutrients. However, it also contains some peptides with opioid properties obtained after proteolytic digestion of β-casein that may increase risk of chronic diseases. There are 13 genetic variants of bovine beta-casein; out of these A_1 and A_2 are the most common in dairy cattle breeds. The A_1 and A_2 variants differ only at position 67, which is histidine in A_1 or proline in A_2 milk. Earlier published reports have indicated that A_1 β casein could be responsible for several health disorders like diabetes, coronary heart disease etc. while A_2 β-casein is generally considered safe for human consumption. In the present study, an effort was made to sequence characterize β casein gene and identify allelic distribution of A_1, A_2 alleles in native cattle of Ladakh region adapted to high altitude and low oxygen condition. The sequencing data of exonic and un-translated region of β casein gene was generated in 25 random DNA samples of Ladakhi cow. The data showed 2 non-synonymous variations in coding region, while 5'UTR was completely conserved. The 3'UTR showed 2 more variations in Ladakhi samples. Further, the genotyping in 85 Ladakhi cattle for A_1, A_2 alleles revealed that in Ladakhi cattle, A_2 allele is predominantly present as reported for some of the other Indian breeds. The frequency of A_2 allele was 0.90 while frequency of A_2A_2 genotype was found to be 0.79 in Ladakhi cattle. Similar to other native breeds, the frequency of A_2A_2 genotype was more prevalent in Ladakhi cattle as compared to heterozygous A_1, A_2 genotype. None of the animal showed homozygous A_1A_1 genotype. The present data strongly indicate that local cattle of Ladakh with higher frequency of A_2 allele and A_2A_2 genotype are natural resource for A_2 milk. Systematic efforts should be made for long term conservation and genetic improvement of this invaluable genetic resource of Ladakh.

SP-73

SCREENING OF POINT MUTATION IN INTRON 9 OF PPARGC1A GENE IN GIR CATTLE

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The objective of this study was to screen the point mutation in intron 9 of peroxisome proliferator activated receptor-γ coactivator-1α (*PPARGC1A*) candidate gene. The gene has been located on chromosome 6 and identified as positional candidates for milk traits. Point mutations in Intron 9 of the bovine PPARGC1A determine two allelic variants T and C. Polymorphism of T>C variant associated with production traits in several exotic breed. In the present investigation, these variants were screened by polymerase chain reaction and restriction fragment length polymorphism (PCR-RFLP) analysis in the indigenous Gir breed. DNA samples (n=65) were analyzed for allelic variants of the PPARGC1A gene. Polymorphism was detected by digestion of PCR-amplified products with *Hae* III restriction enzymes, followed by separation on 3% agarose gels and resolved by ethidium bromide staining. Allele T of the PPARG1A gene occurred at a higher frequency than allele C in this breed. The genotypic frequencies were 0.3538 and 0.6461 for TT and TC genotypes and no animal of CC genotype was observed. The frequencies of alleles T and C were 0.677 and 0.323, respectively.

Keywords: Candidates gene, PPARGC1A gene, Polymorphism.

SP-74

OVEREXPRESSION OF GENES ASSOCIATED WITH HYPOXIA IN CATTLE ADAPTED TO TRANS HIMALAYAN REGION OF LADAKH

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Ladakh is an important part of Trans-Himalayan region located between the Kunlun mountain range in the north and the main Great Himalayas to the south in state of Jammu and Kashmir of India. The local cattle from Leh and Ladakh region, known as "Ladakhi cattle" is a unique germplasm having excellent adaptation potential to high altitude hypobaric stress. In the

present study, an effort was made to evaluate the transcriptional pattern of hypoxia inducing factor-1 (*HIF*-1) and several of its regulated genes in PBMCs of local Ladakhi cattle, Holstein Frisian crosses, Jersey (exotic) maintained at high altitude region and Sahiwal (*Bos indicus*) and Karan Fries (cross bred) cattle maintained in tropical environment. The combined data set indicated increased expression of *HIF-1* and its regulated genes *viz*., glucose transporter 1 (*GLUT1*), vascular endothelial growth factor (*VEGF*) and hexokinase (*HIK*) in high altitude cattle indicating their importance in maintain cellular homeostats during high altitude hypoxia. The data indicated that hypoxia associated genes accumulated under hypoxic conditions is part of an essential adaptive component for the cattle adaptation to high altitude of Trans-Himalayan region. In contrary, higher expression of *HSP70* and *HSP90* molecular chaperons in tropically adapted cattle give tolerance to high ambient temperature prevalent in tropical condition. In conclusion, *HIF-1* and its regulatory genes could be termed as important candidates for producing homeostatic responses to hypoxia in cattle populations reared in higher altitudes of Trans-Himalayan region.

SP-75

CHARACTERIZING BINDING SITES OF HEAT RESPONSIVE MICRORNAS AND THEIR EXPRESSION PATTERN IN HEAT STRESSED PBMCS OF NATIVE CATTLE, EXOTIC CATTLE AND BUFFALOES

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Heat stress adversely affects the health and well-being of dairy animals. It is generally believed that due to evolutionary difference, Indian cattle have better ability to counteract heat stress than *Bos taurus* cattle. In recent past, several studies have shown that animal differs in their capacity to manage heat stress. Several SNPs identified in heat responsive genes have shown to be associated with thermo tolerance in cattle. In the present study, 3'un-translated region (3'-UTR) of two most important heat responsive genes i.e., heat shock protein 70.1 (*HSP70.1*) and heat shock factor 1 (*HSF1*) were sequence characterized in large number of Indian native cattle. The purpose was to identify SNPs/variations, if any, in 3'-UTR of two heat responsive genes in Indian cattle. The 3'-UTR was selected with the understanding that this region is an important regulatory region that may affect the gene function. An effort was also made to identify the miRNA binding sites along with the variations within 3'-UTR of *HSF1* and *HSP70.1* genes in Indian cattle. A fragment size of 528 bp covering 287 bp of 3'-UTR of *HSP70.1* gene was amplified and sequence characterized in 7 Indian cattle breeds. The sequence analysis showed 3'-UTR of *HSP70.1* of Indian cattle to be exactly similar to *Bos taurus*. Three variations were observed when Indian cattle 3'-UTR of *HSP70.1* gene were compared with that of buffaloes. Further, 3'-UTR of *HSF1* gene was sequence characterized in 72 animals of 12 Indian cattle breeds. A fragment size of 492 bp covering 304 bp of 3'-UTR of *HSF1* gene was amplified and sequenced. The comparison with *Bos taurus* sequence revealed a total of 2 SNPs, one at 94 position and other at 266 position.

Further, an effort was made to identify miRNA binding sites in 3'-UTR of *HSP70.1* and *HSF1* genes of Indian cattle. Interestingly, no miRNA binding site was detected in 3'-UTR of *HSP70.1*. On the other hand, a total of 7 microRNA binding sites were identified in 3'-UTR of *HSF1* gene. These 7 miRNA binding sites were well conserved as no SNPs were detected within these miRNA binding sites between Indian cattle and *Bos taurus*. Although, out study could not detect any SNP in the miRNA binding sites of heat responsive genes, such variation may have great influence on gene function and heat stress response in cattle.

In addition, effect of heat stress was assessed on cell viability, cytotoxicity and apoptosis in PBMCs of Sahiwal cows, Holstein Friesian (HF) cows and Murrah buffaloes. The PBMCs isolated from 9 animals (three from each breeds) were exposed to heat stress at 42°C for 1 h and harvested at 30 min, 2 h, 4 h, 8 h, 16 h and 24h time points. The percent reduction in cell viability was highest in HF followed by Murrah and Sahiwal. Similarly, cytotoxicity and apoptosis was significantly ($p<0.05$) higher in HF as compared to Murrah and Sahiwal. In addition, expression profile of 12 heat responsive miRNAs was evaluated in heat stressed PBMCs of Sahiwal cows, HF cows and Murrah buffaloes. The selected miRNAs were responsive to heat stress condition. Most of the miRNAs showed higher fold increase in expression in Sahiwal PBMCs post heat stress in comparison to Holstein cows and Murrah buffaloes PBMCs. The distinct pattern of expression of these miRNAs across cattle types and buffaloes might be influencing the cellular tolerance level of Holstein and Sahiwal PBMCs.

SP-76

GENOME-WIDE SNP IDENTIFICATION IN SAHIWAL CATTLE

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Research in cattle genetics was profoundly changed since the public release of the cattle genome sequence. Genomics has been adopted as a foundational tool for livestock breeding, health, welfare and conservation. Discovery and genotyping of large number of genome wide markers is a prerequisite for the application of genomics in livestock. SNPs are the most widely used markers due to its abundance, high level of polymorphism, high throughput capability and stability. Few reports are available on genome wide SNP information in indigenous cattle breeds. In this study a reduced representation next generation sequencing and genotyping technique using restriction enzymes was used to discover genome-wide SNPs in Sahiwal cattle. The ngs reads after quality control were mapped to bovine UMD3.1 assembly and variants were called using samtools/bcftools. A total of 407,952 SNPs were identified with a variant rate of 1 SNP per 6522 bp. The number of novel SNPs identified was 18836. Annotation of the SNPs found Ts/Tv ratio to be 2.45 and the missense to silent mutation ratio to be 0.53. The identified SNPs can be used for downstream analysis like population structure studies and inbreeding detection thus supplementing to conservation efforts and also can aid in genetic improvement by trait mapping, GWAS and genomic selection.

SP-77

EVALUATION OF ALLELIC DIVERSITY AT DQA LOCUS OF MAJOR HISTOCOMPATIBILITY COMPLEX OF INDICUS AND CROSSBRED CATTLE

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Major histocompatibility complex (MHC) class II molecules are central to adaptive immune response and maintenance of self-tolerance, guiding the development and activation of $CD4^+$ T-helper cells. Several features of MHC gene polymorphism in different livestock species indicate that diversifying natural selection has acted upon these genes. In this study, the genetic diversity at MHC DQ-alpha (DQA) exon 2 locus in indicus and crossbred cattle was investigated using PCR-RFLP, cloning and sequencing. Amplification and sequence analysis of a 193 bpDQA fragment in 62 animals represented by 4 indicus and one crossbred cattle populations revealed presence of 35 DQA alleles which could further be classified into DQA_1 (28) and DQA_2 (7) alleles. An important finding of this study was identification of 20 novel DQA alleles (16 of DQA_1 and 4 of DQA_2). Duplication of DQA locus was evident because of the presence of up to 4 alleles in a single animal. Maximum polymorphism was observed at codon 46 in Peptide Binding Site (PBS) region and codon 27 in Non Peptide Binding Site (NPBS) region with variability index of more than 10. Potential evidence of ongoing positive selection at PBS and purifying selection at NPBS at cattle DQA locus was revealed by dN/dS (Non-synonymous/ synonymous substitution) analysis and estimates of Wu-Kabat variability frequency. Phylogenetic analysis of DQA alleles across different ruminant species revealed trans-species evolution of MHC variants, which suggests exposure to common pathogenic pressure over prolonged periods of time.This study documents high, multiplicative allelic diversity with extreme heterozygosity and duplication at cattle-DQA locus. The results provide significant insights into better disease combating ability and genetic fitness of indicus cattle because of their ability to bind and subsequently respond to a wide array of antigens.

SP-78

MONOCYTE-DERIVED MACROPHAGES OF ZEBU AND CROSSBRED CATTLE HAVE EQUIVALENT TLR4 ACTIVITY

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The present study was conducted to quantify and compare TLR4 activity in monocyte-derived macrophages of zebu (Tharparkar) and crossbred (Holstein-Friesian x Jersey x Brown

Swiss x Hariana) cattle. The cells were either induced with *E. coli* 0111:B4 LPS or kept as uninduced. The TLR4 activity was quantified in terms of IκB-α inhibitory subunit (NFKBIA) mRNA copies using real-time, one step RT-PCR. TLR4 activity of induced cells in case of Tharparkar cattle (N=7) was in the range of 2313085±577929 (N=3) to 2669640±735603 (N=3) copies; of crossbred cattle was in the range of 2255387±726567 (N=3) to 2418580±694600 (N=3) copies while that of uninduced cells in case of Thraparkar cattle (N=7) was in the range of 117±51 (N=3) to 293±103 (N=3) copies; of crossbred cattle (N=7) was in the range of 182±122 (N=3) to 296±88 (N=3) copies. The TLR4 activity of induced cells in both the groups was found to be significantly higher than that of respective uninduced cells ($P<0.0001$). Further, upon comparison, TLR4 activities of induced as well as uninduced cells of Tharparkar were not found significantly different from those of cross-bred cattle ($P=0.7931$ and $P=0.6670$). Here we have quantified and compared, for the first time, TLR4 activity in terms of NFKBIA mRNA copies in monocyte-derived macrophages of zebu and crossbred cattle and found that both have equivalent TLR4 activity.

Keywords: Crossbred, Monocyte-derived macrophages, NFKBIA, Tharparkar, TLR4, Zebu.

SP-79

MONOCYTE-DERIVED MACROPHAGES OF ZEBU AND CROSSBRED CATTLE HAVE EQUIVALENT TLR9 ACTIVITY

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The present study was conducted to quantify and compare TLR9 activity in monocyte-derived macrophages of zebu (Tharparkar) and crossbred (Holstein-Friesian x Jersey x Brown Swiss x Hariana) cattle. The cells were either induced with ODN2006 or kept as uninduced. The TLR9 activity was quantified in terms of IκB-α inhibitory subunit (NFKBIA) mRNA copies using real-time, one step RT-PCR. TLR9 activity of induced cells in case of Tharparkar cattle (N=7) was in the range of 364362±53731 (N=3) to 1896411±169945 (N=3) copies; of crossbred cattle was in the range of 340132±64379 (N=3) to 1730051±114138 (N=3) copies while that of uninduced cells in case of Thraparkar cattle (N=7) was in the range of 117±51 (N=3) to 293±103 (N=3) copies; of crossbred cattle (N=7) was in the range of 182±122 (N=3) to 296±88 (N=3) copies. The TLR9 activity of induced cells in both the groups was found to be significantly higher than that of respective uninduced cells ($P<0.0001$). Further, upon comparison, TLR9 activities of induced as well as uninduced cells of Tharparkar were not found significantly different from those of cross-bred cattle ($P=0.3461$ and $P=0.6670$). Here we have quantified and compared, for the first time, TLR9 activity in terms of NFKBIA mRNA copies in monocyte-derived macrophages of zebu and crossbred cattle and found that both have equivalent TLR9 activity.

Keywords: Crossbred, Monocyte-derived macrophages, NFKBIA, Tharparkar, TLR9.

SP-80

INCIDENCE OF REPRODUCTIVE DISORDERS IN DAIRY CATTLE UNDER JHARKHAND STATE CONDITIONS

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Reproductive disorders adversely affect the future fertility of animals and significantly reduce their productivity. To assess such disorders cattle camps are regularly under taken in Jharkhand state in which maximum animals diagnosed in a short period. The present study was conducted to assess the incidence of diseases like agalactia (failure of milk production or failure of release of milk into teat canal), anoestrus (period of sexual inactivity), anorexia (loss of appetite), cervicitis (inflammation of cervix), cystic ovary (ovary enlargement in absence of corpus luteum), debility (physical weakness due to chronic illness), metritis (inflammation of uterus), repeat breeder (cycling normally with no clinical abnormalities but failed to conceive after three successive inseminations), under developed reproductive organs etc. in dairy cattle presented in camps during 2015-2016. These camps were organized in 1401 villages covered under 699 cattle development centers spread over 20 districts. During these camps total 55,139 cows were presented by 25,319 farmers. The recorded disorders were diagnosed by the veterinarians on the basis of general history, physical examination of animals, clinical signs etc. During general physical examination animal's body condition, behavior, posture, gait, locomotive disturbance, pulse, respiration, temperature, abdominal distension, defecation etc. were observed and/or recorded. Owner's complaints were taken into account while performing general physical examination of animal. The animals presented in the camps were divided into two groups as ailments affected like agalactia, anoestrous, anorexia, cervicitis, cystic ovary, debility, genital infection, under developed reproductive organs etc. and other group was animals presented for artificial inseminations, pregnancy diagnosis, complaints for low milk production etc. The results reveals that 71.20% animals were reported for ailments and remaining (28.80%) for other purposes. Under ailments group highest incidence was recorded for anoestrous 51.31%, followed by agalactia 16.24%, debility 10.59%, under developed reproductive organs 7.59%, endoparasite 5.78%, anorexia 4.82%, repeat breeder 3.30% and cystic ovary, ectoparasite, genital infection, cervicitis was less than one percent. 92.73% animals were presented for pregnancy diagnosis, 3.75% animals were reported for low milk production and 3.52% animals were noticed in heat and such animals were inseminated during camps. The results indicated that incidence of anestrous, agalactia, debility endoparasite and under developed reproductive organs in heifers is considerable and knowledge in terms of animal productivity and their mitigation already available about these diseases needs to extended to farmers.

SP-81

DIFFERENCES IN BRUCELLA ABORTUS S19 VACCINE INDUCED HUMORAL IMMUNE RESPONSES IN HF CROSSBRED AND SAHIWAL ZEBU CATTLE

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Brucellosis, an important zoonotic disease spread widely around the world including India. Immunization with live attenuated *Brucella abortus* S19 strain remained the only important step in controlling the disease in bovines and understanding the role of immune response genes would provide new approach in control of disease by developing safe vaccines and breeding for disease resistance. In the present investigation, we demonstrated the relative expression of cytokines and antigen binding receptors genes important for immunomodulation against *Brucella* in Sahiwal zebu (*Bos indicus*) and Karan Fries (KF), (*Bos taurus* × *Bos indicus*) cattle. Six female calves (4-6 months age) of both groups were vaccinated with *B. abortus* S19 strain and blood samples were collected before vaccination (0d) and 7th (7d), 14th (14d) and 28th (28d) days after vaccination. Indirect ELISA showed significantly high IgG levels after vaccination in both the groups, however, without any significant variation between the groups on different days. Initial immunomodulation was assessed by relative gene expression of seven genes *viz*., TNFα, IFNγ, IL6, IL10, TLR4, NLR1 and MHC-DQA using quantitative PCR (qPCR). The results revealed that almost all the genes had higher expression in KF on 14d and 28d after vaccination compared to 0d. KF also had significantly ($P<0.05$) higher expression of IL10 gene compared to Sahiwal on 28d. The higher expression of IFNγ, TNFα, IL6 and TLR4 in crossbreds might also be important in initial containment of the *Brucella* infection. The study revealed that vaccination with *Brucella abortus* S19 strain was able to modulate an earlier immune response in KF compared to Sahiwal calves, making its efficacy more in Indian crossbreds and it would help in further understanding the molecular mechanism against the *Brucella* in cattle of different genetic backgrounds.

SP-82

GENETIC POLYMORPHISM OF BOVINE β4-DEFENSIN GENE AND ITS ASSOCIATION WITH SOMATIC CELL COUNT

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This study was carried out with an objective of identifying genetic variants in *β4-defensin* gene using PCR-RFLP analysis and to associate them with Somatic Cell Count (SCC) in 127 Deoni cattle. AA, AB and BB genotypes were identified in DEFB4-E1/*Ava*I; and only AA genotype in DEFB4-E1/*Pvu*II and only AB genotypes in DEFB4-E2/*Pvu*II and DEFB4-E2/*Hha*I analysis. The frequencies of genotype were varying from 0.5 to 1 and that of 'A' and 'B' alleles was varying from 0.5 to 0.48. The polymorphism information content (PIC), heterozygosity and allelic diversity was varying from 0.3746 (β4-defensin_E1_*Ava*I) to 0.3750 (β4-defensin_E2_*Pvu*II and β4-defensin_E2_*Hha*I), 0.91 to 1.00 and 0.4992 to 0.5000 in the studied Deoni cattle population. Also, the analysis revealed the significant departure of all markers from Hardy-Weinberg Equilibrium (HWE). The linkage disequilibrium (LD) of different *β4-defensin* gene markers were tested using the χ2 probabilities, which revealed that markers in all possible combination were in LD with statistically significant value at $P<0.05$.

For association studies, milk samples were screened using CMT, EC and SCC tests, which showed significant ($p<0.001$) correlation among them. Based on the screening tests, Deoni cattle were categorized as mastitis susceptible and mastitis resistant, which were significantly ($p<0.01$) differing for EC and SCC. The variance analysis has showed the significant effect of genotypes identified using *β4-defensin*_E1/*Ava*I ($P<0.05$) analysis on electrical conductivity only in Deoni cattle. None of the genotypes of β4-defensin identified using different markers had any influence on somatic cell count in Deoni cattle. Association of genotypes identified using β4-defensin_E1/*Pvu*II, β4-defensin_E2/*Pvu*II and β4-defensin_E2/*Hha*I analysis could not be done due to the monomorphic nature in Deoni cattle.

SP-83

ASSOCIATION OF SINGLE NUCLEOTIDE POLYMORPHISMS WITH MANGANESE, FAT AND MILK PRODUCTION IN CROSSBRED CATTLE

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The present study was proposed to find the association of the identified single nucleotide polymorphisms (SNPs) on milk minerals and constituents after adjusting the records with various significant ($p<0.05$) non-genetic factors in crossbred (*Vrindavani*) cattle. Milk minerals, Phosphorus (P), Calcium (Ca), Copper (Cu), Zinc (Zn), Manganese (Mn), Iron (Fe), Sodium (Na), Potassium (K) and constituent traits (fat and protein percentage) were estimated in crossbred (*Vrindavani*) cows during month of December and March. Effect of non- genetic factors (month of collection, parity, lactation stage and level of Test Day Milk Yield) on milk minerals and constituents were evaluated by using least squares mixed model analysis. Five SNPs namely in database rs109421300, rs43691049, rs109727821, rs109047657 and rs135678421 were identified for investigating their association with traits under investigation. The top and bottom 20 cows were selected out of 120 crossbred cows screened for particular mineral and constituents traits against each individual SNP. The AG (4.64±0.22 %), GG (4.62±0.27%) and AA (2.96±0.17%) genotypes at rs109421300 locus were found to be significantly ($P<0.0001$) associated with fat percentage in crossbred cattle. At locus rs109727821, Mn concentration was found to be significantly ($p\leq0.0001$) associated with highest least squares means for AG (1.64±0.16 mg/L) followed by AA (0.98±0.15 mg/L) and GG (0.77±0.24 mg/L) genotypes. The existing association suggested possibilities to select animals for specific minerals and constituent traits in crossbred population.

SP-84

ESTIMATION OF DRAUGHT ABILITY AND RELATED PHYSIOLOGICAL CHANGES IN KOSALI BULLOCKS IN THEIR NATIVE PLACE

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Although modern automation in agriculture caused a declining trend in the population of draught animals but they are continued to be the most important renewable and sustainable power source for Indian agriculture. Bullock cart is serve as chief source of power for performing agricultural operations and carting purpose in rural parts of India. In the present study, draught performance of Kosali bullocks was evaluated by overall draught ability method. Physiological response of bullocks such as respiration rate (RR), pulse rate (PR) and rectal temperature (RT) were recorded prior and immediately after work for each carting and ploughing trial. Working capacity and heat tolerance of Kosali bullocks were also evaluated and categorized based on working capacity in a day. The overall draught ability (ODA) for Kosali bullocks with an average was 67.69% and can consider average working type of draught breed. Among the studied physiological parameters, respiration rate was most affected after the work. Majority of the bullocks were good working types and its percentage was 45% as they worked in between five to six hours a day. In conclusion, Kosali bullocks are found to have good capacity of heat tolerance and good working types with average type of draught breed.

SP-85

STUDY OF GENETIC POLYMORPHISM OF CYP19 A1 GENE IN SAHIWAL CATTLE

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CYP19 A1 gene is a strong candidate gene for fertility. Fertility is a complex phenotype, which depends on both genetic and Environmental factors. One important fertility factor is the Aromatase cytochrome P450 which is encoded by the CYP19 A1 gene which is directly involved in estradol production. In cattle, this gene has been mapped to band q 2.6 of Chromosomes 10. Therefore, the present study was undertaken in a population of Sahiwal cattle maintained at Livestock Research Station, Kodamdesar, Bikaner (Rajasthan) to detect bovine CYP19 A1 gene variation through polymerase chain reaction restriction fragment length polymorphism (PCR-RFLP) genotyping. Genomic DNA extracted from whole blood of 60 unrelated milking animals through spin column method as per manufacturer's protocol. Quality and concentration of extracted genomic DNA was checked on 0.8% agarose gel and Nano Drop spectrophotometer, respectively. PCR was carried out with specific primers and 405 bp fragment was obtained under optimized PCR conditions. The amplicons were digested with *Pvu* II restriction enzyme and kept at 37°C for overnight and resultant fragments were resolved on 12% PAGE. Thus, three Genotypes and two alleles were detected with Pvu II (AA, AB, BB; A and B). The genotype and Allelic frequency with *Pvu* II were calculated as 0.4833, 0.4166 and 0.10 for AA, AB and BB genotypes and 0.69, 0.31 for A and B alleles, respectively. The result indicates the presence of genetic variability in CYP19 A1 gene in Sahiwal cattle and the suitability of PCR-RFLP for evaluating its role in reproductive traits.

SP-86

MOLECULAR CHARACTERIZATION OF LHR GENE IN RATHI CATTLE

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Dairy breeds of cattle provide an interesting model for the study of LHR since, for decade, there has been a strong selective pressure on milk production, with a clear interference in reproductive performance and a reduction in breeding value for fertility. The PCR - RFLP technique proved successful in identifying genetic polymorphism in population, which will be useful for selecting animals with desired genotypes for better production & reproduction. Luteinizing hormone is a glycoprotein hormone of pituitary origin that regulates gonadal function, including steroidogenesis and gametogenesis. In cattle, this gene has been mapped to Exon 11 of chromosomes 11. Rathi being one of the indigenous milch breed, the study was conducted on 60 lactating cows to identify the allelic variants of LH receptor gene and to determine its frequency. The Genomic DNA was extracted by HiElute Miniprep Spin column method and PCR was carried out with specific primers and 303 bp fragments was obtained under optimized PCR conditions. The amplicons were digested with *Hha* I restriction enzymes and kept at 37°C for overnight and resultant fragments were resolved on 8 % PAGE. Based on the restriction pattern thus, three genotypes and two alleles were detected with *Hha* I (TT, TC, CC, T and C). The genotype and allelic frequency with *Hha* I were calculated as 0.15, 0.50 and 0.35 for TT, TC and CC genotypes and 0.04, 0.6 for T and C alleles, respectively, so this shows that variations exist between indigenous and exotic breeds, which warrants for further investigation.

SP-87

JOINT EFFECT OF SNPS IN INTRON 3 AND EXON 5 REGION OF GH1 GENE ON MILK PRODUCTION AND MILK COMPOSITION TRAITS IN KARAN FRIES (HOLSTEIN FRIESIAN CROSSBRED) CATTLE

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Growth Hormone (GH1) gene has been reported to be a candidate gene for milk production in cattle. The genetic markers related to GH1 gene could be used for early selection of young males for improving milk production and milk composition in dairy cattle. The present study was carried out to study the joint effect of SNPs in intron 3 and exon 5 region of GH1 gene on milk production and milk composition traits in Karan Fries (HF crossbred) cattle. Blood samples were collected from 78 pedigreed animals and DNA was isolated from the samples. PCR amplification of the targeted regions of GH1 gene was done using sequence-specific primers. PCR-RFLP of intron 3 using *Msp I* revealed two genotypes-BB and AB with genotypic frequencies as 0.18 and 0.82, respectively and the frequency of B allele was found to be 0.59. PCR-RFLP of exon 5 using *Alu I* revealed LL and LV genotypes with frequencies as 0.46 and 0.54 and the frequency of L allele as 0.73. Regression analysis of phenotypic data related to test day (TD) milk yield, fat yield and SNF yield revealed that the highest effect of SNPs in intron 3 and exon 5 region was found in TD3 which increased TD3MY by 0.587 and 2.601 kg, TD3FY by 76 gm and 80 gm and TD3SNFY by 61 gm and 224 gm, respectively. Moreover, the correlation of TD3 with FL305dMY was also found to be high. TD4 and TD5 were also found to be good for early selection of animals. Based on the phenotypic information and the identified genetic markers in intron 3 and exon 5 region of GH1 gene, adult animals can be selected at early test days while young Karan Fries males can be selected based on genetic marker information only.

SP-88

PREVALENCE AND SEASONAL VARIATION IN IXODID TICKS ON CATTLE OF LUCKNOW DISTRICT, UTTAR PRADESH

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Ticks are important as vectors of disease throughout the most part of the world. Ticks and tick-borne diseases are a global problem and considered as one of the major challenges to livestock health and performance. Economic losses due to ticks and tick-borne diseases in livestock have long been recognized by farmers, government and researchers. They are among the most efficient arthropod vectors: which transmit viruses, rickettsiae, bacteria and protozoa and are able to cause paralysis through neurotoxic salivary secretions. Many species are quite resistant to environmental stresses and may live for years. They have few natural enemies and have a wide range of hosts.

Considering the economic impact of various ticks species on livestock, the present study was conducted to assess the tick prevalence in north India (UP state), to carryout studies to document allelic diversity across identified gene (IL2, IL4, IFNG and BOLA DRB3) for *R. microplus* resistance in indigenous cattle breed. The overall prevalence of tick infestation in cattle was 60%. The highest prevalence was reported in September (76%) while the lowest was in January (44%) months. Seasonal variation was observed during investigation, highest infestation was found in rainy season, while it is lowest in the winter months. Overall highest percentage of tick infestations was noticed in the animals of less than 1 year age (80%). The variation in resistance to tick infestation is most marked between *Bos taurus* and *Bos indicus* cattle, *taurine* cattle given the same exposure, carry between five to ten times as many ticks as *indicine* cattle.

Tick resistance is mostly manifest against attaching larvae, which attempt to feed often and without success, death occurring mostly within 24 h of finding a host. There is evidence of innate and adaptive immune response to tick infestation and it appears that the relative importance of each differs between *indicine* and *taurine* cattle. Typically, *Bos indicus* animals are more resistant to ticks than are *Bos Taurus*, breeds such as Zebu, Kankrej and some Zebu crosses generally become resistant to *R. microplus* after exposure although some variation occurs among and within the breeds.

SP-89

PERIPHERAL BLOOD LEUKOCYTES OF VECHUR AND CROSSBRED CATTLE HAVE EQUIVALENT *L-SELECTIN* mRNA EXPRESSION LEVEL

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For innate immune system to get an early influx of leukocytes at the infection site was essential for reducing the severity of infection and also for timely control of infection thereby minimizing tissue damage. *L-selection*, an adhesion molecule expressed on the surface of leukocytes is essential for making initial contacts between fast moving leukocytes in the blood stream to the endothelial wall at the inflammation site. *L-Selectin* gene expression in peripheral blood leukocytes was evaluated between Vechur and Crossbred cattle using real-time polymerase chain reaction (qRT-PCR) technique. Blood samples of six apparently healthy animals from both the genetic group were collected under sterile and aseptic condition for total RNA isolation. Total RNA was isolated from peripheral blood leukocytes of all samples under study using the TRIzol method after subjecting the whole blood samples with an RBC lysis solution. cDNA was synthesized from isolated total RNA using the commercial cDNA synthesis kit, which was utilized for two step qRT-PCR using SYBR green chemistry. *L-selectin* and *Beta actin* gene specific primers were designed with either one of the primer overlapping in exon-exon junction resulting amplicon size of 150 bp and 100 bp, respectively. *Beta actin* was used as an endogenous control gene for data normalization and crossbred cattle was used as control samples for relative quantification of *L-selectin* gene expression. Expression analysis of *L-selectin* gene between two genetic groups under present study showed 1.14 fold up regulation in Vechur cattle compared to crossbred cattle. Though it showed a disparity of fold change in Vechur cattle, it was not found to be significantly different and the presence of minor variation could be accounted due to some technical discrepancy. Hence we could conclude that the *L-selectin* mRNA expression levels in peripheral blood leukocytes were equivalent between two genetic group under the present study.

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SP-90

POLYMORPHISM OF SLC11A1 GENE AND ITS ASSOCIATION WITH *MYCOBACTERIUM PARATUBERCULOSIS* INFECTION IN CROSSBRED CATTLE OF TAMILNADU

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SLC11A1 gene (Solute Carrier 11 A1 gene), formerly called as Natural Resistance Associated Macrophage Protein 1 (NRAMP1) plays a critical role in innate immunity favoring bacterial killing by macrophages and mutation of this gene is responsible for susceptibility to a number of intracellular pathogens. The present study was to investigate the polymorphism of SLC11A1 gene by using PCR-RLFP technique to associate with the *Mycobacterium paratuberculosis* infection. Animals were grouped into normal and suspected animals on the basis of serological test and symptoms. A total of 40 blood samples of suspected crossbred cattle and 12 normal crossbred cattle were analysed by using three sets of primers to amplify the exonic region 4-5 (1200bp), 5-6 (600bp) and 11(231bp). PCR-RLFP was carried out using five restriction enzymes *viz., Taq* I, *Rsa* I, *Ava* II, *Hae* III and *Bgl* II. This revealed no polymorphic pattern in exonic regions 4-5 and 5-6. In case of exon 11, PCR-RFLP analysis using *Pst* I revealed presence of three genotypes CC (231bp), CG (231bp, 200bp, 31bp) and GG (200bp, 31bp) confirming C>G transversion in coding region. The genotypic frequencies in pooled samples were estimated as 0.24 (CC), 0.48 (CG) and 0.28 (GG). The frequency of C allele and G allele were established as 0.6 and 0.4, respectively in normal healthy animals and same in suspected animals was as 0.46 and 0.54, respectively. Association study, between allele frequencies of healthy and suspected animals were compared by chi-square test. The result revealed significant ($p<0.05$) differences between the allelic frequency of healthy and suspected animals. The report showed that C alleles were common in healthy animals with the frequency of 0.6 and G allele frequencies were common in suspected animals with frequency of 0.54. This polymorphism observed in exon 11 is due single nucleotide polymorphism (C>G). The C>G transversion in coding region resulted in the amino acid change, which might affect the function of SLC11A1 gene.

Keywords: SLC11A1, Crossbred cattle, NRAMP1, transversion.

SP-91

COMPARISON OF *BOLA-DRB3* GENE SEQUENCE VARIATION BETWEEN PCR-RFLP AND PCR-SBT METHODS IN *BOS INDICUS* BREED AND *BOS INDICUS X BOS TAURUS* CROSSBRED CATTLE

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PCR-RFLP, PCR-SBT and HRM analysis were applied to predict simple detection of *BoLA-DRB3.2* alleles in 894 samples of Deoni, Ongole, Kangayam, Bargur, Jersey crossbred and Holstein Friesian crossbred cattle. PCR-RFLP analysis was performed on 284 bp fragment of *BoLA-DRB3.2* gene using *Rsa*I, *Bst*YI and *Hae*III. The frequency distributions of *BoLA-DRB3.2* alleles were predicted as per the BoLA nomenclature. The difference in *BoLA-DRB3* allelic frequencies of Kangayam, Ongole, Deoni, Bargur, Holstein Friesian crossbred and Jersey crossbred cattle was evaluated using a χ^2 test. The allele frequencies of *BoLA-DRB3* in Kangayam (**6*), Bargur (**6*), Ongole (**15*) and Deoni (**6*) breeds of cattle showed higher frequencies viz., 19.72, 24.00, 22.94 and 19.23, respectively and six common alleles (*BoLA-DBB3.2 *6, *9, *11, *13, *15* and **23*) shared more than 50 per cent of total allelic frequencies. Among the crossbred cattle, alleles **6, *9, *11, *13, *15* and **23* were very less in frequency (1.08, 1.29, 3.23, 4.95, 3.87 and 4.30, respectively) and alleles, **8, *23* and **24* were relatively high in frequency (9.03, 10.57, 7.89, respectively). The common alleles (*BoLA-DRB3.2 *8, *10, *16, *22, *24* and **47*) present in crossbred cattle were less frequent in the native animals. To confirm the banding pattern direct sequencing of *BoLA-DRB3.2* allele was carried out using samples from different PCR-RFLP patterns. Different sequence patterns were observed between *Bos indicus* (Kangayam, Bargur, Deoni and Ongole) genetic groups and *Bos indicus* x *Bos taurus* (Holstein Friesian crossbred and Jersey crossbred) crossbred genetic groups. Further, the sequence pattern observed in crossbred cattle was comparable to sequence of *Bos taurus* and a different sequence pattern was observed in indigenous genetic groups (Kangayam, Bargur, Deoni and Ongole) which was similar among these 4 genetic groups. The sequence analysis of *BoLA-DRB3* exon 2 in all six breeds revealed that, there are numerous variations in exon 2, which led to different restriction patterns. Number of SNP variations varies from three to seven in each sequenced *BoLA-DRB3* alleles. High Resolution Melting (HRM) analyses was attempted to predict the SNP variations that were observed in PCR-RFLP and PCR-SBT technique. The HRM analysis showed different types irregular resolution melting curves without any similar types of pattern due to more of SNPs in the sequence. The phylogenetic relationship tree involving sequences of *DRB3.2* alleles of different species rooted several clades based on the similarity in the nucleotides present in the selected breed. Alleles of Deoni, Kangayam, Ongole and Bargur were found to be clustered in respective separate places showing their uniqueness in the *DRB3.2* alleles among the indigenous cattle. Alleles in Jersey crossbred and Holstein Friesian crossbred cattle represented in a single clade. A third cluster with distinctly mixed clades represented crossbred cattle and indigenous cattle sharing some of the alleles of *DRB3.2* alleles.

Keywords: *BoLA-DRB3*, Alleles, PCR-RFLP, PCR-SBT and Crossbred cattle

SP-92

POLYMORPHISMS IN BOVINE PLCZ1 GENE ARE ASSOCIATED WITH SEMEN QUALITY IN SAHIWAL BULLS

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In dairy cattle, even though both bulls and cows contribute to reproductive efficiency, the bull fertility has been given very less consideration as compared to females. Although fertility is a composite trait, functional and structural analyses of semen can be used to predict the fertility status of bull. The present study was carried out to study genetic polymorphism in exon 8 of bovine PLCZ1 gene and to analyze their association with semen quality traits in Sahiwal bulls. Blood samples were collected from 31 Sahiwal bulls maintained at Artificial Breeding Research Centre, ICAR-NDRI, Karnal and genomic DNA was isolated. The exon 8 region of PLCZ1 gene was amplified by polymerase chain reaction (PCR) using custom designed primers. The products were Sanger sequenced and analysed for variations using multiple sequence alignment. Sequence analysis revealed only one SNP (C91799202G) (as compared to *Bos taurus* reference sequence). The identified SNP was genotyped using PCR-RFLP assay. Functional analysis revealed it be a missense variation resulting in alanine to proline change. Phyre2 tools predicted the SNP to be located in X-Y linker domain. SIFT analysis of the SNP showed the nucleotide change to be tolerated one. Association analysis showed the SNP (C91799202G) to be significantly associated ($P<0.05$) with sperm viability and plasma membrane integrity. Bulls with genotype GG had lowest mean viability and plasma membrane integrity and differed significantly from other genotypes. These results suggest that the identified SNP can be used as a potential marker for semen quality in Sahiwal bulls.

SP-93

MOLECULAR CHARACTERIZATION OF A_1/A_2 BETA-CASEIN ALLELES IN VRINDAVANI CATTLE

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A_1 and A_2 are most frequently observed forms of Beta Casein in dairy cattle breeds. A_1 β-casein on digestion releases an opioid, BCM-7 which has been found significantly associated with type 1 diabetes mellitus (DM-1), ischemic heart disease (IHD), autism and including other immune suppression activities in man. On the other hand, A_2 β-casein is devoid of such adverse effects. In the present genotypic study, Vrindavani cow were genotyped for A_1/A_2 β-casein variants conducted in a population of 354 Vrindavani cows maintained at Cattle and Buffalo Farm, IVRI, Izatnagar. Bovine genomic DNA was extracted from whole blood using phenol-chloroform extraction method. PCR-RFLP method was done to estimate beta casein genotypes using *Dde*I restriction enzyme. The restriction digestion fragments were separated on 3% agarose. The gene, genotypic frequencies and genetic indices were calculated. In Vrindavani cows, all three type of genotypes were observed viz., A_1A_1, A_1A_2 and A_2A_2. Genotypic frequencies of A_1A_1, A_1A_2 and A_2A_2 genotypes were 0.11, 0.47 and 0.42, respectively. The **frequency of A_1 and A_2 alleles** in the herd of Vrindavani cows was **0.35 and 0.65, respectively.** The results revealed that **maximum genotypic frequency** observed was **A_1A_2 (0.47) followed by A_2A_2 (0.42) and A_1A_1 (0.11) in Vrindavani cattle.** The observed **heterozygosity (0.47)** and **PIC value (0.35)** pointed towards the existence of **medium genetic variability (V%)** in the tested population.

Keywords: A_1, A_2, PIC, V% and Vrindavani

SP-94

PRESENCE OF TC/G INSERTION/TRANSITION IN INTRON-III OF GROWTH HORMONE GENE AMONG INDIAN BOVINES

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Bovine growth hormone (bGH) has diverse biological activities and is involved in growth, body composition, metabolism regulation, lactation and in development of mammary glands. bGH gene is approximately 2800bp long having five exons and four introns. Recurrent studies have shown a possible direct relationship between allelic variants of bGH gene with production and reproduction traits. Most of the studies describing *Msp*I polymorphism at the bGH gene locus were in essence focused on *taurine* cattle populations, whereas no systematic effort has been undertaken in the past to generate a comprehensive profile of bGH-MspI polymorphism in Indian (native cattle, Karan Fries and Jersey crossbreds and riverine buffaloes) bovines. This *Msp*I polymorphic site became the focal point of research due to its location in the vicinity of a transcription-binding site of bGH and its association with production and reproduction. Present study attempts to explore the distribution pattern of TC/G insertion/transition in bGH-*MspI* locus across 11 Indian bovine populations. A total of 714 females belonging to Murrah (250), Chhattisgarhi (68), Burgur (49), Nagpuri (48), Gojri (50), Purnathadi (48) buffaloes and Jhari (64), Sahiwal (30), Tharparkar (32), Karan Fries (40) and Jersey crossbred (35) cattle, from different geographic locations of India were included in the study. Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) was performed using following primers [F:5-CCCACGGGCAAGAATGAGG C-3 and R: 5-TGAGGAACTGCAGGGGCCCA-3]. Through custom sequencing, PCR-RFLP polymorphic site for *MspI* restriction endonuclease resulting from a TC/G insertion/transition was confirmed. Result of gene and genotypic frequency in the studied populations revealed that in case of buffaloes only genotype *Msp*I(++) was present while *Msp*I(– –) was absent, with the exception for lesser known population from South India-Burgur buffalo. In Burgur buffalo, it was observed that genotype frequency of *Msp*I(+–) is more frequent as compared to *Msp*I(++), although *Msp*I(– –) was absent, similar to other buffalo populations studied. Result in studied cattle populations were in contrast with that of buffalo population. It was observed that genotype frequency of *Msp*I(– –) is more frequent in indigenous Sahiwal, Tharparkar and Jhari cattle. However, in case of exotic crosses (Karan Fries and Jersey crossbreed) *Msp*I(+ –) were found to be more frequent. Thus we infer genomic architecture for bGH locus is different in cattle and buffaloes and also that TC/G insertion/transition in bGH-*Msp*I locus is prevalent among Indian bovines but has a variable frequency. Results from Bargur buffalo (comparatively phenotypically smaller among the studied buffalo populations) and studied Indian native cattle (majority having medium body size) has *Msp*I(– –) genotype, whereas crossbred has *Msp*I(+–) genotype and large sized buffalo populations has *Msp*I(++) genotype. We recommend that bGH-*Msp*I locus can improve body size through selection of desirable allele in Indian bovines.

SP-95

ANALYSIS OF PROMOTER METHYLATION STATUS OF *DAZL* GENE IN BULLS WITH VARYING SEMEN MOTILITY

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In India, crossbreeding of indigenous cattle with exotic cattle like Holstein Friesian and Jersey has been going on since last four decades to improve milk production. Although it has lead to increased milk yield, the sub-fertility in male crossbred progeny has remained a significant problem. Epigenetic modifications (DNA methylation, histone modifications, chromatin remodelling) are regarded as key players influencing gene expression. The methylation and mRNA expression level of *DAZL*, a gene essential for germ cell differentiation have been significantly negatively correlated in the testes of cattle-yaks hybrids and their parents. Therefore, in this study, methylation profile of *DAZL* gene promoter in bull spermatozoa was analyzed in an attempt to speculate its role in crossbred cattle fertility. Semen samples from Sahiwal, Holstein Friesian and Frieswal bulls (Sahiwal X Holstein Friesian) with varying semen motility parameters were collected and DNA was isolated. Methylation specific primers were used to amplify part of promoter and exon 1 of *DAZL* gene using bisulfite converted DNA. The amplified products were sequenced after cloning in pTZ57R/T vector. Sequence analysis revealed significantly higher DNA methylation of *DAZL* gene in Frieswal bulls with poor fertility (28.26%) as compared to medium (15.21%) and high fertility phenotype (6.52%). In purebred counterparts, Sahiwal and Holstein Friesian, epigenetic marks were more in the former (15.21%) than the latter (4.34%) but in both cases, the values were lower as compared to the poor fertility Frieswal bulls. This suggests that differential hypermethylation of the CpG islands could possibly influence reproductive parameters in bovines.

SP-96

EXPRESSION ANALYSIS OF DEFB4A DEFENSIN BETA 4A IN BOVINE PBMCS DURING INTRA-MAMMARY INFECTION

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The immune system of livestock plays a critical role in the health and productivity of the herd. During an intra-mammary infection, as soon as the physical defences are breached by the pathogens the innate immune components comes into the action which exudes large amount of soluble components in milk to bring out inflammation. The major components of this secretion include ample of polymorphic nuclear cells including neutrophils. The prominent part of this composition includes the defensins, which are cationic peptides involved in innate defense in vertebrates. These are produced at both the levels; by the first line of defense (i.e., epithelial barriers) as well as by the second line of defense i.e. neutrophils. One of the β-defensins, Defensin Beta 4A (DEFB4A) is a biexonic gene. During the infection, the expression of DEFB4A increases in somatic cells of milk as well as in circulating PBMCs. No reports exist on the expression profiling of DEFB4A in mastitic cattle using PBMCs. The present study has focused on generating the expression profiles of DEFB4A in the indigenous cattle breed (Tharparkar) known for its better resistance to intra mammary infections than exotic breeds. A group of 5 animals showing clinical mastitis were compared with 5 healthy animals for DEF4A expression and normalized using two housekeeping genes, GAPDH and RPS15. The PBMCs has been successfully established as the sample to predict the level of expression in infected and healthy cattle.

Keywords: DEFB4A, Tharparkar, Mastitis, PBMC.

SP-97

IMPACT OF ADIPONECTIN (ADIPOQ) GENE POLYMORPHISM ON PRODUCTION AND REPRODUCTION TRAITS OF SAHIWAL COWS

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Adiponectin and resistin are very vital adipokines which influence the energy homeostasis, insulin sensitivity and mobilization of body fat stores. The present investigation was performed

to elucidate the genetic polymorphism in adiponectin gene (ADIPOQ) and their association with production and reproduction traits in Sahiwal cows. For that blood samples were collected from 69 Sahiwal cows and genetic polymorphism in ADIPOQ genes. The polymorphism in ADIPOQ gene was identified by amplifying the promoter (ADIPOQ-I) and intron-II region (ADIPOQ-II) of the gene which revealed amplicons of 977 bp and 961 bp, respectively. The *Tsa*I/PCR-RFLP assay of ADIPOQ-I gene revealed three genotypes in population of Sahiwal cattle. The CT genotype was most frequent (62.32%) followed by the homozygote CC (24.64%) and TT (13.04%) genotypes while frequency of C and T allele was 0.558 and 0.442, respectively. The association study of ADIPOQ-I/*Tsa*I revealed significant influence of genotypes on CI, LP, TMY and DRPY. The *Rsa*I/PCR-RFLP assay for ADIPOQ-II gene revealed undigested fragment of 961 bp (AA genotype). This revealed that the Sahiwal cattle were monomorphic in nature. In conclusion, SNP identified in ADIPOQ gene suggests that ADIPOQ/*Tsa*I might serve as candidate genetic marker for selection of Sahiwal cattle with better milk yield trait. However further studies are required to validate these markers in another breed and population and their association with other production traits required to be verified.

SP-98

POLYMORPHISM IN THE LEPTIN RECEPTOR GENE (LEPR) – PUTATIVE ASSOCIATION WITH PRODUCTION AND REPRODUCTION TRAITS IN SAHIWAL COWS

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The present study was performed to detect genetic polymorphism in leptin receptor (LEPR) gene by PCR-RFLP assay in Sahiwal cows. For that blood samples were collected from 69 Sahiwal cows and genetic polymorphism was analyzed by *Bse*GI/PCR-RFLP method. The amplified fragment of the LEPR gene revealed 197 bp product which on digestion with *Bse*GI restriction enzyme revealed three genotypes; AA genotype showed three fragments of 130 and 67 bp, AB genotype showed four fragments of 130, 93, 67 and 37 bp and BB genotype showed three fragments of 93, 67 and 37 bp. In studied population of Sahiwal cattle, most frequent genotype was AB (47.83%) followed by AA (36.23) and BB (15.94%) genotypes. The allele frequency of LEPR/*Bse*GI in Sahiwal cattle was 0.60 and 0.40 for A and B alleles, respectively. The LEPR/*Bse*GI assay revealed significant association of genotypes with LP, TMY, MY300 and PY in third lactation in which BB genotype showed longest LP and highest TMY, MY300 and PY compared to AB and AA genotypes. In conclusion, SNP identified in LEPR gene suggests that B allele might serve as candidate genetic marker for selection of Sahiwal cattle with better milk yield. However further studies are needed to validate these markers in another breed and population and their association with other production traits required to be verified.

SP-99

DETECTION OF KAPPACASEIN GENOTYPES IN GAOLAO CATTLE USING PCR-RFLP

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Considering the significant role of Kappa Casein gene in stabilizing casein micelle and protein content in bovine milk, the present study was undertaken to investigate the genotypes of kappa casein in 90 Gaolao cattle belonging to organized farm (Bull mother farm, Pohara Dist. Amravati) and field (Pulgaon Dist. Wardha) using PCR-RFLP technique. Gaolao is native cattle breed from Vidarbha region of Maharashtra state. Two different reported polymorphic sites of exon IV of Kappa casein gene were studied. A 379 bp K-casein fragment was amplified using forward and reverse primers viz. 5′- CACGTCACCCACACCCACATTTATC- 3′ and 5′- TAATTAGCCCATTTCGCCTTC TCTGT- 3′, respectively. Similarly, a fragment of 633 bp K-casein was amplified using primers viz. 5′-CAGCGCTGTGAGAAAGATGA -3′ and 5′-CCCATTTCGCCTTCTCTGTA -3′, respectively. The amplified PCR products were digested by restriction enzyme *HindIII*, followed by gel electrophoresis to observe genetic variants (A and B) of K-casein. The digested products of 379 bp k-casein showed two variants A and B with gene frequencies of 0.93 and 0.07, respectively. Three genotypes viz. AA (379 bp), AB (379, 225 and 154 bp) and BB (225 and 154 bp) were observed with a genotypic frequencies 88.89, 8.89 and 2.22 percent, respectively. The digested products of 633 bp K-casein indicated the gene frequencies of A and B variant as 0.98 and 0.02, respectively. Two genotypes viz. AA (633 bp) and AB (633, 423 and 210 bp) were observed in 96.67 and 3.33 percent cows, respectively, with no homozygous BB animals. The results revealed polymorphic nature of K-casein gene in Gaolao cattle. Further association of these polymorphism with milk composition traits may suggest its utility for selection of animals for genetic improvement programme.

SP-100

CONSERVATION OF CODING AND REGULATORY SEQUENCES OF HEAT SHOCK PROTEIN BETA-1 GENE AND ITS EXPRESSION PATTERN IN HEAT STRESSED PBMCS OF INDIAN NATIVE CATTLE AND RIVERINE BUFFALOES

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Heat shock protein β1 (*HSPB1*) is one of the major gene of HSP family that helps in cell survival during stress, regulate apoptosis, cellular development and differentiation. The sequence information of *HSPB*1 gene in Indian native cattle was generated for complete coding as well as 5′ and 3′ UTR region using cDNA as well as genomic DNA. The alignment of 12 cDNA of Sahiwal (SAC), Rathi (RAC), Ladakhi (LAC) cattle and Murrah (MUB) buffaloes revealed high level of sequence conservation between different cattle types and also with riverine buffaloes. Only 4 variations; 2 in SAC (G27T, G275A), 1 in RAC (G38A) and 1 in MUB (T431C) were identified. A characteristic signature motif "Alpha crystallin domain" (ACD), typical of mammalian small *HSBP*1 gene was also observed. Additionally, coding region of *HSPB*1 gene including 5′ and 3′ UTRs was sequence characterized in 181 individuals representing 12 diverse Indian native cattle (*Bos indicus*) breeds and compared with exotic cattle (*Bos taurus*) and riverine buffaloes (*Bubalus bubalis*). The analysis of *HSPB*1 sequences in Indian cattle revealed 5′ UTR of 124 bp and 3′ UTR of 76 bp. Interestingly, both the UTRs showed complete sequence homology with that of *Bos taurus*. Similar to UTRs, the exonic region was also highly conserved as only two SNPs (G151T and C2519G) were detected. Additionally, the heat responsive nature of *HSPB*1 gene was evaluated in peripheral blood mononuclear cells (PBMCs) of Sahiwal cows and Murrah buffaloes. The PBMCs of Sahiwal cows and Murrah buffaloes showed significant induction of *HSPB*1 mRNA post heat stress, albeit at varied level. The present study has revealed extensive conservation of *HSPB*1 sequences across different cattle types. The study has also provided a strong clue that PBMCs of Murrah buffaloes are more sensitive to heat stress in relation to Sahiwal cattle.

SP-101

CATALOGUING THE DIFFERENTIALLY EXPRESSED GENES IN PBMCS OF DISEASED VERSUS HEALTHY NILI RAVI WATER BUFFALO

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In the present study, the differentially expressed transcripts in PBMCs of two diseased groups (tuberculosis and metritis) with respect to the healthy Nili Ravi buffalo (*Bubalus bubalis*) have been catalogued. Peripheral blood from 4 animals of each groups (*Tuberculosis, Metritis and Healthy-control*) were selected and peripheral blood mononuclear cells (PBMCs) were isolated immediately. The 4 samples of each groups were pooled to make 2 samples (representing 2 biological replicates) for each group and total RNA was extracted using *mir*Vana™ miRNA Isolation Kit (Ambion, Life technologies, CA, USA). The sequencing of total-RNA was done using Illumina Hiseq 2500 platform. The pre-processed reads were aligned to *Bos taurus* genome using Hisat2 program (version 2.0.5). The gene and transcript expression were studied using String_Tie program (version 1.3.3b). Target prediction of the differentially expressed miRNA genes was performed using Target Scan online tool. DAVID and Panther online tools were used for pathway analysis of DEG-mRNAs and target genes. A total of 31982 transcripts (including mRNA, miRNA, proein coding, pseudogene rRNA, snoRNA, snRNA) were identified. Comparisons of all the 3 groups showed that 21606 transcripts (total) and 8132 mRNA were common. 231 TB, 193 Metritis and 273 Healthy mRNA transcripts were unique to individual groups. The differentially expressed protein-coding genes were identified as up and down regulated on the basis of log2(FPKM ratios) >2 and <2, respectively. In total 162 differentially expressed (up- and down-regulated) mRNA genes (DEGs) were identified in *Metritis* vs healthy group and 176 DEGs (mRNA) in *TB* vs healthy group. Network analysis identified the immune related genes (viz. HRG, TRIL etc among others) contributing to the systems biology related to the diseases in Nili Ravi buffalo.

SP-102

CHARACTERIZATION OF ATP1A1 GENE: A MAJOR ALPHA ISOFORM OF NA$^+$/K$^+$-ATPASE COMPLEX TOWARDS SEQUENCE VARIATION AND HEAT RESPONSIVE NATURE IN INDIAN NATIVE CATTLE AND RIVERINE BUFFALOES

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Na$^+$/K$^+$-ATPase is a transmembrane protein complex which maintains the balance of Na$^+$ and K$^+$ ions across the plasma membrane. It is a hetero-oligomer composed of alpha (α), beta (β) subunit and gamma (γ) subunit. The alpha (α) subunit has four isoforms; α1, α2, α3 and α4 which are encoded by *ATP1A1, ATP1A2, ATP1A3* and *ATP1A4* genes, respectively. Recently, *ATP1A1* gene has been associated with heat stress in dairy animals but the data with respect to molecular characterization and the genetic structure of alpha 1 isoform is deficient in Indian riverine buffaloes (*Bubalus bubalis*) and Indian native cattle (*Bos indicus*). In the present study, an attempt was made to sequence characterize the genomic region covering the partial intron 17 to partial intron 21 of *ATP1A1* gene in 8 different breeds of riverine buffaloes and 12 native cattle breeds. The sequences obtained revealed a total of 28 variations (26 identified in buffalo breeds and 2 variations in cattle breeds) in the selected regions of *ATP1A1* gene. Out of 26 variations in riverine buffalo, 6 were distributed across 4 exonic regions (T27006876C, C27006599T, T27006345C, T27006330C, G27006309T and T27006240C) and the remaining 20 were found in intronic region while in cattle, 1 variation was distributed in the exonic region (C27007790A) and the other (T27007767C) in the intronic region. All 7 variations found in exonic region were synonymous in nature. The SNPs identified in the study could be explored further for their role in heat stress.

Further, the expression kinetics of four isoforms *viz*., alpha1, alpha2, alpha3 and alpha4 (*ATP1A1, ATP1A2, ATP1A3* and *ATP1A4*) of Na$^+$/K$^+$-ATPase was characterized in heat stressed peripheral blood mononuclear cells of Sahiwal cows, Holstein-Friesian cows and Murrah buffaloes. The expression data of PBMCs was normalized using *B2M, RPS9* and *RPS15* housekeeping genes, identified previously for similar experimental conditions. The result showed immediate increase in the expression of *ATP1A1* and *ATP1A2* mRNA in PBMCs of all animal types post heat stress albeit at varied level. On the other hand, higher CT values for *ATP1A3* and *ATP1A4* isoforms indicated their low expression in PBMCs. Both *ATP1A1* and *ATP1A2* mRNA expression was induced at 2 hr post heat stress in PBMCs of all animal types. *ATP1A1/ATP1A2* mRNA expression was maximum in PBMCs of Murrah buffaloes (7.50/3.14) followed by Holstein-Friesian cows (2.17/2.40) and Sahiwal cows (1.95/1.6) at 2h post stress. Additionally, an attempt was made to assess the *ATP1A1/ATP1A2* mRNA expression in heat stressed buffalo mammary epithelial cells. The qPCR data of BMECs was normalized using *RPL4, RPS23* and *EEF1A1* housekeeping genes. Similar to PBMCs, the BMECs data showed induction of *ATP1A1/ATP1A2* isoforms immediately post heat stress and reached at maximum level (4.65/1.84 folds) at 4h post stress. The expression pattern of *ATP1A1/ATP1A2* mRNA in heat stressed PBMCs and BMECs at different time points was compared with the expression pattern of *HSP70, HSP90, HSP60* mRNA. Though all the three HSPs were more responsive in both the cell types, expression pattern of *ATP1A1/ATP1A2* mRNA were positively correlated with HSPs expression data. The differential induction of *ATP1A1/ATP1A2* mRNA post heat stress in PBMCs and BMECs showed these isoforms to be heat responsive and could be utilized as an additional marker to understand the cellular tolerance of different cattle and buffalo types to heat stress.

SP-103

A REDUCED REPRESENTATION APPROACH FOR WHOLE GENOME SNP IDENTIFICATION IN MURRAH BUFFALOES

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NGS based Restriction-site Associated DNA sequencing (RAD Seq) methods are an alternative to Whole Genome Sequencing (WGS), wherein simultaneous sequencing, genotyping and multiplexing are facilitated. WGS for SNP genotyping is technically unnecessary and a reduction of about 35 fold in cost is possible through RAD seq methods as compared to WGS method.

The present study has been carried out to identify the genome wide SNPs and INDELs in Murrah buffalo genome. A total of 21.2 million raw reads from 4 samples of Murrah buffalo were obtained using restriction enzyme digestion based methods. The raw reads were quality filtered and aligned with Water buffalo genome as reference. The coverage of the read alignment is 10.5%. A total of 219856 high quality SNPs along with 15201 INDELs were identified after filtration for quality and depth. The SNPs identified in the present study will be used for the phylogeny comparison with cattle and yaks and will be of further use in the diversity study, Genome Wide Association Studies (GWAS) and Genomic selection.

SP-104

PRIMARY BOVINE MAMMARY EPITHELIAL CELLS COMPARATIVE STUDY AT 15 AND 60 DAYS POSTPARTUM IN BUFFALOES

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The study was carried out to standardize and study the pBMEC recovery percent in Surti and Jafarabadi buffaloes milk at day 15 and 60 postpartum (pp).10 healthy Surti and Jafarabadi buffaloes of each breed were selected at random from Livestock Research Station, Navsari and Cattle Breeding Farm, Junagadh, Gujarat, respectively. Buffaloes were further divided into four different groups for data analysis and comparisons. In the present study, primary bovine mammary epithelial cells (pBMEC) recovered repeatedly at different stages of lactation in same animal using antibody mediated magnetic bead separation method. As a major finding, the mean difference of Somatic Cell Count was highly significant ($p \leq 0.01$) with advancement of lactation in both Surti and Jafarabadi buffaloes. There was no significant difference ($p \leq 0.05$) observed for mean pBMEC obtained from total somatic cells within or between breeds. The mean pBMEC recovery percent difference between two stages of lactation within and between breed was again found to be non-significant ($p \geq 0.05$). Significant difference ($p \geq 0.05$) in mean RNA yield (µg) was observed with advancement of lactation in Surti buffalo. Milk purified mammary epithelial cells over mammary tissue further can be use to study expression patterns of genes related to milk synthesis during lactation as it gives a real picture of the molecular events involved in milk synthesis.

SP-105

GENETIC VARIANT OF EXON 6 IN LACTOFERRIN GENE ASSOCIATED WITH CLINICAL MASTITIS IN MURRAH BUFFALO

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Lactoferrin is one of the important candidate genes for mastitis resistance. The gene is located on *Bos taurus* autosome (BTA) 22 and consists of 17 exons spanning over 34.5 kb. The present study was undertaken with the objectives to detect single nucleotide polymorphism, identify

allelic variant in exon 6 of lactoferrin gene and to analyze its association with incidence of clinical mastitis in Murrah buffalo. Amplification of exon 6 yielded amplicon of 301 bp size. Comparison of nucleotide sequence of exonic region of lactoferrin gene in Murrah buffalo with *Bos taurus* (NCBI accession number AC_000179.1) revealed 2 non synonymous mutations at 10174 (T>C) and 10177 (A>G) position. PCR-restriction fragment length polymorphism (RFLP) analysis of 301 bp amplicon using *Fok*I restriction enzyme exhibited polymorphic pattern with two genotypes (AA and AB) with respective frequency of 0.625 and 0.375. The frequencies of two alleles, A and B were estimated as 0.81 and 0.19, respectively. The chi-square ($\chi2$) analysis revealed a significant ($P \leq 0.05$) association between incidence of clinical mastitis and genetic variant of exon 6 and the animals with AA genotype was found to be less susceptible to mastitis. The findings indicate potential scope for incorporation of lactoferrin gene in selection and breeding of Murrah buffaloes for improved genetic resistance to mastitis.

SP-106

EXPLORING SINGLE NUCLEOTIDE POLYMORPHISM IN AKR1B1 GENE IN MURRAH BULLS

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Aldo-keto Reductase family 1, member B1 (AKR1B1) gene is reported to be an important candidate gene for bull fertility in buffaloes. AKR1B1 gene is involved in carbohydrate metabolism that converts glucose to its sugar alcohol form, sorbitol, which is subsequently metabolized to fructose to be used by sperm cells as an energy source for glycolysis and glyconeogenesis. AKR1B1 gene has a size of 16,806bp encoding 316 amino acid and has 10 exons. Present study was carried out to explore polymorphism in the Intron-7 of AKR1B1 gene. A sample size of 87 pedigreed Murrah bulls was studied. PCR amplification of the targeted regions was done using sequence-specific primer (F:5′-ACCAGGGCTTACCTGGAAGT-3′ and R:5′-GGTCAATGGGCCTTAGGATT-3′) having an annealing of 56.7°C. PCR amplicon (796bp) were digested using *Nde1* restriction enzyme by incubating in a water bath at 37°C for 14-16 hrs. The digested fragments were resolved in 2% agarose gel using gel electrophoresis. PCR-RFLP results revealed three distinct genotypes AA, AB and BB having variable frequencies. Genotype AA had 0.08, AB had 0.44 and BB had 0.48. Gene frequencies were estimated for its alleles and 'A' allele had (0.31) whereas the 'B' allele was more frequent (0.69) in the studied population of Murrah bulls. Based on the identified variations we report that the studied AKR1B1 locus is polymorphic and its further association analysis with fertility traits is required, which shall be very useful for early selection of young Murrah bulls.

SP-107

GENETIC DIVERSITY ANALYSIS OF BARGUR BUFFALO

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Burgur buffaloes are being maintained by Burgur Lingayat an indigenous Kanada speaking community in the Burgur villages (A&B) of Anthiyoor taluk in Erode district of western Tamilnadu. The buffaloes are good in climbing hills and suitable for grazing in hill terrain or in slopes. Very scanty information is available on characterization of Bargur buffalo population of Tamilnadu State and no adequate literature is available regarding their genetic diversity study. Keeping above in view, the present study was conducted to identify, characterize, evaluate and document the present status of this unique bubaline germplasm. Bargur buffaloes are called as Malai Erumai which means hill buffalo. Burgur buffaloes are medium in size with coat colors varying from black to light brown and brownish black. The animals are maintained under zero input system of rearing where they were allowed to graze in the forest area. The animals housed either in a separate enclosure adjacent to the farmers' house (80%) of in the harvested fields with enclosures (20%). The animals are about 102.10±1.23 cm in height and are able to graze in the hilly terrain due its small size. The breeding males are called as Konan, majority of the famers (>95%) was practicing natural mating with Konans. The animals are mainly reared for manure, milk and the male calves are sold for cara-beef. The Bargur buffaloes are riverine type with 50 number (2n) of chromosomes. This is supported by the Mt D-Loop hyper variable segment haplotype analysis. The haplotypes obtained were compared with ASW, Manipuri, Marathwada, Murrah, South Kanara and Toda buffaloes. A total of 40 haplotypes were observed with a overall haplotype diversity of 0.9524 and nucleotide diversity 0.03894. Three unique haplotypes were observed in Bargur buffalo with a haplotype diversity of 0.9111 and nucleotide diversity of 0.01826. Median joining network analysis revealed clustering of Bargur buffalo with the riverine group. The genetic variability measures of Burgur buffalo across the 24 microsatellite markers are depicted in table 2. A total of 24 loci of neutral microsatellite markers were PCR amplified and genotyped in 48 samples. All the loci studied in the population were polymorphic. Overall average number of alleles was 8±0.55 and average effective number of alleles was 3.85±0.25. The average observed (H_O) and unbiased expected (uHe) heterozygosity were 0.66±0.04 and 0.71±0.032 for Burgur buffaloes. The observed heterozygosity in the studied population was found to be lower than the expected heterozygosity. FIS value was found to be 0.056±0.037. Microsatellite diversity analysis revealed no recent bottle neck in the Burgur buffalo population and gives L-shaped curve. This bubaline germplasm with unique and distinguished phenotypic characters needs to be registered at National level so that suitable breeding strategies/conservation models could be suggested which will support the livelihood of the Lingayat community rearing these buffaloes.

SP-108

EVALUATION OF STR MARKERS BASED GENETIC DIVERSITY ACROSS SAMBALPURI BUFFALO OF ODISHA

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India is among the twelve mega biodiversity centres of the world, possessing world's largest livestock population estimated to be 512 million that accounts for 13% of the global livestock population. According to 19th Livestock Census, present Indian buffalo population is 108.7 million; amounting to 57% of world's buffaloes, which includes 13 registered breeds and several non-documented populations. Odisha state located in eastern parts of India has highly diversified buffaloes, mostly reared on extensive management system and well acclimatized to harsh and humid agro-climatic conditions. There are five major buffalo populations namely, Chilika and Kalahandi- two registered breeds apart from three other populations- Paralakhemundi, Sambalpuri and Manda. Among these, Sambalpuri is one of the important buffalo population distributed in Sambalpur, Jharsuguda and Baragarh districts of Odisha. This unique population offers a great opportunity for genomic dissection to explore their genetic diversity. In this study, the genetic diversity in Sambalpuri buffalo population, was assessed using a set of 23 microsatellite markers and genotyping carried out on DNA samples isolated from 48 randomly collected blood samples. PCR amplified products were multiplexed and run on automated DNA sequencer to record the marker wise genotypes. Total number of alleles across population observed were 275 and mean fixation index (F) was found to be 0.098. CSSM47, ILSTS52 and ILSTS26 loci were observed to be having the highest number of alleles i.e. 19. While lowest, 3 were found at ILSTS19 marker locus. The observed heterozygosity value (H_O) was highest at loci ILSTS89 (0.957) and ILSTS29 (0.932). For both the loci expected heterozygosity (H_e) value was 0.811 and 0.854, respectively. The average observed and effective number of alleles were 11.9 and 5.4, respectively. The mean Ho and He were found to be 0.68 and 0.76, respectively. The Polymorphic Information Content (PIC) values for markers used, ranged from 0.083 to 0.89 with an average of 0.74. Mode shift Analysis of the data indicated absence of bottleneck in this population. Overall the study shows existence of substantial genetic diversity among Sambalpuri buffaloes of Odisha.

SP-109

GENETIC DIVERSITY ANALYSIS OF KILAKARSAL SHEEP BY MICROSATELLITE MARKERS

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Kilakarsal sheep population variability and structure was investigated genetically utilizing FAO recommended 25 microsatellite markers. Estimates of genetic variability such as effective number of alleles and gene diversities revealed substantial genetic variation detected by microsatellite markers. A total of 241 alleles were detected and the actual number of observable alleles ranged from five (BM6526) to a maximum of 16 (MAF70). The mean number of alleles (allelic diversity) was 9.64. The effective number of alleles which is lower than the observed number of alleles, was between 2.279 (OarCP20) and 8.510 (MAF70) with a mean of 4.786 alleles. The average observed heterozygosity (H_o) and expected heterozygosity (H_e) were 0.690 and 0.782, respectively. However, the study evidenced a significant departure from Hardy-Weinberg equilibrium in 13 loci. Such lack seems to be caused by a rather high level of inbreeding (F_{IS}=0.097).

Keywords: Characterization, Kilakarsal, Sheep, Microsatellites

SP-110

VARIABILITY OF MYOSTATIN GENE AND ITS ASSOCIATION WITH GROWTH TRAITS IN MALPURA SHEEP

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Myostatin, a candidate gene used to study growth traits, is a negative regulator of skeletal muscle growth and development in mammals. It is highly conserved member of transforming growth factor-β super family. Present study was carried out to assess the genetic diversity of the *Myostatin* gene, using Polymerase Chain Reaction (PCR) single stranded confirmation polymorphism (SSCP) and its association with growth traits in 529 animals of Malpura sheep maintained at an organized institute farm flock in the semi-arid tropics of India. The fragments having the Promoters, 5'UTR, all 3 Exons, Intron 1 and 3'UTR were assessed for their sequence variability. However, variation at nucleotide level was observed for Promoter, Intron-1, 5'UTR and 3'UTR region. We found total six SNPs – 2 in 5'UTR (c.-37; c.-40), 2 in Promoter region (c.-958; c.-1128), 1 in Intron-1(c.+391/c.373+18) and 1 in 3'UTR (c*202) (Please arrange according to the gene sequence as promoter, Intron, 5'UTR, exon, 3' UTR). Non-genetic factors such as sex of the lamb,

year and season of birth, type of birth and weight of dam at lambing were found to influence the growth traits significantly and explained significant variance (R^2) in the trait. Genotypic association study revealed, that out of 4 variable fragments, only Promoter region had a significant effect ($P < 0.05$) on live weight at 12 month age, average daily gain from 6 to 12 month age (ADG3) and corresponding kleiber ratio (KR3). Almost 5.19 g more daily weight was obtained for genotype CT (P4.2) as compared to genotype CC (P4.1), with obvious advantage for T replacing C at c.-958 and c.-1128 position. This variation should be studied further in different breeds, populations and different locations for confirmation of the putative association, so that this variation can be utilized in breeding program.

SP-111

AGE RELATED EFFECT OF MYOSTATIN INTRON 2 GENE ON BODY WEIGHT OF MAGRA SHEEP

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Variation in biometric traits such as body weight plays a critical role in selection of individuals for the production of future generations and on overall productivity of the livestock. Candidate gene such as myostatin (*MSTN*) has frequently been claimed as a negative determinant of body weight in many livestock species. Therefore the present study was conducted to investigate the presence of genetic variation in intron 2 of *MSTN* gene through SSCP marker and sequence analysis of amplified fragment and to analyze their association with body weight at three different ages. Blood samples were randomly collected from seventy four (n=74) contemporary and apparently healthy animals (lambs) of most diverse genetic background on the basis of available pedigree information from the Magra Sheep breed farm maintained at CSWRI, Bikaner. The body weight information from birth to 6 months of age was also collected along with the respective blood samples. A 311 bp fragment of *MSTN* intron 2 region was amplified at an annealing temperature of 54°C through species specific primer after extraction of quality genomic DNA from whole blood. SSCP marker and sequence analysis of the representative SSCP banding pattern was carried out through standard protocols. The results revealed the presence of three genotypic patterns 'AA', 'AB' and 'BB' having differential gel mobility. An overall five SNP's were detected between two alleles (A and B) after sequencing. Association analysis reflected the significant effect of sequence variation of two alleles on the body weight parameter with highest body weight was observed for 'AB' genotyped individuals at 3 and 6 months of age while no association was detected at birth. The present study concluded that polymorphism in intron 2 of *MSTN* gene affects the body weight of Magra sheep at specific stages.

Keywords: Magra Sheep, *MSTN*, Sequence Polymorphism, Body Weight.

SP-112

IDENTIFICATION OF CANDIDATE GENES AND PATHWAYS UNDERLYING MEAT QUALITY IN BANDUR SHEEP

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Bandur - an indigenous sheep breed from Mandya district of Karnataka is famous for its mutton, which fetches a higher price than mutton from local sheep. Meat quality is not only affected by feed, post mortem processing, fat percentage etc., but also by genetic factors. To identify the genetic factors underlying the mutton quality of Bandur sheep, gene expression profiling of skeletal muscles of Bandur sheep was carried out using RNA sequencing technique. Purified mRNA from four biological samples of skeletal muscles from Bandur sheep were subjected to paired end sequencing on Illumina HiSeq-2000 Platform. The total number of reads for each library ranged from 24,280,035 to 30,330,120 with GC content of 44-50%. The reads were aligned to the reference assembly genome Oar v3.1. Gene expression levels were evaluated by counting the number of Fragments per Kilobase of transcript per Million mapped reads (FPKM). The significant GO terms ($p<0.05$) corresponded to skeletal muscle cell differentiation, AMPK signaling pathway, sequestering of actin monomers, mRNA transcription, brown fat cell differentiation and adiponectin-activated signaling pathway, among others. As expected, 99 GO terms were related to muscle or protein and fat metabolism. Genes previously associated with fatty acid metabolism and tenderness that were identified in this study include *FABP4, ADIPOQ, ADIPOR2, LPIN1, HspB1, DNAJ5, HspA6, CRYAB*. Pathways for general housekeeping functions like RNA transport and degradation, Toll-like receptor signaling pathway, immune system, glycolysis etc, were identified. Certain pathways and genes associated with actin and cytoskeleton were also identified. Other prominent pathways detected that are relevant to meat quality were AMPK signaling pathway, PPAR signaling pathway, calcium signaling pathway, adipocytokine signaling pathway, lipid metabolism, muscle development and differentiation. The identified genes and pathways will form interesting candidates for further research on meat quality in Indian sheep.

SP-113

A MOLECULAR STUDY ON GENETIC POLYMORPHISM OF DGAT-1 GENE IN MANDYA AND HASSAN BREEDS OF SHEEP

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The present study was carried out with objectives of identifying and comparing the genetic polymorphism in Ovine DGAT- 1 gene of Mandya and Hassan sheep breeds using PCR-RFLP technique. A total of 100 unrelated animals comprising of 50 each of Mandya and Hassan breeds of sheep were utilized for the present study. The animals of Mandya breed were selected from farmers flock in the breeding tract (Mandya district). The animals of Hassan breed were selected from different villages of Hassan district. From each representative animal, about 10 ml of venous blood was collected in vacutainer tubes containing 0.5 per cent EDTA. The blood samples were immediately transported to the laboratory at 4°C and genomic DNA was isolated within 24 hrs. A 309 bp fragment of Ovine DGAT- 1 gene sequence spanning part of exon 16, intron 16 and part of exon 17 was amplified by following standard PCR procedure using published primers. The PCR amplified sequence of Ovine DGAT- 1 gene was confirmed through nucleotide sequencing. Upon RFLP analysis using *Alu*I restriction enzyme, polymorphic pattern revealed two alleles viz., allele C (309 bp fragments) and allele T (272 and 37 bp fragments). In the studied population of Mandya and Hassan sheep, the allelic frequencies for C and T were 0.92 and 0.08, respectively. The frequencies of CC, CT and TT genotypes were 0.84, 0.16 and 0.00; and 0.86, 0.12 and 0.02, in Mandya and Hassan breeds of sheep, respectively. Thus, polymorphism for DGAT-1 was observed in Mandya and Hassan sheep breeds. The sequence analysis revealed two SNPs *viz.*, T→A (transversion) and C→T (transition) of Ovine DGAT-1 gene. BLASTn sequence analysis revealed high homology (99 per cent) with that of predicted Ovine DGAT- 1gene (EU178818.1) sequence of Ovine chromosome nine.

SP-114

SEQUENCE CHARACTERIZATION OF OVINE MHC DRB GENE IN INDIAN SHEEP BREEDS USING BIOINFORMATICS TOOLS

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Major Histocompatability Complex (MHC) in sheep is also called as Ovar- MHC and is a central molecule for antigen presentation. Due to its increased importance in disease resistance research, we compared the sequence of MHC DRB (exon 2 and intron 2) gene in four Indian sheep breeds. Sheep breeds viz, Marwari, Malpura, Chokla and Mujaffarnagri were selected for the study. DNA was isolated from blood using Sambrook and Russell (2001) method. Ten samples from each breed were sequenced using automated DNA sequencer. The raw sequences were first assembled using Bioedit and MEGA 6.0 softwares. The final assembled sequences were submitted to NCBI database and accession numbers were assigned to them as KT878759 (Marwari sheep), KT878758 (Malpura sheep), KT764074 (Chokla sheep; Haplotype 1), KT764075 (Chokla sheep; Haplotype 2), KT764076 (Chokla sheep; Haplotype 3), KT764077 (Chokla sheep; Haplotype 4), KT781587 (Muzaffarnagri sheep; Haplotype A) and KT781588 (Muzaffarnagri sheep; Haplotype B). On the basis of dissimilarities after alignment the haplotypes were made. Total four haplotypes were found in Chokla sheep designated from 1 to 4 and two were found in Muzaffarnagri sheep designated as A and B. The sequences were also compared using DNASTAR and MEGA 6.0 software. The sequences showed exon 2 spanning from 8th to 277th base pair, followed by intron 2 consisting of characteristic dinucleotide repeats (consisting GT and AG nucleotides predominantly). The exon region was translated to make protein sequence which was analyzed by MEGA 6.0, Phyre 2 online tool (http://www.sbg.bio.ic.ac.uk/ phyre2/html/page.cgi?id=index) and 3D ligand site (http://www.sbg.bio.ic.ac.uk/3dligandsite/) for prediction of ligand binding site. The disparity index analysis showed that both the haplotypes of Muzaffarnagri sheep showing significant (at $P<0.05$) deviation from same substitution pattern. Phylogenetic analysis showed that the haplotypes of Chokla breed viz., haplotype 1 and 4 to be clustered and haplotypes 3 and 2 to be clustered, together. Both the haplotypes of Muzaffarnagri breed were separately clustered with Chokla 1 & 4 cluster (Muzaffarnagri hap A) and with Malpura breed (Muzaffarnagri hap B). The ligand binding site prediction of all haplotypes among all breeds however does not show any difference and amino acid SER83 and GLN87 showed most confident ligand binding site. This means the variations within the sequences may not be directly reflected in ligand binding site structure; however, these variations may exert their effect *in trans* by altering the affinity of either antigen or during the binding.

Keywords: Ovar- MHC, Phyre 2, Indian Sheep breeds, MHC-DRB, Exon 2

SP-115

GENETIC VARIABILITY PRESENT ACROSS THE CLASS II MAJOR HISTOCOMPATIBILITY COMPLEX DRB3.2 LOCUS IN BEETAL GOAT BREED OF THE INDIAN SUBCONTINENT

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The DRB3.2 locus of the Class II Major Histo Compatibility Complex gene which encodes for a protein molecule which is involved in the process of antigen presentation and which has been reported to possess a very high degree of genetic variability in almost all the species; was studied for the extent of genetic polymorphism present across it in Beetal goat breed of the Indian Subcontinent which is found in Punjab, Pakistan and India; and is used for milk and meat purposes. The exon 2 of the DRB3 locus of the Class II MHC was amplified by using locus specific primers by polymerase chain reaction in fifteen animals (n=15) of the Beetal breed of goats. The PCR conditions followed were: Initial denaturation for 2 minutes at 94°C, followed by 25 cycles of 30 seconds each of denaturation at 940 C, Annealing at 600C and Extension at 72°C. The final extension step was carried out at 72°C for 10 min. Taq Master Mix (5X from NEB) was used for amplification. A PCR product of size 284 bp was obtained which was checked on 1.5 percent agarose gel. The amplified gene product was digested with the restriction enzyme(s) Hae III, RsaI and BstYI in order to check for the polymorphism present across this locus. Each digestion reaction contained 10 U of the restriction enzyme in the presence of the restriction enzyme digestion buffer and PCR product. The reaction was carried out by incubation at 37°C for 90 min. with the Hae III and the RsaI enzymes and at 60°C with the BstYI enzyme. The digests obtained were resolved on 3.0 percent high resolution agarose gels and 10 bp molecular marker ladder (Invitrogen) was run along with for accurate sizing of the digestion fragments obtained. The PCR product was also gene sequenced using direct sequencing reaction procedure (Sanger dideoxy DNA sequencing reaction) using the ABI Big Dye Cycle Sequencing kit. The gene product was sequenced using both the forward and the reverse primers. The 284 bp sequenced product obtained was observed to have 40 snp(s) across this short stretch of 284 bp. Analysis of the snp(s) obtained is being carried out in the study.

SP-116

ASSOCIATION OF POLYMORPHISM IN MHC CLASS II GENE WITH HAEMONCHUS CONTORTUS RESISTANCE/SUSCEPTIBILITY IN MARWARI GOATS

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PCR-RFLP analysis was used to investigate the effect of genetic variation in the Major Histocompatibility Complex (MHC) class II region on resistance of goats to the stomach worm parasite *Haemonchus contortus,* using faecal egg count (FEC) and Dot-ELISA as the measure of resistance. PCR-RFLP analysis of DNA from 207 Marwari goats with the restriction enzyme *Hin1I* revealed three restriction digestion profiles AA (285bp), AG (285bp, 174bp and 113bp), GG (174bp and 113bp) with genotypic frequencies 0.24, 0.42 and 0.34, respectively. Association between genotypes and indicator traits was ascertained by using SAS 9.3 software. At Hin1I locus, the mean EPG was found to be 72 ± 17.79, 144.25 ± 27.58 and 157.86 ± 50.04 for AA, AG and GG genotypes, respectively and the effect of genotypes on EPG and log EPG was found to be statistically non-significant ($P<0.05$). The association between genotypes and dot-ELISA results and their Odds ratios (ORs) in ELISA positive and negative groups were calculated using PROC LOGISTIC procedure of SAS 9.3. At *Hin1*I locus, the frequency of AA, AG and GG genotypes were 0.186, 0.407 and 0.407 in dot-ELISA positive group and 0.309, 0.436 and 0.255 in dot-ELISA negative group, respectively. The *Hin1*I locus showed a statistically highly significant association with dot-ELISA test results ($P<0.01$). The odds ratios (ORs) of AA and AG genotypes versus GG genotype were 2.510 (1.152-5.468; 95% CI) and 1.907 (0.962– 3.781; 95% CI), respectively. The AA genotype showed higher resistance than both AG and GG genotypes. The AA genotype was 2.520 times more resistant than AG and 1.907 times resistant than GG genotypes. This shows that odds of finding AA genotype with dot-ELISA negative group were significantly higher ($P<0.05$) than AG and GG genotypes.

Keywords: *Haemonchus contortus*, resistance, PCR-RFLP, MHC Class II Gene, Marwari goat.

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GENETIC POLYMORPHISM OF MHC CLASS II DRB GENE IN INDIAN GOAT BREEDS USING PCR-RFLP

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The Major Histocomtability Complex (MHC) in goat is also called as Caprine- MHC and is a central molecule for antigen presentation. In the present study, we compared the MHC DRB (exon 2) gene in two Indian goat breeds. DNA was isolated from blood using Sambrook and Russell (2001) method. At MHC class II DRB (exon 2) gene, three SNPs at *TaqI*, *BsaI* and *BsaHI* RE sites were studiedin both the breeds. In Salem Black goat population, for *Taq*I locus, the genotypic frequencies were found to be 0.220, 0.490 and 0.290 for AA, AB and BB genotypes, respectively; whereas, the allelic frequency was found to be 0.465 and 0.535 for alleles A and B, respectively. In case of *BsaI* locus, the genotypic frequencies were 0.930, 0.060 and 0.010 for genotypes AA, AB and BB, respectively; whereas, the allelic frequency was found to be 0.960 and 0.040 for allele A and B, respectively. For locus *BsaHI*, the genotypic frequencies were 0.300, 0.440 and 0.260 for genotypes AA, AB and BB, respectively, whereas, the allele frequency was found to be 0.520 and 0.480 for allele A and B, respectively. In Tellicherry goat Population, for *TaqI* locus, the genotypic frequencies were found to be 0.206, 0.514 and 0.280 for AA, AB and BB genotypes, respectively; whereas, the allelic frequency was found to be 0.463 and 0.537 for alleles A and B, respectively. In case of *BsaI* locus, the genotypic frequencies were 0.879, 0.121 for genotypes AA and AB, respectively, the BB genotype was not found in the population studied, whereas, the allelic frequency was found to be 0.939 and 0.061 for allele A and B, respectively. For locus *BsaHI*, the genotypic frequencies were 0.206, 0.429 and 0.365 for genotypes AA, AB and BB, respectively; whereas, the allele frequency was found to be 0.421 and 0.579 for allele A and B, respectively. This existing variation should be further studied in other breeds of goats.

Keywords: Caprine- MHC, Indian Goat breeds, MHC-DRB, Exon 2, PCR-RFLP

NATIONAL SYMPOSIUM: Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income &
XV Annual Convention of Society for Conservation of Domestic Animal Biodiversity (SOCDAB)
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SP-118

COMPARATIVE EVALUATION OF IMMUNE RESPONSIVENESS TO SHEEP RED BLOOD CELLS, PHA-P AND IBDV VACCINE IN NATIVE CHICKEN BREEDS OF INDIA

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This comparative study was investigated with the aim to develop stocks of native chicken with higher production potential and increased resistance to pathogen, parasites and non-specific stresses. A total of 60 birds comprising two native breeds viz. Aseel and Kadaknath were utilized to evaluate and compare antibody response to Sheep Red Blood Cells by haemagglutination test at 0, 5 and 10 days post primary inoculation, to study in vivo cell mediated immune response to mitogen Phytohaemagglutinin (PHA-P) and to evaluate immune responsiveness to IBDV vaccine. The presence of natural antibodies against SRBC was evident in both the genetic groups. Both Aseel and Kadaknath showed an increase in HA titre upto 10 days post immunization. The HA titre on 10 day was significantly higher in Aseel (1.88±0.10) than Kadaknath (1.09±0.06). The in vivo cell mediated response to mitogen was also higher in Aseel (0.68 mm) than Kadaknath (0.43 mm).There was significant difference between the layer breeds for response to phytoheamagglutinin. The titre values for IBDV were lowest before immunization and got increased during 7, 14, 21 DPI. At 14 DPI the titre value was significantly different in both the breeds in which Aseel exhibited the higher titre value (2.96±0.04) than Kadaknath (2.64±0.06). It was found that at 21 DPI antibody responses was highest in both Aseel and Kadaknath, however differences were not significant.

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EFFECT OF BREED, COCCIDIAL DOSE AND INTERVAL ON DIFFERENTIAL EXPRESSION OF CYTOKINE GENES IN RELATION TO COCCIDIAL CHALLENGE IN CHICKEN

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The relative expression of IL-1β, IL-2, IL-6, IL-17 and IFN-Y genes was studied in Kadaknath, Cobb and Caribro-Vishal chicken in control and treatment groups (T1 and T2) on days 4, 7 and 14 post challenge. Group T1 and T2 were challenged by gavaging 10,000 and 20,000 sporulated

oocyst, respectively to each bird on 21st days of age. The control group was given 1 ml of Hanks Balanced Salt Solution (HBSS). The least squares analysis of variance revealed highly significant ($P<0.01$) effect of breed for IL-1β gene and IFN-Y gene. The effect of dose was significant ($P<0.05$) for IL-6 gene and non significant for remaining cytokine genes. The effect of interval (post challenge) was found to be highly significant ($P<0.01$) for all five cytokine genes. The relative mean fold expression of IL-1β gene for T1 (dose 1) and T2 (dose 2) ranged from 9.91±0.14 (Kadaknath) to 105.78±0.52 (Cobb) and 14.47±0.28 (Kadaknath) to 119.01±0.29 (Caribro-91), respectively. The highest and lowest relative mean fold expression for IL-2 gene for T2 (dose 2) was found to be 242.19±0.40 and 6.25±0.03 in Cobb at days 4 and 14 post challenge, respectively. However, the relative mean fold expression of IL-2 gene for T1 (dose 1) was found to be maximum in Cobb (75.84±0.58) and minimum in Kadaknath (12.77±0.38) at day 14 and day 7 post challenge, respectively. For IL-6 gene, the lowest relative mean fold expression was observed in Kadaknath (8.11±0.05) for dose 1 at day 14 while the highest value was recorded in Cobb (99.04±0.92) at day 7 for dose 2. The relative mean fold expression for IL-17 gene was found to be lowest with a value of 11.04±0.29 (dose 1, day 14) in Kadaknath and maximum was seen in Cobb i.e., 197.40±0.37 (dose 2, day 4). For IFN-Y gene, the lowest relative mean fold expression was found to be 8.11±0.19 (dose 1, day 14) in Kadaknath while the highest value was recorded in Cobb (84.74±0.25) for dose 2 at day 7 post challenge. All the five cytokine genes showed relative up-regulation in the three genetic group responses to coccidiosis.

SP-120

INVESTIGATION OF *cGH* GENE USING PCR-RFLP TECHNIQUE IN BROILER

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Biochemical polymorphism study is a method of determination of genetic variation. This variability could be a basis for selection and subsequent genetic improvement in poultry. The polymorphism in the exon-1 and partial intron-1 of chicken growth hormone (*cGH*) gene was investigated in the broiler by using polymerase chain reaction (PCR) restriction fragment length polymorphism (RFLP) method. The genomic DNA was extracted from 150 samples by using modified spin column technique. The DNA fragment of the growth hormone gene with 776 bp was amplified by PCR using specific primers. Then the PCR products were digested with *Msp*I restriction enzyme and analyzed on 8% polyacrylamide gel. The allelic frequency of exon-1 and partial intron-1 locus for A and B allele were 0.39 and 0.61, respectivealy. The genotypic frequency for AA, AB and BB in Broilers were 0.22, 0.28 and 0.50, respectively. The results of current study indicated that the exon-1 and partial intron-1 of *cGH* is polymorphic in broiler and could be exploited as a candidate gene for marker-assisted selection for growth-related traits.

SP-121

EXPRESSION STUDY OF *IGF1* GENE AND ITS ASSOCIATION WITH LAYER ECONOMIC TRAITS IN RHODE ISLAND RED CHICKEN

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India is the 2nd largest egg producer and the 4th largest broiler producer in the world with total poultry population in the country as 729.2 million and per-capita availability of eggs and meat as 63 eggs and 2.3 kg meat per year, respectively. Chickens with higher circulating levels of insulin like growth factor-I (IGF-I) and higher hepatic IGF-I mRNA have been reported to show higher growth rate in comparison to those with low level of IGF-I. Present investigation was carried out in selected strain of Rhode Island Red (RIR) chicken to evaluate the basal relative mRNA expression of IGF-1 gene in liver and breast muscle and to analyse the effects of level of expression on various growth traits. Data on growth traits *viz.*, age of sexual maturity (ASM), body weights at 20, 32, 36 and 40 weeks of age were recorded and the relative mRNA expression (mean 40-ΔCt values) of IGF-1 gene was studied by qRT-PCR in liver and breast muscle, collected at the age of 40 weeks from 12 birds. The data was analysed by least square analysis of variance by taking level (high or low) of mRNA expression as fixed effect. The LS ANOVA revealed significant effect of level of relative mRNA expression of IGF-1 gene in liver on BW20 ($P<0.01$), BW32 ($P<0.05$) and BW36 ($P<0.06$). The least squares means of body weights at 20, 32 and 36 weeks of age were higher in birds revealing higher expression level, with body weights as 1506.00 ± 40.85 g, 1988.42 ± 90.77 g and 1996.42 ± 103.75 g, respectively. Corresponding body weights in the birds revealing lower expression level were 1274.00 ± 48.34 g, 1675.00±107.41 g and 1657.80 ± 122.76 g. Although statistically non-significant, but the body weights were higher at other ages also in the birds which had higher level of expression in liver. In breast muscle, the LS ANOVA did not reveal significant effect of level of relative mRNA expression of IGF-1 gene on any growth traits. IGF-1 expression may be considered as an important marker for better growth in RIR chicken.

Keywords: Body weights, Chicken, IGF-1 gene, mRNA expression, Rhode Island Red.

SP-122

AMPLIFICATION OF KAPPA CASEIN GENE IN CAMEL

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Kappa-casein, important protein component in mammalian milk, plays a pivotal role in formation and stabilization milk micelles and preventing them from aggregating and

therefore, helping to keep calcium phosphate in solution. The work aimed to amplify 453 bp kappa casein gene by Polymerase chain reaction using suitable pair of primers CSN3-F: 5'-TGTGCTGAGTAGGTATCCTAGT TATGG-3' and CSN3-R 5'-GCGTTGTCTTCTTTGAT GTCTCCT-3'. Amplification of 453bp was not successfully carried out in Bikaneri camel while in Rathi cattle gene fragment was successfully amplified. Amplification of 488bp fragment was successfully carried out by species specific primers in camel CSN3-F: 5’- CAC AAA GAT GAC TCT GCT ATC G-3’ and CSN3-R 5’ GCC CTC CAC ATA TGT CTG 3’. Kappa casein gene fragment amplification could not be achieved in camel by other primer despite of close homology of camel with cattle.

Keywords: Kappa casein, Bikaneri camel, Rathi cattle, Polymerase chain reaction.

SP-123

DETECTION OF POINT MUTATION IN κ- CASEIN GENE IN INDIAN CAMEL (*CAMELUS DROMEDARIUS*) BREEDS

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Single humped camel (*Camelus dromedarius*) is one of the important livestock species triving in the western zone of the country. Under harsh conditions, camels have the capability to produce more milk than any other species and for longer periods of time, while their feed requirements are modest. Casein is a major part of protein in camel milk. The present study was carried out on a total of 112 camels belonging to the four major breeds viz. Bikaneri, Jaisalmeri, Kachchhi and Mewari to detect point mutation in κ- casein gene by PCR-RFLP. The PCR amplification of 488 bp fragment of κ-Casein gene spanning from -137 (promoter) to +351 bp (5’ flanking region) was carried out and genotyped for the g.1029T>C SNP using the restriction enzyme *Alu*I in PCR-RFLP analysis. Three restriction patterns were resolved on 3.5% agarose gels. The pattern 203 bp, 158 bp and 127 bp was resolved successfully for the TT samples, whereas the band 158 bp long is further restricted into two fragments of 120 bp and 38 bp in the presence of cytosine. However based on the available results the TT genotype was the most numerous followed by CT and the CC genotype was the least numerous. The frequency CT genotype in Bikaneri, Jaisalmeri, Kachchhi and Mewari breeds was observed to be 0.357, 0.429, 0.322 and 0.429, respectively. The genotype frequency pooled over breed, was 0.045, 0.384 and 0.571 for the CC, CT and TT genotypes, respectively. The frequency of major allele T was observed to be 0.763 and that of C was observed to be 0.237. The existence of CT genotype in sizable number documents the dynamic nature of the locus g.1029T>C SNP, in Indian dromedary breeds. Almost comparable polymorphism was observed in both the sexes. The three genotypes, *viz* CC, CT, TT, were almost equally distributed among the four Indian breeds (χ^2=3.4529; P = 0.750224; non-significant at 5% probability level of significance). Though the frequency of C allele (Cytosine) in Indian dromedary is relatively low (0.237), still a rapid directional selection might be attempted in favor of the C allele, which is responsible for the creation of an extra putative site for the Hepatocyte Nuclear Factor – 1 (HNF-1) transcription factor. The HNF-1 is reported to be involved in regulation of a number of genes associated with innate immunity, lipid and glucose transport, metabolism etc.

NATIONAL SYMPOSIUM: Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income &
XV Annual Convention of Society for Conservation of Domestic Animal Biodiversity (SOCDAB)
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SP-124

GENERATION OF MANIPURI HORSE AND KUTCHI CAMEL FIBROBLAST CELL LINE FROM SKIN EXPLANTS FOR SOMATIC CELL BANKING

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Fibroblast banks propose a practical approach to preserve precious livestock genetic resources due to advancement of cell culture techniques. In addition, skin cells offer an attraction because of easy accessibility, non-invasiveness and without any limitations of sex or age of animal. Ear marginal tissues from 8 Manipuri horses and 6 Kutchi camels were utilized for establishment of cell lines by attachment cell culture method followed by cell cryopreservation technique. Primary culture was established using explant culture technique using fibroblast specific media (HiFibroXL™). At about 10-14 days epithelial-like and fibroblast-like cells could be seen sprouting from the margins of explants of both Manipuri horse and Kutchi camel. Fibroblast-like cells showed typical fusiform morphology with centrally located oval nuclei. Initially epithelial and fibroblast cells grew together but during subsequent passages fibroblast cells grew rapidly and replaced the epithelial cells. Passaging of cell lines for both Manipuri horse and Kutchi camel was continued using DMEM+Ham's F12 (1:1) media with 10% FBS. Cells exhibited radiating, flame like or whirlpool like migrating patterns and density dependent inhibition during cell proliferation. The growth curve at passage-5 represented typically S-shaped as the cell population passed through a lag phase, a logarithmic phase and a plateau phase with population doubling time of 27.9 hrs and multiplication rate of 0.86 population doubling/24 hrs for Manipuri horse. The cells were cryopreserved from 3rd to 6th passage stocking at least 75 cryogenically-preserved vials (1×10^6 cells/ml) per animal. These newly established cell lines of Manipuri horse and Kutchi camel preserves the genetic resources at the cellular level and provides invaluable materials for genomic, post-genomic and somatic cell cloning research.

Keywords: Manipuri horse, Kutchi camel, Fibroblast, Epithelial, Somatic cell cloning, cryopreservation.

SP-125

NOR-BANDING OF CROSSBRED AND NON-DESCRIPT PIG

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In the present study a total of 63 and 65 number of good metaphases were prepared by lymphocyte cell culture technique in LWY crossbred and non-descript pig.To study number of Nucleolar organizing regions ammonical silver staining procedure as described by Howell and Black (1978) with slight modifications was followed for NOR-Banding technique. Number of NORs detected were 168 and 143 in both genetic groups, respectively. The mean number of NORs per metaphase was found to be 2.67 and 2.20 in LWY crossbred and non-descript pig. LWY crossbred pig had high mean number of Ag-NORs per metaphase compared to non-descript pig. In general it was observed that the highest frequency of metaphases (%) examined had 2 number of NORs, while the lowest frequency (%) had 4 number of NORs. The number of NORs observed per metaphase on secondary constriction of 8th and 10th chromosome pair ranged from 2 to 4. The Chi-square test of significance revealed that the observed frequencies do not differ significantly from the expected frequencies. The results confirmed differences across breeds in occurrence and number of NORs on chromosomes. The mean numbers of NORs present per metaphase vary between the animals, indicating the existence of polymorphism for the number of NORs. A higher number of Ag-NORs were observed on 10th chromosome pair in both the genetic groups. It revealed that NORs were more morphologically distinct and greater on chromosome pair 10th than on 8th pair, which suggests a dominant role of 10th chromosome in the production of ribosomal RNA.

Keywords: Ag-NORs, Large white Yorkshire crossbred pig, Non-descript pig, Silver staining

SP-126

SIGNIFICANT ASSOCIATION OF ACK1 POLYMORPHISM (g.107371 A>C) WITH DIARRHOEAGENIC *E.COLI* ADHESION PATTERN IN NATIVE INDIAN PIGS

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Genetic resistance to diarrhea in piglets due to *Escherichia coli* infection is inherited as a simple dominant Mendelian trait. The loci controlling trait of interest has been mapped by

haplotype sharing to a 2.5 Mb region on pig chromosome 13q41 region. Activated Cdc42-associated tyrosine kinase 1 (ACK1) gene was localized at the same region and considered as a positional candidate gene for ETEC F4ab/ac receptor. The present investigation was conducted to find out polymorphism in porcine ACK1 genes, ascertain the adhesion patterns and their association with allelic variants. The microscopic adhesion test was conducted to screen out the pigs for *E. coli* adhesion pattern. In the present investigation out of 150 animals screened for the adhesion pattern total of 116 animals were positive for adhesion with *E. coli i.e.* adhesive. Among the positive 4% showed strong adhesive, 58% were adhesive and 15.33% were weakly adhesive and 22.66% were found to be non-adhesive. Three SNPs for ACK1 gene were analyses for the genotyping and association study which revealed that the loci g.93222 C>A and g.94600 C>T showed significant departure from HWE. The SNPs investigated in Porcine ACK1 gene revealed that genotypes observed at g.107371 A>C loci were significantly ($P<0.05$) affecting the *E. coli* adhesion pattern. The linkage disequilibrium (LD) of different loci were tested using the χ^2 probabilities, which revealed that locus g.291 C>T (TFRC), rs81218930 C>T (TFRC) and g.93222 C>A (ACK1) were significantly ($P<0.05$) associated with g.107371 A>C (ACK1). The SNP g.107371 A>C was found to be a significant association with adhesion pattern and it was found not to be in HWE indicates its importance in natural selection.

Keywords: ACK1; Desi pigs; *E. coli*; Diarrhea; Microscopic adhesion test; Polymorphism.

SP-127

ASSOCIATION OF RYR1 AND MC4R SNP WITH BODY WEIGHTS IN CROSBRED PIGLETS

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Selection based on growth has been of great importance to the pig industry because of cost associated with feeding and consumer preference for lean meat. A number of candidate genes have been identified as potential markers for growth in pigs. The present study was carried out to investigate association of RYR1 (Ryanodine Receptor 1) and MC4R (Melanocortin-4 Receptor) SNP with body weights in crossbred pigs. A total number of 247 crossbred pigs (75% Landrace X 25% Bareilly local), born at Swine Production Farm, ICAR-Indian Veterinary Research Institute, Izatnagar, Uttar Pradesh, India from 2013 to 2016 were considered in the study. Genotype of each SNP was obtained by PCR-RFLP procedure. The body weight at birth and thereafter at one week interval till 8th week was collected. MC4R SNP had three genotypes AA, AG and GG whereas RYR1 SNP had only two genotypes RR and Rr in population. Association of SNPs with body weights was determined using PROC GLM Module of SAS 9.3 software. Association of MC4R was significant with birth weight ($p< 0.05$) and weight at 1st week ($p<0.05$); and non-significant with other weights. GG (1.08±0.03 kg) genotype had the highest body weight at birth followed by AA (1.02±0.36 kg) and AG (1.00±0.02 kg) genotype. First week weight was the highest in GG genotype (2.50±0.08 kg) followed by AG (2.33±0.06 kg) and AA genotype (2.24±0.09 kg). Effect of RYR1 SNP was non-significant on all the weights.

SP-128

HIGH GENETIC DIVERSITY IN RAJASTHAN DONKEY OF INDIA DIVULGED BY MULTI LOCUS GENOTYPIC DATA

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19th Livestock census of India reported a decrease of 27% in the population donkey compared to population in 2007. Donkey has remained a neglected species with respect to the characterization of different populations in the country as reflected in the list of registered animal genetic resource of India. Only one breed of donkey (Spiti) is listed among the 160 indigenous breeds in the country. Therefore, the need of characterization for this valuable genetic resource is urgent. Thus the genetic diversity of Rajasthan donkey population was investigated by using 20 microsatellite markers. Two of the loci, HMS5 and ASB17, depicted less than 4 alleles and were thus excluded from further analyses. Rajasthan donkey was found to host a moderate level of diversity. This conclusion is evidenced by the number of alleles observed across loci (average 8.16±0.89) and by mean observed heterozygosity (0.688±0.06). Signatures of inbreeding could not be detected by the F_{IS} indices in the Rajasthan donkey population. The population did not suffer any bottleneck in the recent past. The study provides the first scientific assessment of the genetic diversity status of Rajasthan donkey population which will offer a valuable reference for its registration and for designing rational strategies in donkey conservation and breeding programs.

Keywords: Bottleneck, Donkey, Genetic characterization, Microsatellite, Rajasthan.

SP-129

WHOLE GENOME SNP IDENTIFICATION IN INDIAN YAKS

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Yak (*Peophagus grunniens*) is a unique bovine species living in the difficult terrains, which appeared some two million years ago and supplies the indigenous people with most of their daily needs including meat, milk, butter, cheese, wool, fiber, leather, fuel and travel requirements. Indian Yaks are classified into Arunachali yak, Himachali yak, Ladakhi yak and Sikkimi yak based upon

the geographical area inhabitation and so far, only Arunachali yak has been described as a breed in India.

In the present study, a total of 80 samples of Indian yaks belonging to Arunachali yak, Himachali yak, Ladakhi yak and Sikkimi yak were used for the identification of genome wide SNPs and INDELs. High throughput sequencing of the DNA samples were sequenced using Illumina TrueSeq chemistry on Illumina HiSeq 2000 platform. The raw reads obtained were further processed for quality filtration and alignment with the yak genome. The reads obtained from the Reduced representation method covered an average of 12.54% of the yak genome. After filtration for quality and depth, a total of 579575 high quality SNPs along with 50319 INDELs were identified in the Indian yaks using yak genome reference sequence. The SNPs identified in the present study will be used for the diversity study and to study the adaptive characteristics of yak at higher altitude in comparison to cattle and buffalo.

Technical Session-III

Sustainable Utilisation for
indigenous Animal
Genetic Resources
(Value addition, Marketing,
Social Cultural, Ecological issues)

LP-12

INDIGENOUS BOVINE GENETIC RESOURCES: SPECIAL CHARACTERISTICS AND STRATEGIES FOR THEIR PRODUCTIVITY ENHANCEMENT

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India has rich and diverse genetic resources of livestock and poultry in the form of a large number of species, breeds, and strains within a species. India is home to 169 indigenous breeds of livestock and poultry with unique traits, which include 41 for cattle, 13 for buffalo, 28 for goat, 42 for sheep, 7 for horses & ponies, 9 for camel, 7 for pig, 1 for donkey, 1 for yak, 18 for chicken, 1 for duck and 1 for geese. Besides recognised breeds there are populations of livestock and poultry in various geographical locations with unique traits. Cattle and buffalo rearing has been an integral part of the socio-economic and cultural fabric of rural India since time immemorial. As per the Basic Animal Husbandry Statistics (BAHS) 2012, in India there are about 56.7 per cent of world's buffaloes (105.05 million) with 1st position, 12.5 per cent cattle (199.07 million) with 2nd position, 20.4 per cent small ruminants comprising 144 million goats and 72 million sheep with 2nd and 3rd position, respectively in the world.The Indian breeds of livestock are suited to tropical climatic conditions, are able to resist the heat stress, need less water, can walk long distances, survive on local grasses and resist tropical diseases. They can also be turned into high producers given the right kind of feed and environment. Indigenous livestock generally require low maintenance energy. Thus, the impact of climate change will be minimal on low and medium producing animals as compared to high yielding animals.

Bovine milk has fat, carbohydrates, minerals, vitamins and antimicrobial substances and other health promoting agents. Casein makes up to about 80% of the protein in the milk. Beta casein is made up of 209 amino acids linked together in sequence. Milk from Indian zebu cattle and buffaloes contain only A2 allele of beta-casein protein which is considered to be safe for human consumption whereas A1 allele of beta casein is found to have higher frequency in most of *B. taurus* breeds, which has been implicated in certain diseases, viz., type 1 Diabetes Mellitus, ischemic heart disease, arteriosclerosis and neurological disorders, such as autism and schizophrenia. The difference in A1 and A2 beta-casein is the amino acid histidine in A_1 and proline in A_2 at position 67. The indigenous cow's milk has high level of Conjugated Linoleic Acid (CLA Content a vital health promoter) besides a rich source of carotenoids, Vit D and Vit B12 besides antimicrobial substances viz. lactoferrin, lysozyme and immunoglobulins. The content of lactoferrin, well-known antimicrobial and antiviral substance is higher in desi cow milk as compared to crossbred and buffalo milk (Singh *et al,* 2015). Lactoferrin also inhibits fungal and parasitic infections.

India has only 2.4% world's area, 7.3% of the global arable land and 4.2 per cent of world's water. India is home to 17 and 11 per cent of global human and livestock population. Driven by the structural changes in agricultural sector and food consumption patterns in the last few decades, the utility of livestock has undergone a transformation with their importance as a source of quality food has increased. The greatest challenge of the millennium is to produce quality food by increasing production and productivity of agricultural commodities many folds to meet the requirements of exponentially growing population with the same/reduced resource base of land and water. These sectors are evolving in response to surging demand for food due to population growth, sustained income and economic growth, urbanisation, burgeoning middle-income class and changing lifestyles. The task becomes even more onerous set against climate change and limited natural resources and their constraints (water and soil foot print) and reducing cultivable land. The need is to develop technologies that improve productivity and enable farmers to produce more with fewer resources, reducing the impact on the environment.

The assemblage of the breeds and populations having traits and unique characters is a source of food, fiber and a host of other services, and this assemblage is phrased as Animal Genetic Resource (AnGR). The term AnGR encompasses the genetic material of animals covering semen, egg and live animals, DNA molecules, RNA, proteins and other micro physical genetic material (Tvedt *et al,* 2007). It is very essential to maintain genetic diversity to respond to situations like climate change and emerging diseases and to adapt to production systems. Over the centuries, indigenous livestock breeds have adapted to local conditions. Darwinian adaptations of indigenous cattle in relation to their ability to tolerate heat and parasites as well as their ability to survive and produce milk and capacity to work in harsh conditions under poor quality feed and fodder is yet to be fully understood, and exploited for further improvements. The main objectives of the Indian National Plan of Action for AnGR is to ensure a strategic and comprehensive approach in achieving the sustainable use, development and conservation of animal genetic resources, to increase and improve food production and food security, alleviate poverty and contribute to rural development and its role in society for cultural values. At the international level Global plan of action for ANGR, the first internationally agreed framework to halt the erosion of livestock diversity and support the sustainable use, development and conservation of AnGR was adopted by delegates from 109 countries at the International Technical Conference on Animal Genetic Resources for food and Agriculture, 3-7 Sept 2007, in Interlaken, Switzerland.

India has some of the best breeds of cattle with traits for dairy, draught power and dual purposes and best breeds of buffaloes. These breeds are essentially the products of long term natural selection and are better adapted to tropical fodder, environment and diseases, and perform under low and medium inputs in different ecological niches. Thus, indigenous breeds are well adapted to harsh climate, resistant to common tropical diseases and can subsist on poor quality crop residual roughages, grasses and scanty drinking water. Indigenous cows also could also be turned into high milk producers given the right kind of feed and environment. Under the prevailing conditions it is not possible to change the production system to suit them and mimic the systems used in developed countries. The grain based livestock farming has led to diverting of valuable food crops away from human consumption.

Indian Dairy sector

Dairying is an important sub-sector of Indian agriculture and milk group has highest contribution to livestock sector output (68.22%). About 70% of milk is produced by marginal and small farmers owning 2-4 animals. The different production systems like zero input – low output, low input – moderate output, intensive input – high output are characteristics of dairy production system in India (Ramesha and Divya, 2013). Dairy sector has shown a constant and sustainable growth despite limited investment from public and private sector. Perusal of the Fig. 1 clearly shows that the production of milk in India has increased substantially over the years. The annual growth rate in milk production during the year 2015-16 was 6.28% while the average growth rate in milk production in the world is around 1.5%. However, a paradigm shift is required in dairy sector from production orientation to quality and cost orientation in the WTO era (Ramesha and Jayaraj Rao, 2013).

Dairy animals in India are reared with multiple objectives besides providing milk also provide a diverse range of output for agriculture, irrigation, manure and transport, fibre and leather goods and their rearing systems are different from developed countries. The drought prone semi-arid regions are characterized by a major animal component, as animals can exploit resources that cannot support intensive crop cultivation on a sustainable basis. Crossbreeding of indigenous cattle with exotic high yielding breeds started in 1960's and currently the contribution of crossbred cattle to total milk production is around 24per-cent. The adaptation of temperate exotic breeds or their crossbreds out of crossing with Indian breeds need sophisticated and scientific management to exploit their full production potential under tropical climate of India.

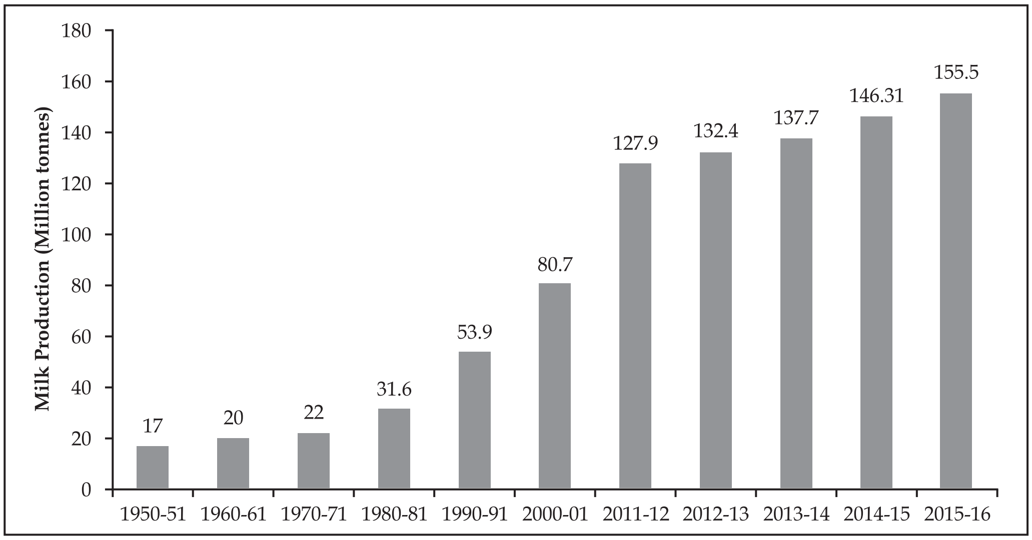

Figure 1. Milk production dynamics in India; Source: Annual Report (2016-17), DAHD & F, Govt. of India

Yet another important problem is the disposal of crossbred males as farmers don't prefer them for draft purpose. Even now about 53 % milk production in India come from buffaloes. The milk productivity of Indigenous cow, crossbred cow, buffalo and goat is only 3.41, 7.33, 5.76 and 0.45 kg/day in the year 2015-16, respectively. The differences in milk production of crossbreds and indigenous milch breeds do not seem to be substantial considering the fact that not much selection has gone into the improvement of indigenous breeds for milk yield. India is the largest milk producer with 160.35 mt (18.5% of the total world milk production) during 2015-16 from 298 million cattle and buffaloes which is 17.54% of the total world bovine population. In contrast, USA and New Zealand are producing 11.7 and 2.7% of milk from 9.47 and 1.1% of total world bovine population. Average milk production/cow/year in developed countries viz. USA, Sweden, Denmark is above 7500 kg while in India is only 1200kg which clearly indicates the need for productivity enhancement in them.

Recently, several measures have been initiated by the government to increase the productivity of milch animals. Among Indigenous breeds, cows producing good quality milk in a lactation have been recorded under Central Herd Registration Scheme for breeds like Gir (3038-3263 kg), Ongole (2000-2544 kg) and Hariana (1671-4015 kg). Even among Maland Gidda-dwarf cattle with body weight of 80-120 kgs, many cows give 3-4kgs of milk per day with regular calving under low input production system (Ramesha, 2013). This indicates that there exists genetic potential for high milk production in indigenous breeds.

Indian breeds abroad

India has contributed richly to the international livestock gene pool and improvement of animal production in the world. Brahman cattle are found in 45 countries while Sahiwal breed is found in 29 countries (Ramesha *et al,* 2007 and Ramesha *et al,* 2008). Many cattle breeds of Indian origin have made major contribution to the development of composite breeds elsewhere in the world. The world's best Gir cows today give 5500 litres of milk on an average per lactation of 307 days (Sharma, 2011). In recent years Brazil has emerged as the world's biggest supplier of improved cattle embryos and semen of Indian origin. The demand for Indian breeds is particularly high from the African and Southeast Asian countries. As these breeds are suitable for the tropical conditions, these countries find the improved cattle germplasm to be ideal for their cattle breeding programmes (Sharma, 2011).

SWOT Analysis of Indian Dairy Sector with special reference to Bovine genetic resources

Strengths: The constant and sustainable growth of livestock sector despite limited investment from public and private sector itself shows the strength of the sector. Bovine genetic resources with high diversity found in India will become handy to utilize environment unsuitable for crop agriculture and to respond to changes in production systems, impending climatic change, and emergence of new diseases and market demand. The low production cost compared to other countries in this sector is another remarkable strength. India is also the world's largest and leading buffalo germplasm holder. The different production systems like zero input – low output, low input – moderate output, intensive input – high output are characteristics of Indian livestock production system. There is huge internal demand for livestock and poultry produce and India is surrounded by countries that are deficit in animal produce, thus offering huge potential for export of livestock and poultry produce.

Weakness: Presently dairy sector is facing the challenge of low productivity of Indian milch animals, higher susceptibility of crossbred cows to various diseases, shortage of feed and fodder, shortage of quality germplasm and continuous shrinkage of grazing land, late sexual maturity of dairy animals coupled with large number of breedable but uncalved female population. The greatest challenge for the dairy sector is to increase production and productivity many folds to meet the requirements of exponentially growing population with the same/reduced resource base of land and water. Prevalence of certain diseases like FMD, Brucellosis and mastitis in dairy animals have major implications for export potential, productivity and safety, quality of livestock products and zoonotic implications. Climate change may have serious impact on dairy animal productivity due to heat stress, loss of habitat in certain areas, change in incidence and pattern of certain diseases, scarcity of quality feed and fodder and needs development of proper mitigation strategies. Wide gap between availability and requirement of proven dairy bulls is another major constraint.

Opportunities: The opportunities in dairy sector include technology driven production enhancement in low producing animals and value addition to livestock produce. Dairy farmers are increasingly focusing on production efficiencies, cost control through increasing scale of operation and adoption of modern technological tools. In the post WTO era, in the knowledge based global economy, quality control, increasing purchasing capacity of food items has made increased demand for quality and safe products with appropriate packaging. The demand for organic milk and milk products, A2 milk is another opportunity for Indian dairying (Ramesha and Jayaraj Rao, 2013).

Threats: Excessive grazing pressure on marginal and small community lands has resulted in almost complete degradation of land. Indiscriminate crossbreeding for raising productivity could lead to disappearance of valuable indigenous breeds. With intensive industrialization of livestock sector in response to market forces, the small producers will find it increasingly difficult to compete with the industrial sub-sector and thus risk losing a significant means of livelihood. Changing climate and depleting natural resources with associated losses in production, reproduction and health in dairy animals is another threat.

Special characters of Indigenous cattle

Indigenous breeds are well known for heat tolerance, hardiness and ability to survive and perform even under stressful conditions and low input regimes. Zebu cattle have the ability to convert low protein, high fiber roughage materials into high-grade foodstuffs with the aid of omasal symbionts. They have the ability to reverse down metabolism during extremes of scarcity but show quick response in the form of better reproductive and productive efficiency when nutrients are plenty. Zebu cattle are efficient foragers and their tight sheath and small teats avoid injuries during grazing. The sloppy rumps in draft breeds make them suitable for quick and hard work. The white or light colored, short, sleek, densely reflecting and glistering coat in indigenous cattle does not attract vectors and dislodge them. Flexible tail tip helps as a brush to repel vectors. Premunity is high and reticulo-endothelial system is well developed in zebu cattle. Usually longevity is more than 15 years with high reproduction rates and more number of lifetime calves and many animals give more than 15 calves in their life time. They have outstanding mothering ability. They calve with ease and dystokia is rarely reported. There is a great degree of genetic variation in indigenous breeds of livestock with respect to their size, productivity growth rate, reproductive efficiency which can be made use for the improvement of livestock worldwide.

Indigenous cattle have lower basal metabolic rate, better capacity for heat dissipation through cutaneous evaporation and thus adaptation to tropical heat and resistance to diseases specially the tick-borne diseases than taurinecattle. Indigenous cattle possess natural resistance to various insects, as their skin has a dense texture, making it difficult for blood sucking insects to penetrate. Several studies indicate the differential disease resistance of indigenous cattle compared to exotic cattle on Theileria parva (Ndungu *et al,* 2005), on tick infestation (Mwangi *et al,* 1998), on symptoms of babesiosis (Aulakh *et al,* 2005). The CRC (2006) work in Australia confirms tick resistance but also shows the poorer temperament in Brahman cattle. Most of the indigenous cattle can withstand and graze even at atmospheric temperatures of 40°C. Aggarwal and Singh (2006) reported Upper (UCT) and Lower Critical Temperatures (LCT) for different breed types as 38°C and 10°C, respectively for Indigenous breeds, 24°C and 2°C for Jersey and crosses, 20°C and 10°C, respectively for Holsteins. Ghosh *et al* (2006) reports temperatures at which milk production starts to reduce as 21°C for Holsteins, 24°/27°C for Jersey and Brown Swiss and 32°C for Zebu type. Due to these special characteristics of indigenous cattle, they are able to conceive after drought while crossbreds fail to conceive after lack of feed and water and many times sent to slaughterhouse (Ramesha, 2003). The study conducted in Kerala Veterinary University showed that Vechur cattle did not show symptoms of heat stress even after exposure to sunlight. There had been only slight increase in body temperature after exposure to sun (Venkatachalapathy and Iype, 2010). The extensive area covered by the dewlap, loose body skin, more sweat glands and hair coat play a vital role in its heat tolerance.

Impact of climate change on Bovine Genetic Resources

Potential impacts of climate change on bovine production in India are yet to be exhaustively studied. Temperature increase in mid altitude and in high altitude is liable to amend pasture production by incrementing the season of pasture production. Local breeds are liable to benefit from warmer winter. In plains and dry land areas, extreme conditions like drought and water shortage may increase substantially. In areas near deserts, livestock deaths due to heat strokes may increase. In coastal zones, due to increasing temperature and sea level, the area available for grazing or fodder production may reduce. In view of climate change, adaptations to changing environment and resistance to incipient diseases will be paramount criteria in livestock production. It is liable to impact housing, feeding, health care, etc. in livestock sector. Climate change is liable to affect disease pattern and epidemiology, ailment and fodder availability (Pilling and Hoffmann, 2011). The water scarcity for livestock production is a serious issue. The climate change is likely to aggravate water scarcity problem.

Genetic improvement and multiplication of bovine genetic resources

In India development and improvement of indigenous breeds has been taken up by various agencies from time to time. These programmes had assisted in increasing the productivity of the AnGR and also helped in conservation of indigenous germplasm. Some of the important programmes aimed at genetic improvement livestock include National Project for Cattle & Buffalo Breeding of Dept. of Animal Husbandry and Dairying, GOI; ICAR Network and AICRP Programmes for genetic improvement of native farm animal breeds. Presently programmes are in operation for cattle (Gir, Sahiwal, Hariana and Ongole), buffalo (Murrah, Nili Ravi, Jaffarabadi, Pandharpuri, Surti and Bhadawari).

Genetic improvement of dairy animals depends on access to genetic variation and effective methods for exploiting this variation. With the help of traditional breeding system, animal breeders have effectively enhanced production traits in their herds by selecting superior individuals as progenitors for the next generations, however, the genetic progress is slow (1-3%) per year. Sustainable improvement of indigenous bovine genetic resources using New generation technologies and innovations coupled with traditional systems of selection is the need of the hour. Technology driven productivity enhancement in low producing animals is the need of the hour. There is an urgent need to improve productivity, reduce inter-calving period, improve conception rates, reduce the number services per conception.

There are many challenges in genetic improvement of dairy animals in India mainly due to mostly small herds with non-availability of recorded data, challenging environment, low inputs and poor management in most of the areas, uncontrolled mating, indiscriminate cross breeding. The ambitious National Dairy Plan (NDP) was initiated in 2012 with a focus on quality dairy animal production through genetic improvement and faster multiplication of superior germplasm with strategies of improving genetic potential of bovines, producing required number of quality bulls, and superior quality frozen semen and adopting adequate bio-security measures etc. Further, strengthening and expanding village level infrastructure for milk procurement and provide producers with greater access to markets is also being taken care adequately under the NDP1.

Improvement of Indigenous cattle and buffaloes could be achieved by selective breeding by incorporating modern genomic tools and production of breeding bulls having high genetic potential, which can be achieved by utilizing progeny testing, genomic selection and modern reproductive biotechnological tools. Modern genetic tools have to be used to increase the percentage of breedable females in milk with improved lifetime productivity. Drought resistant breeds such as Rathi, Sahiwal, Tharparkar should be propagated in different pockets of the country having harsh climate particularly to minimize the effects of climate change. In certain areas the productivity of dwarf breeds like Malnad Gidda, Punganur and Vechur have to be improved through selective breeding and propagated. Crossbreeding of non-descript cattle with high producing exotic cattle is recommended in areas where good marketing facilities for milk and milk products are available especially in areas like Peri-urban and industrial towns, where adequate amount of green fodder and quality feed resources exist. In India the recommended breeds of choice for crossbreeding are Holstein and Jersey. In resourceconstraint areas, grading up of non-descript cattle with high genetic merit indigenous bulls, which are well adapted to the local conditions like Sahiwal, Tharparkar, Red Sindhi, Gir, Deoni, Hariana, Ongole, Kankrejetc in breeding tract is recommended (Sreenivas, 2013).

One of the major problems in buffalo improvement is out of about 54.5 million breedable buffaloes in the country; barely 15-20% are bred through AI while 80-85% is covered by natural service mostly by scrub bulls. Parentage control of breeding bulls in the buffalo improvement programmes is essential. The genetic improvement of buffalo herds in the country can be brought through selective breeding. Networking approach of progeny-testing of bulls associating multiple organized herds as well as farmer's herds, under field conditions could be followed. In certain pockets of states like Gujarat, Rajasthan and Karnataka, Surti is recommended to be the breed of choice, Murrah is generally the breed of choice in the states of Punjab, Haryana and Western U.P., besides few pockets in Punjab where Nili Ravi has sizable population and it also needs to be improved through selective breeding (Sreenivas, 2013). The production potential of low producing non-descript buffaloes could be increased rapidly through mating with superior sires of improved breeds like Murrah, Surti and Mehsana. The low producing non-descript buffaloes can be replaced with relatively high producing buffaloes conforming to the characteristics of well-defined breeds through grading up with superior breeds in 5 to 6 generations (Singh and Barawal, 2010). Marker assisted selection (MAS) and genomic selection could be utilized to select at an early age. Genetic progress can be hastened with the use of tools such as SNP chips, high thorough-put genome sequencing and microarray.

For many years worldwide, dairy cattle breeding programs were mainly oriented towards milk yield traits and have not given due weightage for fertility traits. In India, the main focus has been on production traits, and now time has come to include both fertility and lifetime productivity and profitability instead of milk production alone (Ramesha and Divya, 2013). Reproductive techniques, such as multiple ovulation, embryo transfer, micromanipulation and gene transfer in the embryo, transgenesis, cloning might enable us to modify the genetic composition of an animal by means other than standard breeding techniques. The production of a calf with preferred sex is a long-cherished dream of dairy farmers. Semen can be sexed with greater than 90% accuracy with use of a flow cytometric cell sorter. The higher cost per dose of semen combined with a reduced conception rates are the limiting factors but improvements in sorting capacity, fertility and reduction of semen cost are expected in coming years. Imported sexed semen is being used in many states.

Epilogue

Indigenous livestock have evolved over a long time in the diverse, stressful, tropical environment with adaptive traits. This situation enables them to live and engender in these conditions. Indigenous livestock breeds are not able to compete with "improved breeds" in terms of production on the other hand, they fulfil a much wider range of functions and support farming community with wider range of quality products. The milk productivity of indigenous cattle and buffaloes could be enhanced substantially by adoption of various modern technologies for selection and faster multiplication of genetically superior germplasm and adoption of improved animal management strategies.

Note: The article includes content of earlier presentations of the authors in conferences/ winter school.

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LP-13

ROLE OF LIVESTOCK AND POULTRY IN ENHANCING FARMERS INCOME IN NORTH HIMALAYAN REGION OF INDIA

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Introduction

The Indian Himalaya; with a breadth of 250-300 km and stretch of over 2500 km from Jammu and Kashmir in the west to Arunachal Pradesh in the east; covers an area of about 5,33,604 km^2, which is inhabited by 39.62 million people. This region represents 16.2% of the total area and 3.86% of the total population of the Indian Republic and is of crucial importance by virtue of being rich and unique centres of cultural and biological diversity (Resource information database of the Indian Himalayas). But north Himalayan region comprises three northernmost Himalayan mountain states of India: Jammu and Kashmir, Himachal Pradesh and Uttarakhand. The percent share of geographical area of these states with respect to Indian Himalayan region are 41.65, 10.43 and 10.02%, respectively whereas it comprises around 10.08% of the total geographical area of India. These temperate and hilly regions contain a considerable proportion of land at high altitudes. Livestock farming in these areas has primarily been of a migratory nature, and depending on the availability of pasture, people move with their animal holdings in summer to highland pastures, coming down to the lower hills and valleys during the winter. To a large extent this practice continues particularly for sheep and goats. Although agriculture is the prime source of livelihood for a majority of rural population in the North-Himalayan region of India, dependence on livestock, horticulture and forestry as an alternative source of income is significant. The percent share of different livestock and poultry of north Himalayan region to that of total population of India is presented in Table 1.

Further, because of social and religious acceptance, the consumption of meat is relatively higher in this region, and that of milk and milk products is lower. Coupled with the traditional meat-eating habit, increasing per capita income, urbanization and changes in life-style, the region is deficit in production of livestock products. Some states in the region depend on inter-state trade in livestock to meet the domestic demand. In the official site of Animal Husbandry department, Himachal Pradesh, the tentative receipt of milk procured from neighboring states is about 1.00 lakh to 1.5 lakh litres of milk daily. J&K is also importing huge bulk of animal products from the neighboring states viz. Rajasthan, Punjab, Haryana, etc. However, responding to the burgeoning demand for livestock products in a sustainable manner is a big challenge, but the widening gap between the demand and supply of livestock products can be bridged by introducing changes in production structure or by encouraging scientific interventions, either of which can correct the imbalances in the long-run. It is evident by comparing the 18th and 19th livestock census of north Himalayan region, that there is decrease in livestock population but the figures are quite impressive for poultry population (Table 2).

Hardly any investigational work has been carried out on temperate animal husbandry in India, and a package of practices based on scientific investigations for improvement of livestock productivity is lacking. Also, it is well known fact that environmental factors affect livestock production. It occurs through change in altitude, the mean annual temperature, seasonal and diurnal variations, rainfall, humidity and atmospheric pressure. The climatic factors, coupled with poor grazing, scarcity of green fodder, particularly in winter, traditional systems of stock management, genotypes that have not been improved, and fairly high morbidity and mortality rates appear to be the major constraints in livestock development. These factors account for the low productivity of the animals in the region. But by curbing the above constraints, doubling of farmer's income is possible in the coming future.

Table 1. Details of different livestock and poultry species of North Himalayan region (19th livestock Census, 2012)

Attribute	Population of India (million numbers)	Population in North-Himalayan region (million numbers)	% share of North Himalayan region to India
Total Livestock population	512.05	18.84	3.68
Cattle	190.90	6.95	3.64
Buffalo	108.70	2.44	2.25
Sheep	65.06	4.56	7.01
Goat	135.17	4.50	3.33
Pig	10.29	0.027	0.27
Camel	0.4	0.0011	0.28
Mithun	0.29	0.00098	0.34
Yak	0.07	0.057	82.10
Horses and Ponies	0.62	0.175	28.38
Mules	0.19	0.086	45.64
Donkey	0.32	0.026	8.16
Poultry	729.2	14.02	1.92

Table 2. Comparison of livestock and poultry population for 18th and 19th livestock census

State	18th livestock census 2007 (in millions)	19th livestock census 2012 (in millions)	Percent Change
Total Livestock Population			
Jammu and Kashmir	10.98	9.20	-16.21%
Himachal Pradesh	5.21	4.84	-7.10%
Uttarakhand	5.14	4.79	-6.81%
Poultry Population			
Jammu and Kashmir	6.68	8.27	+23.80%
Himachal Pradesh	0.81	1.10	+35.80%
Uttarakhand	2.602	4.64	+ 78.41%

Contribution of livestock to people of Northern Himalayan region

The livestock provides food and non-food items to the people.

✓ **Food:** The livestock provides food items such as milk, meat and eggs for human consumption. India is number one milk producer in the world. It is producing about 163.7 million tones of milk in a year (2016-17). Similarly it is producing about 74.75 billions of eggs, 8.89 million tonnes of meat in a year. The value of milk group and meat group at current prices was Rs 4,06,035 crores in 2013-14. As per statistical data, Animal Husbandry department of Himachal Pradesh, the contribution of livestock products during the year 2015-16 was 12.83 lakh tonnes of milk, 81.17 million eggs and 4005 tonnes of meat. As perDADF, 2015 during the year 2012-13, the total milk production for J&K state was 1630.56 thousand tonnes, meat production was 34.07 thousand tonnes (recognized sectors) and egg production was 6715.41 lakh numbers. Likewise as per statistics cell, Department of Animal Husbandry, Uttarakhand, for the year 2014-15, the total meat production from sheep and goat was 20.500 and 88.201 lakh kg, respectively.

✓ **Fiber and skins:** The livestock also contributes to the production of wool, hair, hides, and pelts. Leather is the most important product which has a very high export potential. India is producing about 47.9 million kg of wool per annum. As per statistical data, Animal Husbandry department of Himachal Pradesh, 2015-16, total wool production was 1411 tonnes. As per DADF, 2015 total wool production for J&K for year 2012-13 was 7680.61 kg. Likewise as per statistics cell, Department of Animal Husbandry, Uttarakhand, for the year 2014-15, the total wool production was 468.93 thousand kg.

✓ **Draft:** Bullocks are the back bone of Indian agriculture. Despite lot of advancements in the use of mechanical power in Indian agricultural operations, the Indian farmer especially in hilly terrains still depend upon bullocks for various agricultural operations. The bullocks are saving a lot on fuel which is a necessary input for using mechanical power like tractors, combine harvesters etc. Pack animals like camels, horses, donkeys, ponies, mules etc. are being extensively used to transport goods in north Himalayan region in addition to bullocks. In situations like hilly terrains, mules and ponies serve as the only alternative to transport goods. Similarly, the army has to depend upon these animals to transport various items in high areas of high altitude.

✓ **Dung and other animal waste materials:** Dung and other animal wastes serve as very good farm yard manure and the value of it is worth several crores of rupees. In addition it is also used as fuel (bio gas, dung cakes), and for construction as poor man's cement (dung). Now-a-days, vermicompost and vermiwash are getting popular for organic livestock farming, which can act as additional source of income for farmers with additional advantage of preventing nuisance caused by these wastes.

✓ **Storage:** Livestock are considered as "moving banks" because of their potentiality to dispose off during emergencies. They serve as capital and in cases of landless agricultural laborers many time it is the only capital resource they possess. Livestock serve as an asset and in case of emergencies they serve as guarantee for availing loans from the local sources such as money lenders in the villages.

✓ **Weed control:** Livestock are also used for biological control of brush, plants and weeds.

✓ **Cultural:** Livestock offer security to the owners and also add to their self esteem especially when they are owning prized animals such as pedigreed bulls, dogs and high yielding cows/ buffaloes etc. The livestock in these areas are mostly owned by communities like Gujjars, Bakarwals, Gaddis etc.

✓ **Sports /recreation:** People also use the animals like cocks, rams, bulls etc for competition and sports. Despite ban on these animal competitions the cock fights, ram fights and bull fights are quite common during festive seasons.

✓ **Companion animals:** Dogs are known for their faithfulness and are being used as companions since time immemorial. When the nuclear families are increasing in number and the old parents are forced to lead solitary life the dogs, cats are providing the needed company to the latter thus making them lead a comfortable life.

Role of livestock in farmers economy

The livestock plays an important role in the economy of farmers. The farmers in these hilly regions maintain mixed farming system i.e. a combination of crop and livestock where the output of one enterprise becomes the input of another enterprise thereby realize the resource efficiency. The livestock serve the farmers in different ways:

Income: Livestock is a source of subsidiary income for many families especially the resource poor who maintain few heads of animals. Cows and buffaloes if in milk will provide regular income to the livestock farmers through sale of milk. Animals like sheep and goat serve as sources of income during emergencies to meet exigencies like marriages, treatment of sick persons, children education, repair of houses etc. The animals also serve as moving banks and assets which provide economic security to the owners. At farm level, cash can be generated regularly from direct sales of livestock products, such as milk, eggs and manure, occasionally from the sale of live animals, wool, meat and hides and from fees for draught power or transport services. Census figures 2011 signify that about 73% of the population of J&K lives in rural areas and are associated with agriculture and allied sectors including livestock rearing as main occupation. It is estimated that livestock and its derived foods and other products contribute about 6.13% to this Gross State Domestic Product (GSDP) in the year 2010-11. In Himachal Pradesh, the contribution of Animal Husbandry sector to GSDP is 1.29% for the year 2015-16. As per statistics cell, department of animal husbandry, Uttarakhand, the grand total income generated in the year 2014-15 from wool production and meat production is 38256.37 lakhs.

Employment: A large number of people in these regions being less literate and unskilled depend upon agriculture for their livelihoods. But agriculture being seasonal in nature could provide employment for a maximum of 180 days in a year. The land less and less land people depend upon livestock for utilizing their labour during lean agricultural season especially in snow covered regions.

Food: The livestock products such as milk, meat and eggs are an important source of animal protein to the members of the livestock owners. Animal products are primarily a source of proteins and essential amino acids, but when they are a major constituent of the human diet they also contribute a significant proportion of total calories. In the areas, where diets are composed of only a small number of staple foods, animal products are of great importance in preventing malnutrition as they are concentrated sources of the limited essential amino acids available in vegetable proteins of staple foods.

Social security: The animals offer social security to the owners in terms of their status in the society. The families especially the landless which own animals are better placed than those who do not. Gifting of animals during marriages is a very common phenomenon in different parts of North Himalayan region. Animals are also used for various socio religious functions. Cows for house warming ceremonies; rams, bucks and chicken for sacrifice during festive seasons; bulls and cows are worshipped during various religious functions. Many owners develop attachment to their animals. Livestock is considered as an asset value to rural families, as it provides a means of security at times of crises. It also helps when the rural families are affected with natural calamities like floods, drought, cyclones, earthquakes etc., where in the livestock enterprises comes as a rescue to the rural farmers and sustain them in the above crises. In the rural areas financial services such as credit, banking and insurance are virtually non-existent. In these areas, livestock play an important role as a means of saving and capital investment, and they often provide a substantially higher return than alternative investments. A combination of small and large livestock that can be sold to meet petty-cash requirements to cover seasonal consumption deficits or to finance larger expenditures represents a valuable asset for the farmer. Possessing an animal of their choice gives women considerable satisfaction.

Draft: The bullocks are the back bone of Indian agriculture especially in hilly terrains. The farmers especially the marginal and small depend upon bullocks for ploughing, carting and transport of both inputs and outputs.

Dung: In rural areas dung is used for several purposes which include fuel (dung cakes), fertilizer (farm yard manure), and plastering material (poor man's cement).

Challenges in North Himalayan region of India

Livestock of these areas are mostly dependent on locally available feeding resources like top foliages and unclassified grasses in the village, grazing land/forest area for feeding of their livestock round the year. Private dairy farms started with improved breeds of cows failed in the mid-hills due to lack of quality feed and proper health services. The major constraints in livestock development in the area are –

- Deficiency of quality feed and folder,
- Poor conception rate (from AI),
- Prolonged age at first calving (4-6 years),
- Unhygienic housing/resting place of animals,
- Poor disease management system,
- High morbidity and mortality in livestock, (parasitism)
- Little knowledge about vaccination against animal diseases.
- Unorganized markets for livestock

If new concepts viz. dry livestock farming, organic livestock/poultry farming, vermicompost, backyard poultry farming were given due attention along with marketing in the policy framework, and curbing the above constraints can help farmers in raising their incomes in the near future.

Conclusion:

Livestock contributes lot to the economy of North Himalayan region but has the potential to double it by adopting modern scientific technologies and by curbing the constraints of these regions. Among all the land related activities in mountain and hill farming system, dairying and poultry farming indeed is a cream activity with a lot of potential for socio economic development of the hill farmers.

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LP-14

VALUE ADDED MARKETING OF LIVESTOCK PRODUCT FOR ENHANCING FARMERS' INCOME

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Value Addition in Livestock Product

Mankind has been utilizing different animal species from the dawn of civilization for a variety of purposes viz. production of milk, meat, wool, egg and leather etc. These products are either useful in raw form or in value added form. Value-addition describes economically adding value to the product by changing its place, time and form to characteristics that are more preferred in the market place. Another way of explaining is that what happens when you take a basic product and increase the value of that product, usually the price by adding extras in the manufacturing process, or by tacking on extra products and/or services.

Value can be added using one or two approaches i.e. first innovation (improving existing process, methods or services or creating new one). Second is Coordination i.e. arrangements among those who produce and market the products. Coordination links producers, wholesalers, retailers and consumers.

Need of Value Addition

Adding value to farm commodities is becoming an important income-enhancing strategy for producers. Commodity prices will be similar in the future to what they have been in the past, but periods of excess supply and low prices will occur. New risk-management tools will need to be developed (Dobbins *et al*). Many producers will look for ways to be economically viable through voluntary, incentive-based solutions. Producer's greatest opportunities may lie in activities that add value to their products and move their point of first sale downstream toward consumers. Adding value to bulk raw commodities is one way for producers to keep a larger share of the margins associated with further processing and market development. Progressive producers respond to market developments, determine what factors will drive the future of their industry, and use these results to their advantage by adapting to change.

Value-added products can help dairy farming becoming a more viable enterprise, more visible to the public and open up new markets, but equally more risks involved when selling value-added versus marketing directly to your local milk cooperative.

Global Experience of Value Addition in Livestock Products

Global value chains, led by retailers and food processors, are increasingly dominating the agriculture and food sectors. Multinational retailers for example, work with importers and exporters and more and more, control how products are grown. Control of quality, food safety standards and traceability along the supply chain requires vertical co-ordination. A relatively small number of companies organize the global supply of food and link producers in developed or developing countries to consumers all over the world. Food safety is a global issue of increasing concern for governments, food producers, food processors and handlers, as well as consumers. There is a big gap in price fetched for the raw product by producer and finished products sold by retailer to consumers.

Four different methods can be used to add value to producer's raw commodities such as

(1) Selling into open markets for normal distribution channels of marketing and processing,

(2) Investing in a portfolio of food companies

(3) Using production or marketing contracts, and

(4) Forming of producer-owned businesses.

Marketing

The key to the success of value-added products is to market a high quality product that is reasonably priced and available in a convenient location for the consumer to purchase. You must deliver your product with a consistent quality and have sufficient supplies to meet the demand. Remember that the consumer will react negatively to your product if you do not maintain your quality standards and/or timely deliver sufficient supplies.

Value-added products can be a good way to increase farm income, give farm more visibility and help to expand to new markets. Careful business planning and adhering to state regulations will also ensure the success of new venture.

Thus the key to the success of value-added products is to

- Market a high quality product that is reasonably priced and available in a convenient location for the consumer to purchase.
- Product must be delivered consistently and have sufficient supplies to meet the demand.
- A certification for food quality and safety.

Open Market Distribution and Processing Channel

Food marketing channels include all the institutions and processes by which food moves from the producer to the end user. Perishable products, such as fresh produce, move through shorter channels, whereas more storable products, like frozen pizza, utilize longer distribution channels. The purpose of middle men has been to smooth the flow of goods from manufacturers or growers who produce large quantities of a few items to consumers who desire to purchase small quantities of many items. However, as retail chains have grown larger and more concentrated, food processors have found it advantageous to negotiate with and distribute directly to large retail customers (Connor, Schiek, and Uhl) *et al,* Over the last 20 years, food processors have provided innovative, easy-to-prepare foods with convenient packaging, because consumers desire product quality, variety, food safety, and nutrition. In addition, fulfilling consumer's desires will necessitate closer coordination and communication between producers and processors.

Preparation convenience is a key feature of foods purchased by busy, affluent households. In fact, the number of food service meals eaten away from home has increased by 50 percent in the last 20 years. Therefore six significant growth trends in consumer demand have been identified: more convenience, ethnic-identify foods, aging of the population, low-calorie foods, fresh foods instead of frozen or canned, and healthy natural foods (Connor *et al*). Value-adding producers should focus on products that fill these consumer desires or market niches. By utilizing value-added precepts for business development, producers can identify the desires of consumers and target markets, rather than taking the commodity to the market and hoping that consumers will like it and use it. Target markets are tightening as retailers and consumers pay more for a narrower range of eating experience. Hitting these target markets means that value-adding businesses must know their consumer's desires.

Livestock Products Requiring Value Addition

Meat

Total meat production in India is 6.7 MT and growth rate in meat production is 7.31%. Out of total animal slaughtered percentage of different livestock is as cattle 10.6%, buffalo 10.6%, sheep 24.1%, goat 58.8%, pig 95%, and poultry 90%. Per capita meat consumption is 5.5kg/person/year while world meat consumption is 42kg/person/year and 80.3kg/person/year in developed countries. Livestock contribution in GDP is 4.1%. India's trade in livestock & livestock products is in live form. India is not even contributing 1 percent to global export of livestock market. India is thus very small player in global market. Total meat processing capacity of India is over 1 million per anum, remaining meat sold in fresh and frozen form.

Value added meat products

Animal byproducts, traditional meat products, Enrobed meat products, Cured and smoked meat products, Dried meat products, Chunked meat products, Ground meat products, Designer meat, Emulsion meat products, Restructured meat products etc. There are few meat products with longer shelf life such as Cured & smoked chicken, chicken patties, chicken meat spread, chicken pickle, cooked chicken stock (one minute curried chicken, cost effective, instant use by working couple, old people and highly useful at the time of instant need. Meat is high in protein, low in fat, source of essential Amino Acid, good source of I, P, Cu, Zn & B_{12}, Dark meat & skin is higher in fat than white.

In case of dairy products, one can add extra value to milk by processing and marketing products, such as cheeses, packaged milk, yogurt, ice cream or butter.

Dairy Value Addition

For successful value addition the following points are necessary –quality of raw material, correct formulation, optimum processing, right packaging, storage stability, flavor and colour changes, nutritional value, product specification and regulation etc.

When considering the production and marketing of value-added dairy products, one should consider the capital outlay, time commitment, market share and the fact that your business may not make a profit in the first five years. Following point should be kept in mind while starting value addition to livestock products-

- Product you want to sell
- Target audience and how will I market the product
- Location(s) convenient to the consumer
- Profit potential of the product
- Consumer paying capacity
- Quality of the product?

Value-added products can help your farm become more viable, more visible to the public and open up new markets but there are more risks involved when selling value-added versus marketing directly to your local milk cooperative.

Farmers can take classes, or attend seminars on making the products that they are interested in marketing. Food technologists can also offer guidance on the processes and production of milk products.

BAIF Role in Value Added Marketing of Dairy Products

BAIF is working in the field of research & development since 1967 with the mission to enhance farmers' income through dairy cattle & buffalo breeding through its Cattle Breeding Centre. All the programmes of BAIF have focused on enhancing farmers' income through its holistic approach i.e. agriculture, livestock, horticulture, sericulture and natural resource management. Income enhancement is possible only if farmers are having productive animals. To increase the production of Indian cattle BAIF has started its crossbreeding programme in 1970 through artificial breeding (AI) i.e. crossbreeding with HF and Jersey to local & non-descript and upgrading indigenous cattle & buffalo is main focus of BAIF program so that farmers income can be increased as a result of increase in milk production. BAIF is not directly involved in adding value to milk, but carries through Self-help group (SHG). BAIF is contributing in value addition by providing various services to the farmers as follows

- Training to the farmers & SHG member on milk by products, how to prepare khoa, cheese, paneer, ghee etc. from milk so that income of the farmers can be increased.
- Guidance to the producer on production and process of milk by products.
- Farmers/SHG members are undergoing different trainings, workshop, demonstrations on products preparation and initiating interest in marketing.

Value Addition in Poultry

In the domestic market the consumption of poultry meat is low due to the low purchasing power of people. Just 25% population living in urban areas consumes about 75-80% of eggs and poultry meat. The per capita consumption of egg is 100 and poultry meat is 1.2 Kg per person per annum in urban areas. In rural area it is only 15 eggs and 0.15 Kg poultry meat. The output of eggs is increasing at the rate of 4-6% and broiler at 8-10% per annum. It accounts for about 3% of the total GNP and 10% of the total GNP attributed to livestock product with growth rate of 15-20%

Poultry sector is one of the fastest growing segments of Agriculture sector in India. Driving this expansion is a combination of factors - growth in per capita income, a growing urban population and falling real poultry prices. Compared with meat, poultry industry has registered significant growth. India ranks fifth in the world with annual egg production of 1.61 million tones and 18th largest broiler production. Indian poultry meat products have good markets in Japan, Malaysia, Indonesia and Singapore.

India has gifted the world the species like Red jungle and Silver jungle fowls, out of whose progenies, domesticated and crossbreed have emerged the "Pure lines" of today. Transformation has involved sizeable investments in breeding, hatching, rearing and processing. Farmers in India have moved from rearing non-descript birds to rearing hybrids which ensure faster growth, good livability, excellent feed conversion and high profits to the rearers. The industry has grown largely due to the initiative of private enterprise, minimal government intervention, considerable indigenous poultry genetics capabilities, and considerable support from the complementary veterinary health, poultry feed, poultry equipment, and poultry processing sectors. India is one of the few countries in the world that has put into place a sustained Specific Pathogen Free (SPF) egg production project. Some of the value added poultry products are : mention only the names salted chicken egg, Albumen rings, Egg roll, Egg crepe, Egg waffles, Pickled egg and Designer egg.

Some trends affecting poultry markets are - Consumer preference for convenience to save the time, attractive packaging, products for the children- funny shapes, convenient for microwave, preserving freshness etc.

Recommendations

As the poultry industry is among the fastest growing in the world, its potential to attract big-time foreign investment is negligible and that is why it needs greater integration, better cost-effectiveness and improvement in the distribution. Indian poultry industry needs good branding system in order to increase the consumption of chicken. More retail outlets, mass gathering and creating awareness home to home about the nutrient values of chicken and egg. Develop mechanism to counter anti-meat lobbies. Developing efficient independent, authority for disease monitoring and biological quality control.

Livestock Niche Product Marketing

The farm share of profit in the food systems is falling. But there is an opportunity to turn that around. The "mass market" is breaking up in market segments – groups of consumers seeking unique products with specific attributes. Some are willing to pay premiums for those attributes. Many market surveys in US & Europe found that over half of consumers would pay a premium for food produced in a more healthful and environmentally sound manner. This offers an opportunity for farmers to go beyond producing cheap, undifferentiated commodities to adding value and earning premiums by delivering unique products that are highly valued by different groups of consumers. That may be food that tastes better. Perhaps it is locally produced and fresher or is produced in a way that improves its flavor. It may be food that is healthier or perceived as consistent with a healthier lifestyle – such as products raised without pesticide, hormones, and antibiotics. This is an area where products from indigenous livestock breeds have an offer to enhance farm incomes and make economic justification for raising indigenous breeds.

Future Prospects

Value addition of the livestock products is the best way to enhance the farmer's income. If farmers are directly involved or trained in value addition of different livestock products but the constraints such as Less preference for frozen meat by consumer, insufficient cold chain facilities, lack of well-organized marketing system, less demand for value added products, lack of infrastructure facilities for storage and processing, fluctuating export trade, high import duty etc. Besides these constraints there are some challenges like poor process, marketing condition, microbial problem, bio-insecurity of products, quality deterioration and inadequate focus on quality & safety structure should be overcome.

In summary, producers should stay attuned to the needs of the marketplace, they should see themselves producing consumer products instead of farm commodity products. To establish a value-added business, one must be very careful about:

- Start by choosing something you love to do.
- Establish good relations with customers to identify products that will appeal to them.
- Maintain consistent supply of high quality products.
- Make sure that products will be in high demand over the long term.

- Partner with people possessing good technical expertise.
- Carefully hire consultants with expertise, experienced project manager.
- Have a complete plan prior to start & make long-range plans.
- Plan on more time, effort, and expense than expected.

Way to Attract Indian Youth towards Family Dairy Business

In today's scenario youth are diverting from farm jobs to non-farm jobs. Therefore everyone should focus on how to attract youth to dairy farming or dairy business? There is only way to attract them towards dairy business by introducing new schemes as well as new technologies in dairy sector, giving some relaxation, different means of increasing income from dairy and paying more remunerative prices. The whole business of farming has to be commercially viable. Today's youth is modern, they go for commercial dairy farms, they build proper shed, milking through milking machines, good practices so that youth is interested in farming in a village.

Following are the strategies to be adapted to enrolle Indian youth for family dairy business-

- Government should allow free trade agreement with other countries.
- Dairy should be considered as the part of agriculture so whatever benefits agriculture sector gets that should arrive to the dairy sector too. The subsidized loans available for agriculture should also be available for dairy.
- Cooperatives are owned by the small milk producers, so they should be given relaxation from all kinds of taxation.
- Opportunities in the fields of animal husbandry should be introduced such as improved technologies of small-scale poultry and dairy farming can be introduced.
- Financing the dairy farming through bank under different financing schemes. Such as establishment of small dairy unit, purchase of dairy processing equipment's, transportation facilities of dairy products, cold storage facilities, vet. Clinics, dairy parlors or dairy outlets etc.
- Youth should realize that Animal Husbandry is a very attractive business with small land size or even for landless.
- Generate more employment opportunities in dairy sector.
- Such as Amul is launching innovative programmes like the "cow to consumer" to make the dairy sector "contemporarily cool" and commercially viable for today's youth who are moving to cities and reluctant to join the milk industry. In 1970, per capita of milk consumption in India was 111 gm and today it is 350 gm, it is growing at the rate of 2 percent per annum. The demand for milk by 2050 would touch 540 million litres and to meet India's demand in the coming years there is a need to make the dairy industry commercially viable for India's youth, as said Sodhi.
- Codex alimentarius standards of food safety can be popularized in the case of perishable commodities. For this purpose, the young farmers should establish Gyan Chaupals or Village Knowledge Centers. Such centers will be based on the integrated use of the internet, FM Radio and mobile telephony.
- Relaxation, in terms of regulation and policies, the industry seeks from the government?

The industry is going through a golden period as it is passing through a very excellent demand with good supply from procurement side. As far as the demand is concerned, urban India is buying more and more branded products whether it is wheat, egg or dairy product. The retail price of milk has increased around 60 percent in the last three to four years. Thus, the farmers are also getting handsome returns. It encourages them to increase their productivity. In India, milk production is increasing at the rate of 4.5 percent per annum while the demand is surging around 10-12 percent. So, it is good for the industry and the youth.

Keywords: value addition, livestock products, marketing, farmers' income, poultry

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LP-15

SUSTAINABLE UTILIZATION OF INDIGENOUS SMALL RUMINANT RESOURCES OF NORTHERN INDIA

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The contribution to the food production from the livestock sector is increasing day by day due to various factors like population growth, urbanization, changing consumer preferences, income growth etc. The economic contribution of small ruminants to marginal and landless households and livelihood security is much higher than is imagined. Small ruminants (i.e., sheep and goats) are widespread in the tropics and the domestication process for sheep and goat genetic resources is not a new phenomenon and occurred thousand years ago. Developing a concept of sustainable utilization requires a deeper understanding of AnGR diversity within its economic, social and ecological context. Sustainable use means the use of components of biological diversity in a way and at a rate that does not lead to the long-term decline of biological diversity, thereby maintaining its potential to meet the needs and aspirations of present and future generations. Locally adapted breeds are of considerable interest since they represent potential reservoirs of adaptive fitness traits that may contribute to the future of sustainable productivity in a changing climate.

Sheep (*Ovis aries*) are believed to be the first animals to be domesticated, followed by the dog and goat. India has contributed magnificently to the international livestock gene pool and enhancement of animal production in the world. It has played a significant role in determining and maintaining the socio-economic and cultural status of the rural masses. Economic contributions of sheep and goats have been well recognized in animal-agriculture. Goats have an inherent capability to utilize coarse fibrous fodder much more efficiently than sheep (Devendra, 2007 and Liang and Devendra, 2014). The choice for rearing sheep and goats by rural farmers is mainly attributed to their small size, low initial capital and input cost and animal's adoptability to adverse dry climate. Also high quality nutritional products and food security are provided by these animals to rural masses in developing countries. In addition to food security, they are a boon for millions of farmers during unanticipated economic catastrophe or uncertainties to maintain their livelihood and social status (Devendra and Chantalakhana, 2002 and Devendra, 2010; 2013). Goats and sheep also have been used to keep a check on unwanted weeds in plantations, orchard crops and in range lands. Besides, their dung and urine adds to improve the richness of soil. The present caprine and ovine diversity is the upshot of thousand years of conscious selection and breeding efforts made to address the variable need of human being of diverse agro-climatic regions. This diversified germplasm is decisive to face future challenges and to sustain most of agro-ecosystem and production system and is also important for system resilience and improving efficiency in variable production environments. Indigenous genotypes are primarily found among pastoral/ extensive farmers and mixed crosses among smallholders. During the course of evolution these indigenous animals have developed superior heat tolerance as well as disease resistance. Skilled to cover long distances during migration, indigenous sheep breeds are relatively better adapted to local climatic conditions and can uphold extremely high temperature during summer season as compared to crossbred sheep. Hence, the crossbred and exotic sheep have to be grazed during cooler hours as they start panting during hot summer months.

The population of sheep is 65.06 million and Goat is 135.17 million which contributes to 12.71% and 26.40% of total livestock population, respectively according to 19th Livestock Census 2012 (DAHD, GOI). India ranks 2nd and 3rd in goat and sheep population in the world (FAOSTAT, 2016). Genetic resources of 42 breeds of sheep and 28 breeds of goat available in India as reported or updated by NBAGR in 2017 and it is characterized by variations in agro-climatic conditions led to development of various breeds and synthetic strains.

The North India region comprises of Jammu and Kashmir, Himachal Pradesh, hilly regions of Uttaranchal and vast alluvial plains regions of Punjab and Haryana. Largely the flocks are small and stationary but about 20% of the flocks are migratory and are comparatively bigger in size. The stationary flocks graze in harvested fields, along the waterways, in forests and in permanent pastures on common grazing land whereas the migratory flocks graze on foothills and in the valleys in winter and move to high altitude forests and alpine meadows in summer.

Sheep Genetic Resources of Northern India

The important sheep breeds are Bhakarwal, Changthangi, Gaddi, Gurej, Karnah, Poonchi and Rampur Bushair, Munjal and Hissardale. Different breeding strategies have been adopted in different regions for improving wool production, quality and body weight in sheep. The breeds are as follows:

Name	Home tract	Utility
Bhakarwal	Jammu and Kashmir	Meat and Wool
Changthangi	Jammu and Kashmir	Meat and Wool
Gaddi	Himachal Pradesh	Meat and Wool
Gurej	Jammu & Kashmir	Carpet wool
Karnah	Jammu & Kashmir	Fine wool
Poonchi	Jammu & Kashmir	Carpet wool
Rampur Bushair	Himachal Pradesh	Carpet wool
Munjal	Punjab	Meat and Carpet wool
Hissardale	Hissar, Haryana	Wool

Goat Genetic Resources of North India and their characteristics

The goat of the temperate Himalayan region grows fibres of superior quality, where rainfall is low and possesses the finest quality of under coat called "Cashmere" or "Pashmina". The goat breeds found in north and northwestern regions are reasonably large in size and primarily of dairy type. The breeds are as follows:

Name	Home tract	Utility
Chegu	Himachal Pradesh	Meat and Pashmina
Changthangi	Jammu and Kashmir	Meat and Pashmina
Gaddi	Himachal Pradesh	Meat and Fibre

Critical Issues for Sustainable use of small ruminants

Small ruminant production, in the context of sustainable livelihood of the poorest is facing a number of grave problems in India. The important ones are:

- Poor awareness regarding the importance of small ruminants in the livelihood system
- Lack of knowledge of market and marketing system
- Lack of knowledge for scientific management of small ruminants
- Absence/lack of active animal keeper organizations
- Pressure on fodder resource bases
- Inadequate veterinary health services
- Lack of adequate focus on genetic improvement
- Reduced access to credit and insurance
- Poor inter-departmental coordination

Strategic options to strengthening sustainable use of local small ruminant

Sustainable utilization of small ruminants can be strengthened by considering the following conditions:

- Choice of small ruminants and better use of locally adapted breeds
- Official support and increased resource use
- Choice of production system
- Matching production to available feed resources
- Build up of numbers
- Knowledge of market and marketing systems for linking production, products and by-products to market
- Targeting poverty and improved livelihood
- Prioritizing the development of the small-scale and traditional sector;
- Continuing to re-orient the role of governments in creating an appropriate enabling environment;
- Making more appropriate production technology available through research and extension;
- Continued investment in human resources development, especially farmers;
- Improving resource management by smallholder farmers;
- Increasing beneficiary participation in efforts and rewards.

Conclusion

Small ruminants play a pivotal part in the livelihood of small and marginal farmers, landless agricultural labourers in Northern India. Most breeds have been developed based on traditional knowledge, natural selection and improved through human interventions by animal keepers for adjustment to particular agro-ecological conditions. To date some of small ruminant breeds are at risk in the Northern region of India. However, there are still large gaps in the phenotypic and genetic characterization of small ruminant populations in this region and in the documentation of their population status. Adaptive traits of the breeds have not been studied thoroughly. There is a high potential to improve the productivity of the small ruminant flocks through both genetic improvement and management interventions. Future of indigenous breeds in India lies in appropriate approaches for conservation and suitable action programmes which maintains their unique characteristics of specific species. The greatest challenge in the near future for sustaining the use of small ruminants will be the supply of adequate feed resources in times of rapidly increasing feed prices and low contribution of rangelands to the diets.

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LP-16

SUSTAINABLE MANAGEMENT OF SHEEP GENETIC RESOURCES IN INDIA

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Introduction

Small ruminants are the key component among the livestock sector that plays a significant role in sustainable livelihood of landless and small holder farmers in India. Rural human population constitutes 72.22% out of which majority are dependent directly or indirectly on the agriculture and livestock related occupations. The total sheep in the country is 65.06 million that accounts for nearly 12.7% of total livestock population in India. Being the world's second most populous country, India has huge pressure on its food resources. This pressure is increasing with limited agricultural land, however with 24.8% of the agricultural contribution to gross domestic product (GDP) during 2013-14 at current price; the livestock and poultry (512.05 and 729 million numbers, respectively) sectors are proving to be key factors for India's food security. There are social stigmas associated with beef and pork among the majority Hindu community and the second-most populous Muslim community, respectively. The contribution of sheep in total meat consumption in India is only 7% (DAHD & F AR 2016-17). Sheep breeding programs of the past had the major objective of fine wool production, followed by carpet wool and meat. A number of crossbred strains were developed by crossbreeding of Indigenous stock with exotics. Since 1990, the Network Project on Sheep Improvement (NWPSI) focussed on improvement of indigenous breeds by intensive selection. Since 2009 Mega Sheep Seed Project (MSSP) also works for genetic improvement of the sheep in field, using elite germplasm at the farm units. These projects are still running in the right direction. However, a major challenge towards profitable and sustainable sheep rearing today is their market connectivity *i.e.* "linkage", which has not received much emphasis in sheep improvement programmes.

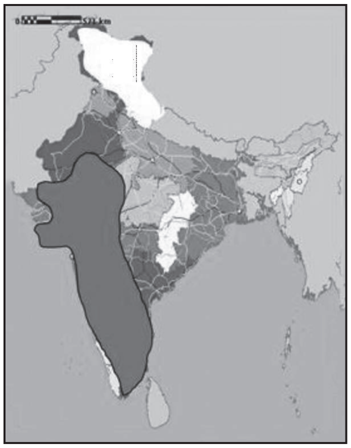

Fig 1. Sheep Producing zones in India : > 80% Population of sheep thrive in Drought prone area.

Present status of sheep and its importance to Animal Husbandry

Sheep Husbandry contributes significantly not only for numbers but also for sustainable livelihood options in the country. The analytics on sheep population and drought prone zones in India conveys the picture that sheep population is more in the drought prone areas, thus acting as the buffering zone for human sustainable livelihood (Figure 1).

It has been observed recently that the sheep population has increased in the areas of Andhra Pradesh/Telangana where farmer's suicides due to crop failure were more. Sheep is the lifeline in areas where crop failure is a commonplace. According to the Livestock Census 2012, Andhra Pradesh (including Telangana) ranks first in sheep population with nearly 40.57%

sheep population followed by Karnataka (14.73%) and Rajasthan (13.95%). Sheep in true sense act as security option and remain always ready for cash option with the farmer. Hence, a jargon of ATM is also associated with sheep flock.

Leading states in sheep population (Livestock Census 2012)

State	Population ('000)	% share
Andhra Pradesh/Telangana	26060	40.57
Karnataka	9339	14.73
Rajasthan	9007	13.95
Tamil nadu	4470	7.36
J&K	3284	5.21
Maharashtra	2533	3.97
Gujarat	1641	2.62
INDIA	**65060**	**100**

Agriculture and allied sector contributes for 48.9% employment according to Economic survey (2013-14). Livestock contributed 16% to the income of small farm households that indicates importance of livestock sector as a whole. Agriculture sector contributed 15.6% to National GDP (BAH&FS 2015). The livestock sector contributed over 4.1 per cent of the total GDP in 2012-13, that nearly accounts for 29.5% of the agricultural GDP (BAH&FS 2015) indicating a significant contribution of the livestock. Presently, sheep is mainly reared for mutton purpose due to the constraints of appropriate market for the wool and higher shearing cost. As far as meat production from sheep is concerned, Andhra Pradesh ranks first with 28.68% contribution followed Telangana by (27.88%) and Rajasthan (9.48%) and slaughter rate in sheep has been on rise consistently. During 2015-16 a total of 3,82,17,670 sheep were slaughtered that lead to per animal productivity estimates to be 12.70 kg during 2015-16.

Leading states in mutton and wool production (BAH&FS 2016)

S. No	States	Mutton Production (million kg) 2015-16	States	Wool ('000 kg) 2015-16
1	Andhra Pradesh	139.26 (28.68%)	Rajasthan	13414.61 (30.8%)
2	Telangana	135.36 (27.88%)	Karnataka	8191.42 (18.8%)
3	Rajasthan	46.03 (9.48%)	J & K	6865.65 (15.8%)
4	Tamil Nadu	36.48 (7.51%)	Telangana	4562.41 (10.5%)
5	Karnataka	28.55 (5.88%)	Gujarat	2282.65 (5.2%)
6	West Bengal	17.59 (3.62%)	Himachal Pradesh	1408.87 (3.2%)
7	Uttar Pradesh	15.77 (3.24%)	Maharashtra	1389.89 (3.2%)
INDIA		**485.53 (100%)**	**INDIA**	**43581.34 (100%)**

The meat production from sheep and goat in India as estimated (BAH&FS 2016) is 485.53 and 942.91 million kg, respectively, that constitutes 7% and 13% contribution to 7000 million kg of total meat produced in country. Share of sheep meat towards total meat production of the country has been quite stagnant since last few years with 7.33% in 2007-08 to 7% in 2015-16.

Wool as a commodity from sheep is losing its value due to many reasons. First is its utility as an important by-product due to easy and cheap availability of the synthetic fibres. Secondly, the income generated from wool is non-significant as far as the primary producer is concerned.

However, still the wool fetches a great value at market. During 2015-16 estimates of wool production was 43.6 million kg that reduced from last year production of 48.1 million kg. It has remained almost stagnant from 43.9 million kg in 11th plan to 43.6 million kg in 2015-16 (BAH&FS, 2016). During last decade, more than 42 million kg of raw wool was produced annually in the country of which about 2.5 million kg was of fine quality. India's per capita/year consumption of meat is 5.11 kg (FAO, 2009), and it will increase in the coming future. As far as wool production is concerned, Rajasthan ranks first with 30.8% contribution followed by Karnataka (18.32%) and Jammu & Kashmir (15.8%). Sheep husbandry is popular among many nomadic tribes In India, although it has been a key source in their sustainable livelihood but could not reach its true potential. This sector has been infected with the pests of poverty, illiteracy, absence of market, middlemen and absence of proper scientific management of the sheep flocks. In the near future, with advent of new technologies, streamlining of the market, access of market for sheep owners, formation of co-operatives by farmers, micro-credits, boom in the information technology, the future of sheep husbandry seems to be bright.

Diversity of Sheep Genetic Resources in India

There are 42 breeds of sheep and are found across the country and are well adapted to specific agro-climatic region. Details of the sheep breeds classified on the basis of agro ecological regions *viz.* a) North temperate region; b) North Western arid and semi-arid region; c) Southern peninsular region; and d) Eastern region are depicted below. In our country a sizable population of sheep are non descript due to indiscriminate breeding and intermixing of breeds.

Breeds of sheep in different agro-ecological regions in India and their major utility*

North Temperate	North-Western Arid and Semi-Arid	Southern Peninsular	Eastern
Bhakarwal (CW)	Chokla (CW)	Bellary (MCW)	Balangir (MCW)
Changthangi (CW)	Jaisalmeri (MCW)	Coimbatore (MCW)	Bonpala (MCW)
Gaddi (CW)	Jalauni (MCW)	Daccani (M)	Chottanagpuri (MCW)
Gurez (CW)	Kheri (MCW)	Hassan (M)	Ganjam (MCW)
Karnah (AW)	Magra (CW)	Kachakatti (M)	Garole (MP)
Kashmir Merino(AW)	Malpura (MCW)	Kanguri (M)	Tibetan (CW)
Poonchi (CW)	Marwari (MCW)	Kilakarsal (M)	Kendrapara (MP)
Rampur Bushair(CW)	Muzaffarnagari (MCW)	Madras Red (M)	
	Nali (CW)	Mandya (M)	
	Patanwadi (CW)	Mecheri (M)	
	Pugal (MCW)	Nellore (M)	
	Sonadi (MCW)	Nilgiri (AW)	
	Munjal(M)	Rammand White (M)	
		Tiruchy Black (M)	
		Vembur (M)	

*Within parenthesis is the major utility of the breed: (AW) Apparel wool; (CW) Carpet wool; (MCW) Mutton and Carpet wool; (M) Mutton; (P) Prolificacy

Sheep Breeds of Arid Region

In India there are two types of arid regions: 1) Hot Arid and 2) Cold Arid. Hot arid region comprises of Western Rajasthan, Western Gujarat and adjoining areas of AP and Karnataka. The cold arid region comprises of Jammu Kashmir (Northern Part) and Leh Laddakh. In the hot arid region Magra, Marwari, Jaisalmeri, Patanwadi, Pugal and Chokla sheep breeds are found. These are heavy breeds with migration capability and good carpet wool and mutton producing quality. The cold arid region has only one breed of sheep and that is Changthangi. It is distributed in the

Changthang region of Leh. Animals are usually shorn twice a year, generally in May/June and September/October, but in some cases shearing takes place only once a year, in July/ August. Greasy-wool production ranges from 1 to 1.5 kg per animal per year. The wool is of a good carpet/ medium apparel quality of Ladakh.

Why do we need to conserve sheep genetic resources?

Pastoralists and small and marginal farmers are somehow or other are dependent on the livestock those have been their companions since ages. They symbolises their culture, knowledge systems and societies. These animals are unique with respect to tolerance to biotic and abiotic stresses. These animals and breeds continue to produce meat, wool and other produce without much input on feeding, care and veterinary assistance. Today, in the time of competition, the focus of farmer as well as government is diverted towards the high producing breeds which can meet the demand and in turn the diversity of the sheep breeds. This small number of high producing breeds leads to narrowing the genetic base, as native breeds are neglected in response to market forces. The diversity of animal genetic resources is essential to satisfy basic human needs for food and livelihood security. Genetic diversity defines not only animals' production and functional traits, but also their ability to adapt to different environments, including food and water availability, climate, pests and diseases. It has also been found that the Indian sheep breeds are more resistant to the gastrointestinal parasites as compared to the crossbreds or exotic sheep. There are many sheep genetic resources which are unique (Table below) and popular among the local (Bhatia and Arora, 2005). Thus we need to preserve this trait which is possible only if we can save these breeds form extinction.

Some unique sheep breeds of India*

Breed	Unique characteristics
Changthangi	Fiber fineness
Chokla	Fine carpet quality fleece
Magra	Lustrous carpet quality fleece
Mecheri Chennai Red	High quality skin and mutton
Mandya	Excellent meaty conformation, high quality and meat palatability.
Nellore	Tallest sheep breed of India.
Garole	High fecundity- twins and triplets common. Survival under saline conditions.
Marwari, Deccani Jaisalmeri	Hardy and capable of walking long distances during migration.

*Source: (Bhatia and Arora, 2005)

Enhancing the per animal productivity of the sheep

Average carcass yield from sheep is relatively low in India with national average of 12.7 kg, whereas the world average is 16 kg for carcass yield. In India, Assam has lowest average of 7 kg, and Himachal has highest average of 20 kg. Apart from this the increased slaughter rate is also a thing of concern, if population shows a declining trend. In the past, efforts towards enhancing body weight through selection within indigenous and crossbred population has been attempted. The results of cross breeding on the whole, revealed that percent improvement in body weight up to 6 months of age is conspicuous in different crossbreds over contemporary natives but only marginal improvement was observed at 12 months of age. This is indicative of the fact that crossbreds/new synthetics require high plane of nutrition and if they are managed on the same feeding regimen as for natives, the differences which were conspicuous up to 6 month age became marginal at the age of one year. Due to non-availability of required plane of nutrition, mutton type strains developed by crossing Suffolk and Dorset with the indigenous breeds could not outdo the natives under village management conditions despite the improvement in body size as well as in wool quality and quantity. Results on growth performance of native breeds reveals that Malpura and Muzaffarnagri of North Western breeds and Nellore and Mandya of Southern breeds have great potential for their use as improver breeds for mutton production. Improvement of sheep through breeding strategy will also depend upon socio-economic and ecological considerations, existing genetic resources, their productivity, possibility of their improvement through selection within a breed, upgrading with indigenous improver breeds, or replacing an indigenous breed with an existing breed if it is arising from similar ecological region and thus will be adaptable, or cross-breeding for evolving new breed combining the adaptation and hardiness of local breed and higher productivity of the exotic breed.

Per Sheep More Sheep

Considering the importance of multiple births in sheep breeding in special reference to mutton production, Garole, an indigenous prolific breed of sheep, was introduced at CSWRI, Avikanagar during 1997 for improving reproductive efficiency of native sheep (Sharma *et al,* 2004). The results indicated that twining percent in Garole X Malpura (GM) half-breed ewes were 52.24 % and lamb born, as triplets were 7.46%. The average number of lambs born per ewe lambed was 1.64 in GM and 1.08 in Malpura sheep (Kumar *et al,* 2006, Mishra *et al,* 2007). It was observed that the body weight at different ages of GM half-bred was on lower side compared to contemporary Malpura lambs. This was however the first report that also signified the importance of enhancing Malpura inheritance to 75% for better live weight gain and mothering ability in prolific crosses. The overall percent gain in prolificacy in GM was 52.38, which increased to 75.73 in third parity (Mishra *et al,* 2007). The FecB gene carrier GM was backcrossed with Malpura ewes to produce the GM x Malpura (GMM). The GMM crossbreds ewes were able to produce >50% twin lambings and higher body weight as compared to half-breds but problem of low milk yield of dam for feeding twins/triplets and to enhance the live weight gain during pre-weaning stage persisted. To address this issue, Patanwadi sheep of Gujarat (a heavy sheep breed of Saurashtra, famous for higher body weight and milk) was introduced. By implementation of structured breeding plan, a high performing triple breed cross in terms of increased prolificacy, more litter weight, more milk per dam and adaptable to sub-tropical climate has been developed at CSWRI Avikanagar, which was named "Avishaan" on 04th January 2016. This newly developed prolific sheep is a composite cross possessing 12.5% Garole, 37.5% Malpura, 50% Patanwadi inheritance in which *FecB* gene has been introgressed successfully. The average body weight of the lambs is 3.3 kg at birth, 16.8 kg at weaning and 25.9 kg at six month age (Sharma *et al,* 2016). More than 54% Avishaan females produced 2 lambs and 2% produced 3 lambs in a lambing leading to 57% prolificacy with litter size at birth 1.61. Avishaan ewe excelled the local Malpura sheep in terms of ewe productivity efficiency at 3 month age by 32.5%. They also produced 50% twin lambings at farmer's door. Results obtained so far in case of newly developed prolific sheep are encouraging and igniting a new way ahead for profitable sheep husbandry. In times to come, prolific sheep may prove a boon towards enhancing the economic returns per sheep for livelihood security of Indian sheep keepers.

Current challenges with the Indian sheep husbandry sector

1. **Bottom-up approach in sheep breeding policies:** With so much of cultural, linguistic and biological diversity, India cannot afford to have one policy for all the sheep husbandry sector. In India, each state government has its own policy for livestock breeding as agriculture is a state subject. There are 42 breeds of sheep in India and diversity between these breeds is very high that influenced by the agro-climatic condition of each region. Usually each state government has

a well-crafted breeding policy considering locally available needs and germplasm. However, the execution of the policy fails due to the policy not being given priority, inadequacy of funds and infrastructure and no direct control over the wish and will of farmers to adopt the government policy. A bottom-up approach is an essential requirement, whereby there is a need for the breeding programs to be chalked out at grass root level that will include Panchayati Raj structure. Given sufficient funds for operation, such a program will be able to deliver the best results.

2. **Linkages between livestock producers and market:** The genetic improvement programs for sheep have primarily been aimed at improvement of the live body weight and wool yield. However, in general farmers are not much benefitted from having higher or lower weight animals, as their animals are seldom sold on a live weight basis. Thus having no incentive for producing animals of higher body weight, livestock keepers do not show much interest in adoption of the superior sheep germplasm. To address this problem, linkage with the market is essentially required. Study at ICAR-CSWRI Avikanagar on Malpura sheep breeders indicated that farmers sell their lambs at 3 to 4 months of age for the price ranging between Rs. 1200/- to 2500/- (Malpura Project AR 2012-13), and the average weight of lambs is more than 15 kg. The average price for live weight at the Delhi abattoirs is Rs. 240/- per kg live weight. Market to producer linkages needs to be set up from government organization and or NGOs. Establishment of breeders' organizations, especially for small ruminants should be a priority. In this scenario, where weight of the animal carries less importance than the number of animals sold, the high genetic worth germplasm like *Avishaan*, can prove to be highly profitable.
3. **Coverage under genetic improvement program:** The number of breeds covered in the program and coverage of the population is not realistic looking in to the actual breeding population. Today MSSP and NWPSI covers only 10 breeds out of 42 enlisted. This is less than 25% coverage. Not only this, but the population covered under each program is very small, due to unavailability of the budget. Thus a strong support from government side in terms of with huge funding is essential for increasing the coverage of the sheep population so that gains can be predicted and realized in true sense.
4. **Revival and conservation of grazing resources:** Sheep being the animals of poor farmers are reared on zero input systems in India. The country's pastures have reduced from about 70 million ha in 1947 to about 38 million ha in 1997 (PCI 2011). The remaining grazing lands have either already degraded or are in the process of degradation. With shrinking grazing resources and extensive agriculture production, there is severe pressure on common grazing land. State policies in restricting the encroachment of the common property resources (CPRs) for grazing land needs to be strengthened. The grazing land should not be allotted at all for human settlement or industrial purpose. The challenge is to revitalize the degrading common fodder and pasture resources in the country and improve their productivity. Stall feeding (with fodder and concentrate) to sheep is one option; however, this is unrealistic looking in to the poor economic condition of the shepherds. These days, entrepreneurs are entering in the sheep rearing business, where stall feeding is the only option left due to non-availability of the grazing land. Many entrepreneurs share their good experience with semi-intensive system of rearing. Shifting from extensive to semi-intensive and then to intensive system of rearing has the challenge of profit making due to the poor market infrastructure and supply chain in this sector.
5. **Minimum support price for sheep produce:** The sheep mainly produce the wool and meat as primary products, however the prices are not fixed. Although meat receives better prices

in market, but the wool from majority of the breeds is sold at very low cost. Many a times it was observed that the cost of shearing is also hardly recovered from the sale of wool. Again the problem is with linkage, where wool is not sold at the right platform. However, being a natural fibre, wool is a prime product should receive a fixed minimum support price (MSP). This will help sheep farmers to think over their produce and opportunities for marketing will increase.

6. **Diversified sheep produce and marketing:** Sheep has been traditionally reared as a family business, without actually thinking about its economics in India. The pastoralist system was the only stakeholder of sheep in India. However, with shrinking grazing land, losing interest of new generation in sheep raising and low returns as compared to the hard work requirement, now the time has come, when the sheep husbandry needs a boost. Sheep provides a multitude of produce about which farmers hardly think. Apart from meat and wool, the sheep manure can be a major source of income, if it is properly marketed. One such example is "AVIKHAD" prepared at ICAR-CSWRI Avikanagar, where sheep manure with wool waste is processed and packed for sell to the kitchen gardens, etc. Apart from this, the coarse wool that is not used for any production, can be best utilized for making toys, mats, etc., targeting the right customers. A breeder's cooperative organization formulated for managing such business along with sell of live animals on a fixed rate can prove worth.

7. **Need of abattoirs:** Sheep skin/hide can be utilized for making purse, and other leather products. Bone, blood obtained from the sheep also fetches good market value for making meals for poultry and fish, given right processing. However, all these things to happen require right processing of the sheep in the slaughter house, linked with marketing. Therefore, scientific abattoirs with facility for processing of each produce of sheep needs to be constructed at every important city with sufficient two way linkages to farmers and market.

Conclusion and recommendations

Sheep husbandry is the backbone of India's rural economy. A few steps in the right direction with considerable economic investment are essentially required to rejuvenate this lifeline. There is a need to focus on sheep productivity in a sustainable manner with emphasis on profitability and institutional support.

- A sincere effort from government as well as other developmental agencies for addressing issues such as market viability of the sheep husbandry, linkages of sheep produce with the market, availability of feed and fodder, availability of superior males for breeding, management and healthcare are required.
- Scientific approach for management of breeding, lambing, nutrition, housing and healthcare must be followed for reducing the losses and fetching more returns from sheep rearing.
- Farmer participatory approach should be followed by working hand in hand with the farmers on their sheep flocks with scientific data recording and management. Genetic improvement of sheep for mutton and wool using both farm and field units should be strengthened.
- Prolificacy may be incorporated in the breeds wherever possible using developed germplasm with high growth such as *Avishaan*, looking in to the fact that nutritional and environmental stress is avoided at best possible and availability of milk with nourished ewes.
- Co-operative approach in sheep husbandry may be tried at least at a village level and adopted for better breeding practices, fixation of the prices and net economic benefit to the end user.

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CULTURAL AND SOCIAL ISSUES IN CONSERVATION OF INDIAN LIVESTOCK

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Introduction

India is officially the most sustainability minded country in the world as per the global Greendex report (2014) by National Geographic. We, as Indians, take pride in our strong cultural heritage. A look at Indianism shows that we worship the sun, wind, land, trees, plants, and water that are the very base of human survival. Likewise, respect and conservation of wildlife—garuda, lion, cattle, peacock, mouse, and snake – these are part of our cultural ethos from time immemorial. Ancient texts like the scripture *Vishnu Samhita* contains direct instructions dealing with biodiversity conservation. Even we have firm faith that "Religion protects and nurtures nature". As a matter of practice, India is a culturally rich and diverse country where a large percentage lives as diverse communities in their respective social structures completely depending on their environment to ensure their livelihoods. The erosion of livestock and poultry biodiversity is part of a larger problem of unsustainability, whereas cultural richness supports sustainable use of the environment and thereby promotes its conservation.

In contrast, the global expression of the concerns for sustainability and conservation are only of recent origin. 'Sustainability' as a concept appeared first, in 1992. Only subsequently, the rich contributions and the crucial role of 'communities' and the value of 'traditional knowledge' of communities were appreciated by international bodies. Here are some glimpses of the developments in the recent few decades that have a direct bearing on conservation in general as well as conservation of livestock breeds, especially in view of the cultural ethos of our country.

The 1992 Earth Summit held at Rio de Jeneiro is a recent effort by the international community of 172 countries for a global plan of action for sustainable development. Soon after this, the UNESCO sponsored the Convention for Safeguarding the Intangible Cultural Heritage, adopted by the General Conference in 2003; it called for safeguarding knowledge and skills that are recognized by communities, groups, and individuals, as forming part of their cultural heritage; these are transmitted from generation to generation and constantly recreated; these are crucial for the sense of identity and continuity of communities and groups; also, these are in conformity with human rights, and sustainable development. This is commonly known as traditional or indigenous knowledge. Soon after this, the UN Declaration on the Rights of Indigenous Peoples, endorsed by the UN Human Rights Council in 2006, recognized that "respect for indigenous knowledge, cultures and traditional practices contributes to sustainable and equitable development and proper management of the environment". In India, the Biological Diversity Act was prepared considering the above as well the cultural strength of the country and contains a framework provision for the protection of rare knowledge of indigenous communities. All these developments are of recent origin in comparison to the long tradition and cultural ethos of nature conservation followed in India since time immemorial.

What is Culture / Cultural Issues

Culture is the shared knowledge, behavioral norms, values and beliefs that help people to live in families, groups and communities. Broadly speaking, culture is the set of rules for interpreting experience. Cultures help define ethnic groups as people who share ideas, language and beliefs because they come from the same country place. Cultures can also define groups within countries by example like Religion (being Jewish), Occupation (the military), Regions (Southern culture), and such other special statuses.

It can be said that 'cultures are rich, complex, and diverse'. Moreover, cultural values and beliefs are rooted in specific traditions often overlaid by religion. Tools are now available for identifying 'Cultural Resources in a Community'. Such is the possible impact of cultural values on livestock utility especially under the Indian conditions that "Society can be benefitted by considering 'cultural resources' and 'animal genetic resources' together for the given eco-system". For this we need to understand the socio-cultural factors that play an important role.

Socio-Cultural factors

By definition, socio-cultural factors are the customs, lifestyles and values that characterize a society or group. Socio-cultural aspects include concepts of beauty, education, language, law and politics, religion, social organizations, technology and material culture, values and attitudes. An understanding of socio-cultural factors is crucial in developing strategies for livestock utilization including marketing wherever there is a need to seek actions from particular groups. Formation of Breed society is a glaring example where socio-cultural factors play an important role.

Social problems

Social problems are the general factors that affect the society. A social problem is normally a term used to describe problems with a particular area or group of people. Social problems affect real life; it affects how people react to certain situations. For example, poverty, especially the factors that contribute to it, is a social problem. The main causes of social problems that would affect conservation of livestock are: unemployment, poverty, urbanization, lack of education, superstitious beliefs, caste discrimination, environmental contamination, ethnic conflict, health disparities, inequality and loss of sustainability etc.

Cultural issues in a Community

A community is an expressive manifestation of culture in the social groups. For centuries, indigenous communities – spread out globally but particularly in India - always used and adjusted their agriculture in the event of changes in climate or the surroundings. There is, however, imminent threat of losing the communities themselves to outright annihilation or due to their amalgamation in the mainstream and thereby losing the very culture and the traditional knowledge of the communities. With the rampant commercialization of natural resources, traditional knowledge that always managed to maintain the sustainable levels of resources has been sidelined. Issues of privatization and 'bio-piracy' are now major areas of concern. The existing policy and legal mechanisms to protect traditional knowledge usually does not involve these communities. Hence little is done to safeguard local community needs, values and customary laws relating to traditional knowledge and genetic resources of indigenous and local communities that is necessary for conservation and sustainable development of indigenous breeds.

Challenges of the modern times

Recent few decades noticed technical challenges and strong market forces that are reducing the role of communities in sustainable use of livestock or its conservation. The powerful combination of scientific reductionism and capitalism is driving food production into limitless intensification and scale. Developments in agricultural science are reducing the role of communities that are more closely associated with production systems at the ground level. Through the lens of reductionism, the readers are focused increasingly on the biology of the resources with less reference to how they will be integrated into the agricultural community of life. This separation is becoming stronger with the developments in molecular genetics. Scientists in this field now direct their interest less to the farming system and animals and more to the tissues, cells, and especially to the protein and base molecules. Funding is largely from private industry, thereby the relationship with the farmer has further reduced. Moreover, gene technology researchers in the food chain are frequently unaware of the importance of the community of life and good husbandry that have been foundations of settled agriculture for millennia. In fact, current research specifically aims to breach the species boundaries and to transfer genes from any other species on earth into the traditional agro-diversity species. Further, the business employers of researchers, having their main focus on shareholder profit, are often out of touch with the rhythms of nature and are not trained to think in terms of environment/ nature or in terms of sustaining the communities.

A second major challenge in farming in recent decades is the attempt, through the intensification of livestock management systems, to overcome the natural boundaries of life cycles like by the use of synthetic hormones to increase milk and meat production. The result of animal research today, when applied to animal production, largely tends to rupture the established management system in some way and, thus, upsets traditional biological boundaries. In a way, the future is being traded for present consumption. One growing effect of this on humans is to view livestock as disposable. The term "animal husbandry" is scarcely relevant to livestock farming any longer, as the flow of innovative management techniques now produces systems so intensive that they are frequently exploitative of the animal and destructive of the environment. The fact that society now has consciously to think and work about the need to conserve domestic animal genetic resources or has to put up the institutions like NBAGR reveals the destructive nature of current livestock usage.

The consideration that the unique genetic forms existing as breeds and races may be of value one day, thereby justifying conservation is in contrast with making "utility now" the only value in public decision-making. It is argued that a civilization based solely on 'immediate economic benefit' by breaking biological boundaries and disregarding the community of life, is already in the process of losing its own cultural heritage. This is not justified. Fortunately, the cultural strengths in India have the capacity to strengthen sustainable use of the resources. Innovative means have to be generated/followed to strengthen the 'cultural resources' of the country that will automatically save and strengthen the 'animal genetic resources'.

The principal decision makers are no longer farmers but business executives, who are remote from the farm. The emphasis on cheap food is the principal driver that leads to increased competition and unsustainable practices. Farmers as well as their breeds are disappearing. The advent of gene technology and transgenic livestock is reviewed with the prospect of extensive manipulation of animal form and function and abuse of genotypes as animals are redesigned, suffer, and lose all dignity. We need to look for alternatives to this system and must assess what do we have in store, or in human memory. Indian cultural practices could be an answer.

Indian Culture is in tune with Nature Conservation

Today, when people throughout the world are perturbed by the degradation of the environment and the disastrous consequences of this, traditional ethics of nature conservation could be looked upon as a resource of inspiration and guidance for the future. Environmental conservation - for the present generations in India - is a way of life. Historically, conservation of nature and natural resources was an innate aspect of the Indian psyche and faith, reflected in religious practices, folklore, art and culture permeating every aspect of the daily lives of people. Some of the fundamental principles of ecology-the interrelationship and interdependence of all life-were conceptualized in the Indian ethos and reflected in the ancient scriptural text over 2000 years ago; it says, *'This universe is the creation of the Supreme Power meant for the benefit of all His creation. Each individual life-form must, therefore, learn to enjoy its benefits by forming a part of the system in close relation with other species. Let not anyone species encroach upon the other's rights.'*

Hinduism, Buddhism, Jainism, Christianity, Islam; and others place great emphasis on the values, beliefs, and attitudes that relate to the cross-cultural universality of respect for nature and the elements that constitute the universe. The concept of sinning against nature exists in various religious systems. Many of the rituals were traditional strategies to preserve the intrinsic relationship between man and nature. The worship of trees, animals, forests, rivers, and the sun, and considering the earth itself as Mother Goddess, were part of the Indian tradition.

One of the finest examples of traditional practices in India based on religious faith which has made a profound contribution to nature conservation and livestock conservation has been the maintenance of certain patches of land or forests as 'sacred groves' dedicated to a deity or a village God, protected, and worshipped. These are found all over India. Sacred groves must have been a very effective way of preserving tropical biological diversity as new species of plants that have disappeared from everywhere else are discovered in these 'sacred groves'. There are also examples of sacred hillocks or ponds attached to temples in many parts of India especially in Himachal Pradesh as noted on the migratory routes of Gaddi sheep on the Dhauladhar range.

All these accounts vividly show how the ancient culture and traditions of Indian society contributed to the conservation of natural ecosystems, and the plants and animals that inhabited these. The impacts have obviously been also on conserving the local livestock breeds. In brief, Indian literature effectively mirrors the ethos of its deep and sympathetic understanding of animals through innumerable stories. Even amongst these one could pertinently mention are the *Hitopadesha, the Panchatantra* which are abound with references to the animal world. Animals in these stories have been endowed with such qualities that provide lessons in morals and are relevant even to human beings in day-to-day life.

Furthermore, some twenty-two centuries ago Emperor Ashoka decreed that it was a king's duty to protect wildlife and the trees of the forests. He got edicts inscribed on rocks and iron pillars throughout his kingdom, prohibiting the destruction of forests and the killing of various species of animals. This historical evidence, surviving to this day, is the first recorded measure on conservation anywhere in the world. In more recent historical times, Mughal Emperor Babur's memoirs (*Baburnama*), Guru Nanak's hymns on *'Baramasa'* (the seasons) depicting each month with a dominant bird image, and Emperor Jehangir's memoirs showing his keen interest in the wildlife provide fine illustrations of the Indian tradition. The love for nature has been handed down the ages, becoming an integral part of the Indian psyche.

This long tradition and belief in the conservation of nature is also vividly alive in contemporary times. One of the most successful conservation movements in India today is the Chipko movement spearheaded by the womenfolk in Garhwal in the Himalayas. This simple yet effective action eventually saved 12,000 sq. km. of a sensitive water catchment area. Such care at the community level has a positive impact on conservation of nature and local indigenous breeds. There was a similar Appiko movement in the southern state of Karnataka where the activists used local folklore to reach out to the masses and reminded the people of the need to conserve sensitive ecosphere, which is the abode of several plant species and livestock strains.

Further, it must be emphasized that the indigenous people are not primitive or backward; they may be poor and disadvantaged in many other ways, but they have a tremendous understanding of ecosystems and the factors that sustain them. They still look upon life as a gift to be celebrated; and this ancient Earth as one to be praised, worshipped and also celebrated. They are the one to whom the earth is not something to be used, not a possession or an object for exploitation but a living entity, an object of reverence, and the relationship is one of sacred trust and loving intimacy. It reveals the intimate sense of togetherness and harmony that exists between man and nature in indigenous and tribal societies. Recent 'discovery' of a new strain of cattle *Nallamalla Poda* [yet to be registered as a breed] in Telangana is a testimony of the perseverance and sustenance of these cattle by the tribal communities in the regional milieu.

Communities or ecosystems are the topics of high priority for many environmental biologists. They, together with all who live close to the earth, including farmers and livestock producers, are aware of the community of life with all of its mutual dependencies and integrations. Domestic poultry and livestock have, for millennia, been sustainers of agriculture, of society, and of civilizations. The practice of caring for domestic animals and birds forces recognition that human life is dependent on the biosphere, and rural people everywhere have developed respect for biological boundaries and communities. Farming systems throughout the world are part of an integrated whole in which human ambitions are tempered by natural boundaries. Leaders of most simple societies have learned that survival and, more particularly, quality of life in a civil society, depends on living peacefully within the limits imposed by the natural boundaries.

Consideration of unique adaptation of indigenous breeds to local feed, disease challenges, topography, climate, and management conditions, and the experiments at crossbreeding has provided the lesson that livestock in natural environments cannot be separated from the joint interactions of historic culture, local ecosystem and values of the people. Hence, there is a need to empower the poor without trying to change their livestock and management systems, which are closely tied to their values and culture. The poor need help in building viable community structures such as Breed Societies to take on conservation of the breeds at their own level.

Cattle and Culture

Cows contribute to human material welfare in more important ways than milk production alone. Despite the marginal status of milking in the symbiotic syndrome of the cattle production system in the country, cows are revered on religious considerations even though the awareness on the superiority of the regional adaptability of the locally adapted breeds is not well understood/ appreciated. The issue of 'cow culture' in India has many overtones at social, economic and even political level, and cannot be dealt in a few pages like this article. It is, of course, noted that, as the awareness on superiority of the local cattle breeds is increasing, community level support is being extended to saving the breeds. There is hence a dire need to identify the local lesser known breeds and bring these on the national map. This will not only provide policy support to their development and conservation but also work as an impetus to the local community to save their own cattle genetic resources.

Socio-culture and Breed Conservation

India's cultural strength has historically supported conservation of animal biodiversity. Ingrained in human mind and expressed in day-to-day activities, Indian cultural resources have variously led to 'conservation' as a way of life. To bring home the point, two expressive examples are cited as 'Success Stories' in two different eco-cultural landscapes, i.e.

(1) Timbaktu Collective which illustrates the strength of farmers' opinion rising from their practical daily requirements, and

(2) Banni Breed Association which shows the traditional surviving instincts being transformed to enhanced utility of the Banni buffalo and rejuvenating the Banni based production system.

Culture supports conservation of Hallikar cattle in Timbaktu Collective

In an interesting case, the farmers of the Anantpur (AP) area were to decide on the type of cattle that would suit their agricultural requirements. During 2007, Timbaktu (an NGO) took the initiative and the farmers were shown the (high) production system of crossbred HF cattle in the vicinity, but they selected Hallikar cattle which the community people said would provide some milk but more valuable draught power without the need for elaborate feed/fodder or veterinary care requirements. More than 900 cattle heads were searched and purchased from nearby Karnataka. After use for 3 years it was recorded that the number of Hallikar cattle had increased in the area – being the locally adapted breed. As a matter of fact, the farmers have naturally been groomed – right from their childhood – with such socio-cultural strength that they are generally aware of the superiority of more sustainable local breeds that provide some milk, ensure a calf almost every year, and sure draft power for the needed agricultural and transport operations in the village. "There is no need for veterinary care or a doctor for these local breeds and these cows meet all our requirements" said the Hallikar keeper at the Sheshampally village near CKPally in Anantpur district of Andhra Pradesh. He obtained the Hallikar cows through Timbaktu Collective [www.timbaktu.org], and used these cows for ploughing as well. The impressive logic and wisdom of the farmers is but a manifestation of their socio-cultural strength.

Culture supports development and conservation of Banni buffalo

Maldhari community who live in the Banni grasslands of the Kachchh district in the State of Gujarat in India are the custodians of the biodiversity rich Banni grassland ecosystem and have protected and nurtured it for over 450 years. The Maldhari way of life has co-evolved with the Banni ecosystem, and indigenous livestock- the Banni buffalo, Kankrej Cattle, Kachhi-Sindhi Horse which are uniquely adapted to the region and has evolved through a dynamic and complex inter-relationship between the Maldharis and the Banni region. The Maldhari, the Grassland and animal genetic resources of Banni are mutually inter-dependent. Banni pastoralists expressed in their 'Cultural Protocol' that "Through our traditional knowledge relating to our breeds we have, over centuries, been able to develop particular characteristics that enable the animals to survive and thrive in the difficult conditions of Banni, while maintaining high yields. Our knowledge extends to what we feed our animals; we raise the bulls in a way that allows them to start servicing at 2.5 years of age. The milk that our animals produce is entirely organic with no chemical additives. Mostly we treat our animals using our traditional medicine. We rely on our traditional forms of medicine for our animals. For example our knowledge includes techniques for the safe delivery of calves, treatment of sick animals using the herbs and grasses of the Banni and providing our animals certain foods to heal them. We take pride in this knowledge and want to preserve it for our future generations".

It's indeed the cultural strength of the Banni pastoralists that earlier helped in sustainably continuing the Banni breed and subsequently, as a community approach, they formed a robust Banni Breeding Society (*'Banni Pashu Uchherak Maldhari sangathan'*), and now developing and conserving the breed more effectively.

Berari Bakri Breeders' Association and other case studies

Berari goats are located in parts of Maharashtra state and the Khandwa, Khargone and Burhanpur districts of Madhya Pradesh. A Breed Society named as "Berari Bakri Breeders' Association, Khargone, MP" was formed in 2015 by the Berari keeper's community who initially came together by virtue of cultural affinities and social coherence.

Just as the local cultural practices have strengthened the local social system & also saved the Hallikar, Banni or the Berari breeds we have very many examples & case studies in our country where culture plays a big role. Some cases are cited below.

>> A Padam Shri awardee Shri Magraj in Barmer noted that poverty was rising and the socio-cultural system disintegrating as people started moving out from villages to nearby cities, and the only reason he noted was the loss of the local good Tharparkar cattle. Under the banner of an NGO named SURE [Society for Upliftment of Rural Economy], they undertook to developing and strengthening community based approaches for conservation of Tharparkar cattle. They established breeders' associations in 15 villages, raised young Tharparkar bulls and distributed 34 selected bulls in the undertaken villages for natural service. Each service was recorded. A total of 2091 Tharparkar progenies were born (in 2008). Under the community awareness programme regular meetings of the breed association members were arranged to solve the local problems for the development of Tharparkar breed. The project succeeded mainly on the basis of local socio-cultural strengths.

>> An NGO **Jal Kranti Trust** by one Mr. MansukhBhai Suwagia in Junagarh (Gujarat) worked for improvement and conservation of Gir cattle by spreading and raising the number of purebred Gir cattle. Under an innovative scheme developed by him *'Gir ghar ke Aangan Mein'* ['Gir in each house'], they supported and more than 60% of the houses in Jamka village had at least one Gir cow. Number of quality Gir cows were raised and various products from the cows were utilized as a source of earning by the villagers. This increased awareness for improvement of Gir cows and also their conservation.

In addition, there are many other examples of association between culture and conservation. One example is that of natural resource conservation at the village of Mendha in Gadhchiroli district of Maharashtra. In 1987, the villagers renewed their efforts at biodiversity conservation. It was decided that no commercial exploitation of the forests, except for Non-Timber Forest Produce, would be allowed. Further, villagers would themselves regulate the amount of resources they could extract from the forests and undertake measures to tackle soil erosion. The important aspect of this community was that the villagers decided for themselves. Basic force behind the conservation was the strength of **culture of the villagers**. Another case study is that of the sacred groves in Rajasthan where several species of plants are protected that itself offers protection to birds and animals. There are several communities in the States of Manipur and Assam in the North-Eastern part of India which is home to diverse tribal and other ethnic groups. Here, the Meetei community meets a substantial proportion of its resource requirements from a relatively small catchment area in which they have been living for a long time. They live in complete harmony with nature and with the motive of sustainable harvesting. Conservation is hence a part of the local culture. It has also been noted that certain religious beliefs and practices help in the conservation of nature, biodiversity and livestock especially cattle.

All the above success stories are testimony to the fact that India has positive socio-cultural strengths that can lead to conserving the local breeds for supporting local livelihoods and thereby rendering the local production systems more sustainable. In brief, India offers a positive socio-cultural atmosphere for community based working to conserve and develop local breeds. In the same vein, Jallikattu - the sport - cannot be left out in our discussions on 'culture and conservation'.

Jallikattu as a case study

In the attempts at conserving the breeds through scientific methods, India has had more failures than successes so far. The reason is that 'conservation is known to be a complex process'.

It can be managed only by a multi-dimensional approach *i.e.* by acting in several directions, with several alternative paths, all leading to saving the breed from further dilution. Owing to the amount of work that needs to be done in developing alternatives, banning an already existent and functional system like Jallikattu must be seen from 'conservation' point of view as well. The Jallikattu events held at Dindigul and Avaniyapuram a year ago and the discussions held offered some lessons. Jallikattu could have its place in conserving the native Pulikulam or Kangayam breed of cattle if proper judicious adjustments are made to save cruelty to animals and injuries to people. Jallikattu becomes an incentive for rearing a breed – it is surely an effective system of breeding. The bull that wins is declared the temple animal and it can be used by farmers to mate their cows. The offsprings of the bull winning the Jallikattu will be decidedly stronger.

Jallikattu may not be a scientific technique to conserve the breeds, but its role in conservation of the local breed can not be ignored in view of the importance of local cultural practices.

How to infuse cultural strengths to conservation of livestock breeds

Following steps are needed:

1. There is a need to take further steps to preserve, protect, and promote the traditional cultures and knowledge of the indigenous people.
2. Local knowledge and the local strengths must be provided the opportunity for education and scientific study.
3. There is a need to involve related non-government organizations as at times it is easy for NGOs to interact and get across to tribal people and local communities and they can work in unison with the local culture.
4. There is need to sensitize and educate concerned officials at the state and especially at the local levels to understand and respect the culture differences.
5. Ways and means have to be developed so that benefits can be shared from accessing traditional knowledge.
6. Indigenous people should be fully involved in every stage of policies and plans related to sustainable development.
7. Young people should be encouraged to learn more about their cultural heritage and traditions.

Lastly, it needs be underlined that conservation of Cultural Resources and conservation of Animal Genetic Resources are both intertwined and can be achieved only through the empowerment of indigenous communities and their development for long term sustainable benefits to the Indian people.

Epilogue

India is the cultural hub of the world and offers culture based means and methods to develop and conserve local livestock breeds – such techniques are superior to the scientific based 'number increasing' methods for conservation. It is appreciated that conservation of nature and natural resources was an innate aspect of the Indian psyche and faith, it is reflected in religious practices, folklore, art and culture permeating every aspect of the daily lives of Indian people. Based on this current strength, now, as the awareness is increasing regarding the superiority of local breeds in the local milieu, it is necessary to understand and support the communities by taking a joint approach with NGOs and individuals are who are coming forward to develop and conserve the local breeds including by forming breed societies.

LP-18

SCOPE AND PROSPECTS OF CARPET WOOL PRODUCTION IN ARID ZONE OF INDIA

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In India, sheep is an important livestock species and it contribute immensely to the agrarian economy by providing gainful employment and income to large number of rural poor especially socially backward, marginal and landless labourers. The sheep rearing has importance in geographically difficult regions including arid, semi arid and mountainous areas where crop and dairy farming are not economical and viable. India ranks third in sheep population and account for nearly 6% of world sheep population, currently India has 65.06 million sheep as per Livestock census 2012. The wool production is almost stagnant in the country for last one decade, however, the slight increase was achieved in wool production to about 48 m kg in 2013-14 from last year 46.1 m kg (BAHS, 2014).

In India sheep are mostly reared for wool and meat. A number of rural based industries use wool and sheep skins as raw material. In addition to this, sheep manure is an important source of soil fertility. Sheep rearing is important source of livelihood and income generation activity for economically poor, uneducated, socially backward and migratory people (Suresh *et al,* 2011). This sheep sector ensure them self-employment and family labour under extensive system and act as cushion at the time of drought and famine (Kumar et al, 2013). However, in country the handmade carpet alone exports have crossed Rs. 8559.01 crores during 2014-15 fiscal year. Woolen industry provides employment to about 2.6 million people. Out of total production of raw wool in the country about 70% is carpet grade, 20% coarse grade and 10% apparel grade (Karim and Shakyawar, 2011). In world scenario the 37% of world is classed as fine wools, 22% as medium wools, and 41% as coarse wools. Two thirds of wool is used in manufacture of garments and about one third in carpets, upholstery and rugs. (Naqvi, 2013). Besides this sheep also significantly contributes to mutton production which increased to 441.14 m kg and total export earning of Rs. 250 crores from meat and animal casing and processed meat.

Sheep genetic resources in India

There are 42 well defined breeds of sheep in India which can be divided mainly into four regions on the basis of the agro climatic conditions and type of sheep available. Out of these regions, North Western, Central arid and semi arid region is important from the point of carpet wool breeds. These region comprises the state of Punjab, Haryana, Rajasthan, Gujarat, plains of Uttar Pradesh and Madhya Pradesh having carpet wool type sheep breeds viz Chokla, Nali, Marwari, Magra, Jaiselmeri, Pugal, Malpura, Sonadi, Pattanwadi, Muzaffarnagri, Jalauni, Hisardale and Kheri. These region has second largest population of sheep of four regions and wool produced is mostly suited for manufacture of carpets. The produced wool is mostly suited for manufacture of carpets. It was reported that nearly 50% of Sheep population of this region produces 2/3 of carpet grade wool and Rajasthan alone with 16 million sheep contributed 40% to Indian wool production (Acharya, 1982). Out of total sheep population 90.8 lakhs in Rajasthan

75.7% are in arid zone and one third wool (15 m kg) of country is produced in this area. Breeds like Magra and Chokla are excellent in quality wool and have inherent potential of 2.25 to 2.50 kg wool/sheep. There is great demand of wool in arid Rajasthan for yarn production. India ranks 6th amongst clean wool producer countries and 9th amongst greasy wool producers. Indian wool is almost exclusively of broader micron and used in manufacturing of carpets and rugs. The produced wool is mostly suited for manufacture of carpets.The different sheep breeds of different agro climatic zone are mentioned in Table-1.

Table-1. Sheep breeds of India in different regions

S. No.	Region	Sheep breeds
1	North Temperate	Changthangi (CW), Bhakarwal (CW), Gaddi (CW), Gurez (CW), Karnah (AW), Kashmir Merino (AW), Poonchi (CW), Rampur Bushair (CW)
2	North-Western Arid and Semi Arid	Magra (CW), Marwari (MCW), Chokla (CW), Malpura (MCW) Jaisalmeri (MCW), Jalauni (MCW), Kheri (MCW), Muzaffarnagari (MCW), Nali (CW), Patanwadi (CW), Pugal (MCW), Sonadi (MCW), Munjal (MCW), Hisardale (MCW).
3	Southern Peninsular	Bellary (MCW), Coimbatore (MCW), Daccani (M), Hassan (M), Kanguri (M), Kilakarsal (M), Madras Red (M), Mandya (M), Mecheri (M), Nellore (M), Nilgiri (AW), Rammand White (M), Tiruchy Black (M),Vembur (M)
4	Eastern	Balangir (MCW), Bonpala (MCW), Chottanagpuri (MCW), Ganjam (MCW), Garole (MP), Tibetan (CW), Kendrapara (MP)

Within parenthesis is the major utility of the breed: (AW) Apparel wool; (CW) Carpet wool; (MCW) Mutton and Carpet wool; (M) Mutton; (P) Prolificacy.

In north-western arid and semi arid region sheep farming extensively depends on pastures and rangelands for the nutritional requirement (Suresh *et al,* 2007). Sparse vegetation and low carrying capacity and in most of the year's drought condition compel sheep breeders to migrate in surrounding states for livelihood. The migration was mainly temporarily and started with the initiation of crisis of grazing and ends with onset of monsoon (Narain and Kar, 2005). This resulted to decline in wool production in this region from 28.5 million to 18.9 million kg in last decade (2002-2011). Since 80's the sheep population increase to 1.5 times from 48.4 million to 65.06 million. The major growth of sheep population observed in south peninsular region having coarser wool breed mainly reared for meat production. This can cause to drop off per unit wool production from 0.9 Kg/ sheep/ year to 0.7-0.8 kg/per sheep/ year. Although, over the years wool production increases with marginal growth rate of 1% from 40 million to 45.4 million kg.

Table 2. State wise wool production of India for period 2001-02 to 2010-11 (000'S Kg)

State	2004-05	2005-06	2006-07	2007-08	2008-09	2009-10	2010-11	2011-12	2012-13
North western arid and semi-arid region									
Rajasthan	15049	15405	15685	15451	12664	12529	12277	13192	14007
Haryana	1304	1136	1121	1121	1200	1246	1287	1333	1370
Punjab	566	712	513	435	451	485	506	532	558
Gujarat	2950	3123	2962	2996	2857	2919	2918	2819	2664
U P	1965	1459	1461	1481	1503	1523	1543	1420	1456
M P	681	431	428	401	381	370	372	413	442
Sub Total	**22515**	**22266**	**22170**	**21885**	**19056**	**19072**	**18903**	**19709**	**20497**

Southern peninsular region									
A P	3678	3978	4230	4407	4507	4605	4832	4924	5030
Karnataka	5484	5598	5599	5631	7137	7165	7179	7779	8020
T N	750	750	750	25	25	31	1	1	1
Maharashtra	1620	1640	1667	1677	1707	1726	1448	1469	1503
Sub Total	**11536**	**11966**	**12246**	**11740**	**13376**	**13527**	**13460**	**14173**	**14554**
Eastern region									
Arunachal Pradesh	16	14	14	12	15	16	14	17	18
Bihar	378	220	231	241	250	260	260	266	267
Chhatisgarh	255	244	245	165	165	166	114	104	107
Jharkhand	148	150	146	147	149	136	149	202	159
Sikkim	4	2	1	1	1	1	1	1	1
W B	659	666	673	680	687	697	705	713	722
Sub Total	**1460**	**1296**	**1310**	**1246**	**1267**	**1276**	**1243**	**1303**	**1274**
North Temperate region									
H P	1600	1603	1605	1607	1618	1614	1642	1648	1649
J & K	7120	7400	7400	7040	7133	7282	7382	7530	7681
Uttaranchal	349	353	355	360	368	353	362	371	400
Sub Total	**9069**	**9356**	**9360**	**9007**	**9119**	**9249**	**9386**	**9549**	**9730**
Grand Total	**44575**	**44884**	**45085**	**43881**	**42819**	**43124**	**42991**	**44734**	**46055**

(Source: State Animal Husbandry Department)

Wool Production and Utilization

According to Government of India (GOI) estimates, for fiscal year (FY) 2012-13 (April-March) raw wool production was 46.1 million kilograms (kg), which has decreased in the last 10 years due to a lower sheep population. The GOI 2012 livestock census reported that since 2007 the sheep population declined by 9.07 percent to 65 million. The average annual GFY is 0.9 kg per sheep, much lower than the world average of 2.4 kg per sheep. Sheep farming is generally unorganized, and lacks sufficient veterinary or extension services. Most wool is produced in Rajasthan, Karnataka, Jammu and Kashmir, Andhra Pradesh, Gujarat, Himachal Pradesh, Maharashtra, and Uttar Pradesh.

In general, Indian wool is coarse, and considered to be of low quality (28 microns and above); it is primarily used to manufacture hand-made carpets. India's agro-climatic conditions do not favour higher quality wool production. Only some areas that border the Himalayas produce finer grade wool. Out of the total production of raw wool about 70% was carpet grade which is mostly used in hand knotted, tufted and woven carpets. Woollen industry in India is small in size as compared to cotton and synthetic fibre based industry, wool and woollen activities in rural areas are having important position. The woollen industry including carpet sector contributes more than Rs. 8559 crore (Anonymous, 2015) in export earnings. Moreover the industry provides employment and source of sustenance to about one million people mostly belonging to low income group.

Presently, the total wool production in India is not enough to meet the total requirement of raw wool for woollen industry. The bulk of Indian wool is of coarse quality and is used mostly in the hand-made carpet industry. Carpet industry need by utilizing all the carpet grade wool produced in the country which is only 1/3 of total consumption of 70 million kg of raw wool. To meet the growing demand indigenous wool production increases from 38.8 million kg to

49.5 million kg by the end of last decade (1992-93 to 2001-02). The maximum wool production was observed to 50.5 million kg in 2002-03 and afterwards recorded declination due to draught condition and fall down to 47.9 million kg in year 2013-14 (Table-4). Over the period of IX and X plan the compounded annual growth rate (CAGR) of a negative 0.4%. After wards by the end of X plan wool production increase to 45.1 million kg with marginal growth of 1%. In starting years of XIth plan wool production further drop down and reach to minimum to 42.8 million kg in year 2008-09. The current wool production in India 47.9 million kg and it is expected that it will produce 65 million kg of wool by 2050. Rajasthan is still main carpet grade wool producing states in India (Table 3).

Table 3. Major carpet grade wool producing states in India (2014-15)

S.No.	States	Wool Production (Qty. in million kg.)
1	Rajasthan	15.03
2	Jammu & Kashmir	8.71
3	Karnataka	7.75
4	Andhra Pradesh	5.04
5	Gujarat	2.58

Source: Animal Husbandry Department, Ministry of Agri.

Table 4. Wool Production in India during different years

Year	Wool Production (Million Kg)
1995-96	42.4
1996-97	44.4
1997-98	45.6
1998-99	46.9
1999-2000	47.9
2000-01	48.4
2001-02	49.5
2002-03	50.5
2003-04	48.5
2004-05	44.6
2005-06	44.9
2006-07	45.1
2007-08	4.9
2008-09	42.8
2009-10	43.1
2010-11	43.0
2011-12	44.7
2012-13	46.1
2013-14	47.9

Source: Animal Husbandry Department 2015

Wool Import: The production of wool in the country is not sufficient to meet the demand of the wool industry including carpet sector and most of it is being imported from Australia, New Zealand and many other countries. The present requirement of different segments of Indian woollen industry is likely to grow further because of higher domestic as well as export need of woollen items (Table-5). There has been a shift from imports of fine quality wool to low quality wool in recent years. This is on account of consumer preference for hand tufted carpets in the US and other western markets. Cheap wool import from the Middle East is also constantly growing and is mixed with indigenous wool to make hand tufted carpets. Import of raw wool from Australia, New Zealand and many other countries are given in Table-6.

Table 5. Import of raw wool in different years

Year	Quantity (M. Kg)	Value in crores (Rs)
2006-07	99.56	1077.45
2007-08	93.07	1089.51
2008-09	65.73	1031.86
2009-10	68.26	1000.77
2010-11	94.77	1434.65
2011-12	76.29	1876.87
2012-13	77.16	1801.90
2013-14	89.6	1967.72
2014-15	96.5	2125.74

(Source: DGCI&S, Kolkata)

Table 6. Import of raw wool from different major countries in 2014-15

S.No.	Country	Quantity in tones
1	Australia	17084
2	Pakistan	8089
3	New Zealand	7422
4	Syria	11225
5	Italy	3432
6	Turkey	1424

(Source: DGCI&S, Kolkata)

Woollen industry: The woollen industry in the country is of the size of more than Rs 10,000 crores and broadly divided and scattered between the organised and decentralized sectors. There are around 958 woollen units in the country, majority of which are in the small scale sector. The industry has the potential to generate employment to the 12 lakh person in organised wool sector. Further, there are 3.2 lakh weavers in the carpet sector. Today India is the world's largest producer and exporter of handmade carpets in terms. Around 70-75% of carpets manufactured in India are exported and handmade carpets are exported to more than 70 countries in the world, the US being the largest importer (Table-7). Indian carpets are known worldwide for their excellent designs, fascinating colours and quality. The four major regions making hand-knotted carpets are Jammu and Kashmir, Jaipur-Agra-Gwalior, Bhadohi, Mirzapur and Warangal-Eleru. But the, country's major carpet production is at Bhadohi-Mirzapur and Jaipur, amounting to about 80%. However, the major carpet yarn production centres are Bikaner (70-80%), Bhilwara, Kekri, Beawar in Rajasthan, Panipat (Haryana) and Bhadohi (UP). Most of the yarn produced in different centres is sent in scoured stage to Bhadohi where it is dyed in desired shades. The yarn number generally spun is 2 to 5 Nm and the wool utilized for such spinning varies from 32 to 37 micron.

Table 7. Major countries importing handmade carpets and other floor covering from India

S.No.	Country	Values in crores (Rs)		
		2012-13	**2013-14**	**2014-15**
4	USA	2501.52	3117.22	3701.81
5	UAE	304.83	648.87	1309.89
2	Germany	657.76	665.51	680.25
8	UK	548.29	484.49	457.88
1	Australia	179.42	201.71	220.07
6	Netherland	96.65	113.74	141.79
3	Canada	118.81	141.29	131.24
7	Italy	83.99	98.89	102.24
8	Others	1386.03	1638.70	1744.14
	Total	**5877.30**	**7110.42**	**8459.01**

Source: DGCI & S, Kolkata Data

Wool Mandis: The largest *mandi* for wool trading is located at Bikaner as the surrounding area produced very good quality of Chokla and Magra wool beside regular qualities of wool ranging from 30 to 38 micron and very much suitable for production of carpet and durries. The very good quality of wool is also coming from Barmer, Jaiselmer, Kolayat in Bikaner *mandis* (Table-8). Weaving of carpet started in Bikaner in Bikaner jail before independence where some very high quality carpets were made and exported overseas also these carpets were very popular in royal families of Rajasthan and other parts of India. Hand knotted carpets were also made in some nearby villages but approximately 10 years back some companies started with modern carpets like hand tufted, handloom, broadloom and shaggy with their quality wool. Total 250 mills in Bikaner is manufacturing 120 million kg yarn of Rs. 2100 crore for manufacturing carpets. So in coming few years Bikaner will be a great industrial hub of Rajasthan for woollen yarn and carpets production.

Table 8. Arrival and sale of wool in Bikaner mandis (CWDB) in million kg

S.No.	Year	Arrival	Sale
1.	2011-12	10.01	9.77
2.	2012-13	18.83	18.73
3.	2013-14	17.30	17.29

Exports: India does not export raw wool, but does ship intermediate and finished products such as woollen yarn, fabric, clothing, and carpets, which generally have increased in the last few years due to price competitiveness. India exports various woollen products like tops, yarn, fabrics, Ready Made Garments and Carpets. Carpet enjoys maximum share of total export. The aggregate export of woollen items from wool tops to finished products like textiles, clothing, blankets and carpets is currently estimated around Rs. 7000 Crores. During the 11th Plan period, the growth was hindered owing to variety of factors. However there are good opportunities for export growth. Primary sectors which can look forward for export growth are textiles, woven clothings, knitwears and carpets. In order to build growth tempo, the action for reform should be expedited which may also attract FDI to reinforce export outlook through joint ventures for better access to major markets. Major importers of intermediate products included the United Kingdom, United States, South Korea, Japan, Germany, Italy, and United Arab Emirates. The

United States and many western European countries import apparel and clothing, while woollen carpets are mainly exported to the United States, United Arab Emirates, and western Europe (Table-7). Hand tufted and hand-made carpets are the largest share of Indian finished product exports.

Table 9. Exports of woollen items from country in different years (Rs. Crores)

Year	Woollen Yarn, fabrics, Made ups	Ready Made Garments	Carpet (Excluding silk) Handmade	Total
2006-07	379.28	1636.54	3891.47	5907.30
2007-08	373.57	1409.54	3725.79	5508.90
2008-09	456.51	1742.97	3505.37	5704.85
2009-10	424.63	1838.09	3442.93	5705.65
2010-11	501.20	1510.92	4706.68	6718.77
2011-12	725.20	1654.69	4051.21	6431.09
2012-13	659.03	1617.43	5340.77	7617.23
2013-14	684.70	1888.60	6255.83	8829.21
2014-15	1234.61	1901.76	8301.56	11437.90

(Source : DGCI&S, Kolkata)

Role of ICAR-Central Sheep and Wool Research Institute in improving carpet wool type

Central Sheep and Wool Research Institute, Avikanagar was established in 1962 is engaged in research, enhancing productivity of sheep and rabbit and its product utilization, transfer of technologies to sheep breeders. Arid Regional Campus (ARC) was established at Bikaner in the arid ecosystem of Rajasthan in 1974. During early phase, ARC had been involved in developing technologies related to pelt production from Karakul and its crosses with native breed Malpura, Sonadi and Marwari. Now this campus is responsible to carry out the research activities for carpet wool production. The major breeds Magra, Marwari and Chokla are being improved by selective breeding for quality of carpet wool.

Important sheep breeds of arid region: Performance and improvement programme

1. *Magra Breed:*

Magra is an important carpet wool breed of Rajasthan, and is found in its purest form in Bikaner and adjoining areas of Nagaur, Churu and Jhunjhunu districts. The sheep produces extremely white and lustrous fleece. The wool therefore produced by Magra is most suitable for carpet production and is in great demand due to its lustre. Magra sheep is being improved through selection under research project since 1996-97. An elite flock of Magra has been established with more than 300 breedable ewes. The project was further strengthened by having external funded project from Central Wool Development Board, Ministry of Textile, on Strengthening of ram rearing centre of Magra sheep at ARC to produce more number of superior breeding rams to fulfill the need of the farmers for genetic improvement of their animals. The rams are being selected on the basis of selection index incorporating six month body weight and first six monthly greasy fleece yield. Every year nearly 100 superior breeding rams are being supplied to farmers/Government agencies for genetic improvement in the animals in field. The overall performance of different economical traits of Magra sheep is given in following Table- 10.

Table 10. Performance of Magra at Arid Region Campus, Bikaner

S. No.	Traits	Performance
1	Birth Weight	3.0 Kg
2	3 Month Weight	16.0 Kg
3	6 Month Weight	25.0 Kg
4	9 Month Weight	29.0 Kg
5	12 Month Weight	31.0 Kg
6	First Six Monthly Greasy Fleece Yield	950 g
7	Second Six Monthly Greasy Fleece Yield	1050 g
8	Annual Greasy Fleece Yield	2200 g
11	Fibre Diameter	32.0 µ
12	Staple Length	5.15 cm
13	Medullation	40-45%

Source: CSWRI-50 years of Research (1962-2012)

2. Marwari breed

Marwari is one of important carpet wool producing sheep breed of North Western arid region of India. The breed is hardy and well adapted to harsh and erratic climatic conditions of hot arid region. This breed is largest in number and distributed widely in Jodhpur, Jalore, Nagaur, Pali, Barmer districts of Rajasthan and some parts of Gujarat. The Marwari project became the part of Network Project of Sheep Improvement from August 1993. Since then Marwari breed is being improved for carpet wool production through selection at Arid Region Campus of CSWRI, Bikaner. An elite flock of Marwari has been established with more than 400 breed able ewes. The rams are selected on the basis of selection index incorporating six month body weight and first six monthly greasy fleece yields. The body weight at six month improved by 41.94 percent i.e. from 15.9 kg to 22.6 kg over the period after start of Network Project. The adult annual GFY was improved from 1209 g to 1484 g since inception of Network Project (Table-11). The survivability of animals improved a lot over the years and 96% was recorded in all age groups. The twinning in Marwari breed of sheep is not common feature but twinning percentage in Marwari was enhanced up to 22% in comparison to 2-3% in early years. The available male lambs born in spring, season were ranked on the basis of selection index constructed from 6 months body weight and 6 months greasy fleece weight. The superior breeding rams produced in the project were supplied to the State Animal Husbandry Departments/Govt. Agency/Farmers/NGO/Developmental agency for the genetic improvement in the farmers' flock.

Table 11. Average Performance of Marwari at Arid Region Campus, Bikaner

S. No.	Traits	Performance
1	Birth Weight	3.0 Kg
2	3 Month Weight	16.0 Kg
3	6 Month Weight	23.0 Kg
4	12 Month Weight	32.0 Kg
5	First Six Monthly Greasy Fleece Yield	565 g
6	Second Six Monthly Greasy Fleece Yield	783 g
7	Annual Greasy Fleece Yield	1484 g
8	Fibre Diameter	33-35.0 µ
9	Staple Length	5.17 cm
10	Medullation	50-55%

3. Chokla breed:

Chokla a renowned carpet wool-producing sheep breed and primarily reared for its quality wool and its suitability for migration. In addition to their superior quality wool the animals of this breed are hardy and well adapted to arid and semi-arid environment. The wool produced by Chokla sheep is heterogenous and is generally mixed with coarser fleece of other sheep before utilization as carpet wool. The All India coordinated Research project on sheep breeding was initiated in 1971 at CSWRI, Avikanagar. Since then Chokla was the one of the native breed used for cross breeding with exotic animals for developing different crossbred such as Avivastra and Bharat Merino. From 1991 AICRP on sheep breeding has been converted into Network Project on Sheep Improvement to undertake survey, evaluation & improvement of indigenous sheep breeds. The Project "Evaluation & Improvement of Chokla Sheep for Carpet Wool" was started in April 1992 and continued up to 2013 aiming to improve wool yield. In Year 2013, it was decided to shift the Chokla flock to Arid Region Campus, CSWRI Bikaner which is nearer to its breeding tract to effortless dissemination of superior germ plasm to end users.

Table 12. Performance of Chokla sheep at CSWRI, Avikanagar

S.No.	Traits	Performance
1	Birth weight	2.82 kg
2	Weaning weight	14.29 kg
3	Six month weight	24.83 kg
4	Twelve month weight	30.29 kg
5	First six monthly GFY	1438 g
6	Adult Annual GFY	2386 g
7	Average fibre diameter	34.84 μ
8	Medullation	33.87%
9	Staple length	6.48 cm

Chokla flocks were kept under semi-intensive system and there is significant improvement in the body weight at different ages over the years. Six month body weight of 24.83 kg, 12 month body weight of 30.29 kg was achieved with change in concentrate supplementation regime during the period 2009-2011. The results showed that superior carpet wool producing Chokla is also having immense growth potential. However, major emphasis remains on improving carpet wool production. Overall least square means in 2009-11 for first six monthly GFY and Adult annual GFY were 1.438 kg and 2.386 kg, respectively (Table-12). Since 1992, a total of 250 rams were sold to the farmers/Govt. of Rajasthan/NGOs for breed improvement programme.

4. Pugal Breed:

Pugal is a medium carpet wool producing sheep breed of Rajasthan which is only present in Bikaner district. The communities responsible for maintaining this breed are Raika, Muslim, Rajput, Jat and Meghwal. Pugal sheep animals are known as "Rataanaa" in the field. The animals of this breed are generally found mixed with Magra, Nali and Jaisalmeri sheep in the flocks and percentage of pure Pugal breed animals in farmers flock ranges from 5-70%. The population of Pugal sheep is declining very fast because of farmers' choice to use Magra breed rams in their flocks. A National Agricultural Technology Project (NATP) entitled "Characterization and conservation of Pugal sheep" was initiated at ARC of CSWRI, Bikaner in 2000 and completed in 2004 to characterize and conserve the breed. The conservation of elite germ plasm could be of great use to re-develop the breed, if it extinct completely in future due to indiscriminate breeding with other breeds and continuous trend of reduction of Pugal sheep population in the fields (Dass *et al*, 2005). The average performance of Pugal breed based on field data is given in Table-13

Table 13. Performance of Pugal sheep at Field level

S. No.	Traits	Performance
1	Birth Weight	2.62 Kg
2	3 Month Weight	17.9 Kg
3	6 Month Weight	23.5 Kg
4	12 Month Weight	29.7 Kg
5	First Six Monthly Greasy Fleece Yield	557.5 g
6	Second Six Monthly Greasy Fleece Yield	513.8 g
7	Annual Greasy Fleece Yield	1618.3 g
8	Fibre Diameter	34.4 μ
9	Staple Length	6.07 cm
10	Medullation	59.1%

Crossbred Sheep developed for carpet wool

Avikalin: At CSWRI Avikanagar, a crossbreeding experiment for improving carpet quality wool production was initiated in 1964-65 involving exotic fine wool breed (Rambouillet) and native extremely coarse wool breed (Malpura). Since the beginning of 1975 the half bred have been pooled and interbred and the new strain arising out of this base having 50% Rambouillet and 50% Malpura inheritance were named as Avikalin (Singh *et al,* 2006). The crossbreeding of extremely coarse and hairy breeds like Malpura with Rambouillet has shown that half-breds from such crosses yield more wool of excellent carpet quality than native Malpura. The Avikalin strain evolved out of this crossbred base is able to produce about 2 kg greasy fleece annually of 25-micron fibre diameter, 25 percent medullation and about 4.5 cm staple length. The wool produced by Avikalin is superior to the carpet wool produced by indigenous breeds.

Improvements in Magra breed in farmers flock in field condition

A field unit of Magra sheep has recently been started at Arid Region Campus, CSWRI, Bikaner under Network project on Sheep Improvement, ICAR, New Delhi. The Technical Programme of NWPSI is conceptually based on selection and Progeny Testing of indigenous sheep breeds with the involvement of field flocks in its native tract. The unit will have four centres from which one will be the ram-rearing centre. Each of the other three centres will cover a population of about 1500 sheep. About 9000 sheep of 92 flocks in all the centres have been registered in this programme and first health coverage in form of ET vaccine has been administered to around 10,500 sheep and goat in field. (Patel *et al*, 2013). The field performance of Magra sheep in terms of body weights of lambs & adult animals and wool yield were recorded to assess the production level of Magra flock in its native tract. The overall means of birth weight, three, six and twelve months weights were 3.06 ±0.34, 12.51±0.19, 19.05±0.33 & 27.25±0.31 kg, respectively. The average adult body weights for two and more than two years age were 33.57±0.29 and 36.13±3.83 kg, respectively. Three shearing in a year is practiced in project area, the average GFY in one clip were observed to be 497, 504 and 503 gm for female, male and overall mean, respectively (Patel *et al*, 2014). The programmes will certainly going to have a positive impact on productivity of this breed in adopted villages.

Constraints faced by wool sector:

i) Raw Wool Production

- Low priority of state Governments in development of wool sector.
- Lack of awareness, traditional management practices, lack of education and poor economic conditions of wool growers.
- Shortage of pasture land which force breeders to migrate their flock from one area to another throughout the year.
- Uneconomical return of the produces to sheep breeders particularly from sale of raw wool, milk, manure, mutton, skin etc.
- Lack of motivation for adopting modern methods of sheep management, machine shearing of sheep, washing & grading of raw wool etc.
- Inadequate production and processing facilities of specialty fibres i.e. Pashmina goat wool and Angora rabbit wool.

ii) Marketing of Raw Wool

- Inadequate marketing facilities and infrastructure.
- Ineffective role of state wool marketing organizations in wool producing States.
- Absence of organized marketing and minimum support price system for ensuring remunerative return.
- Minimum return earned from sale of wool by wool growers.

(iii) Processing of Wool

- Inadequate quantity of quality raw wool.
- Out dated and inadequate pre-loom & post-loom processing facilities.
- Inadequate dyeing facilities in wool potential areas.
- Need of designing & diversification of woollen handloom products.
- Dearth of technicians & trained manpower.
- Inadequate testing facilities and quality control measures.
- Transfer of technology is inadequate.
- Lack of operational and technical bench marks.

Conclusion and Recommendations

The problems of sheep farmers are that their views are generally not taken in to consideration while preparing a plan/scheme for sheep production in country. The policy makers should have face to face discussion with sheep farmers before preparing any programme for sheep improvement and their socio-economic upliftment. The following issues are to be taken into consideration.

- The established carpet wool breeds in the country are some time getting diluted due to intermixing with heavy bodied breeds for higher body weight and mutton yield, therefore, there is need to introduce incentive schemes for higher wool yield animals like Chokla, Magra, Nali, Marwari and Jaisalmeri.
- To bring overall improvement in wool production from carpet wool breeds, the implementing agency must encourage the evaluation of indigenous carpet wool breeds of sheep.

- There is need of setting up of Common Facility Centres (CFCs) for machine wool shearing and creating processing facilities for wool and woollens products.
- Increase employment in wool and allied industry and fulfil requirement of skilled manpower and also trained to wool growers with new techniques.
- Strengthening of State Wool Marketing Organizations for marketing facility for raw wool and to ensure remunerative returns to wool growers.
- Since selection within breeds of sheep seems the most favourable method at present for genetic improvement. Selective breeding; upgrading the inferior breeds by use of native improved breeds and Marker Assisted Selection for enhancing wool yield may be adopted in region.

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SP-130

COMPARATIVE MILK METABOLITE PROFILING FOR EXPLORING SUPERIORITY OF INDIGENOUS COW MILK OVER EXOTIC AND CROSSBRED COUNTERPARTS

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Cow milk and products from the native cattle are used in India for health promoting, disease-preventing and therapeutic purposes since ancient times. In the backdrop of this knowledge, claims are made that the Indian cow is a very unique species. Therefore, this research was conducted to generate the milk metabolite composition of Indian (Sahiwal), exotic (Holstein Friesian) and their crossbred cow from the same livestock farm, under similar production system and using identical methodology to provide scientific data for the superiority of indigenous cow milk, if any. The milk composition of indigenous cattle raised in extensive system of management under zero input was also included for the comparison. Percentage of fat, total solid and lactose was highest in the Sahiwal milk as compared to that of HF or crossbred under intensive feeding, whereas variation in protein was much closer. Grazing indigenous cattle produced milk richer in all these components. Fifty fatty acid traits were compared. Cholesterol did not differ across the groups. Majority of milk saturated fatty acids (SFA) differed significantly ($p>0.05$) between farm managed Sahiwal, HF and crossbred cattle. HF milk had significantly higher proportion of saturated fatty acids (75.9%) as compared to crossbred (72.5%) and Sahiwal (68.2%). It was due to the higher proportion of all the three groups of SFA in the HF milk. The trend for total unsaturated fatty acids was just the reverse. It was contributed by MUFA as total PUFA was similar in farm managed cows. The $\omega9$ desaturase indices were significantly lower in the HF and crossbred cattle as compared to that of Sahiwal. Intensive and extensive system of management largely influenced milk FA composition. SFA was lowest in the grazing cattle (62.1%). Their milk can be considered as an augment source of unsaturated fatty acids (38.6%) with higher concentration of MUFA (31.4%) and PUFA (7.2%). Milk was enriched with higher concentration of α–linolenic acid. The $\omega6/\omega3$ ratio (2.7) and the atherogenic index (33.9) were significantly lower than the cattle under intensive management. No ($p>0.05$) difference was observed in the Mineral and vitamin composition of the milk among the farm managed cattle were not statistically significant. Milk of grazing indigenous cows had significantly higher ($P<0.05$) concentration of minerals (Zinc, Iron, Phosphorous and Copper) and all the vitamins except vitamin B5 (Vitamin A, 2 times; β-carotene, 2.29 times; ascorbic acid, 2.9 times and vitamin E, 4.3 times). Significant difference ($P<0.05$) in the amino acid profile of the Sahiwal and HF breed was not observed except for His, Ser, Gly, Lys and Tyr. The total and essential amino acid and content (g/100 g of milk) was highest for the grazing indigenous cattle. The study reveals metabolite characteristics that can be used to promote the use of indigenous cattle under extensive system of management and can be an important tool to maintain native genetic resources characterized by low production levels.

NATIONAL SYMPOSIUM: Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income &
XV Annual Convention of Society for Conservation of Domestic Animal Biodiversity (SOCDAB)
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MEWARI CAMEL: MILK PRODUCTION AND QUALITY

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The *in situ* sustenance of Mewari breed of camel is chiefly due to the production and sale of camel milk. The milk production potential of the breed at the organized farm has been documented by the Centre in it's earlier publication and here we present the first ever systematic recording of the milk production in the breeding tract. Thirty one she-camels were continuously recorded for a period of eleven months. Morning milk production was recorded weekly at the farmers door step. The average per day milk yield in Mewari camels was observed as 4.029±0.027 litres. The milk yield was high in initial four months averaging about 4.5 litres per day and it reduced to 3.6 litres per day in 11th month of lactation. The analysis of milk quality was also carried out and the concentration of Fat, SNF (Solid Not Fat), Protein, Lactose and Ash was recorded as 3.50%, 6.49%, 2.21%, 3.55% and 0.73%, respectively. The pH was recorded as 6.31. It is clear from the data that the Mewari camels are producing on an average 8 litres of milk per day with 3.5% fat. The selection of elite animals for breeding and proper feed supplementation can further increase the milk production and add to the income of camel farmers in the breeding tract.

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COMPOSITION OF EQUINE MILK IN COMPARISON TO DIFFERENT MILK SPECIES

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Milk composition of mammalian species varies widely depending upon genetic, physiological, nutritional and environmental factors. To assess the compositional differences in milk of equines (horse mares and donkey mares) and other different milk species, milk during early lactation was collected from donkeys (12), mares (11), sheep (5), HF cows (14), camel (16) and buffaloes (10). Milk composition of Marwari mares & exotic donkey mares was observed to be almost similar. Further, equine milk contained significantly ($P<0.05$) low fat as compared to sheep, HF cows, camel and buffalo milk but lactose content was at par in milk of all the species studied. Protein content in equine milk was significantly ($P<0.05$) low than sheep and buffalo milk. It was observed that there was significant variation in milk composition of various species studied. Average milk yield (2 hour) of Marwari mare and Exotic donkeys was 0.475±.05 and 0.400±0.04 kg, respectively. Milk yield was non-significantly high in mares as compared to donkeys. Milking is more frequent in mares than other milk species studied. It is also necessary to separate the foal from the mare for some time before the milking process. Mares can be milked up to 5 to 8 times per day depending upon the stage of lactation.

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EFFECT OF AREA SPECIFIC MINERAL MIXTURE FEEDING ON MILK YIELD AND COMPOSITION OF DAIRY ANIMALS OF JAIPUR DISTRICT OF RAJASTHAN

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The present study was conducted to observe the effects of area specific mineral mixture supplementation on milk yield and milk components of dairy animals of four tehsils of Jaipur district of Rajasthan over a period of two months. Eighty five cattle (64 in treatment group, 21 in control group) and 115 buffaloes (92 in treatment group, 23 in control group) were selected randomly from four tehsils of Jaipur district (Bassi, Chaksu, Phulera and Kotputli). Animals from treatment group were fed area specific mineral mixture @ 50 grams/animal/day for a period of 2 months; whereas animals from control group were not supplemented. Both the groups were kept in same managemental condition. Milk yield of these animals was recorded by workers in morning and evening through structured questionnaire. Milk yield and milk components such as milk fat and milk solids not fat were also evaluated from milk samples collected at village level through milk society. In this study, area specific mineral mixture supplementation resulted in increased milk yield particularly during early, mid and later stages of lactation and also affects value of milk component i.e. fat and SNF.

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HOUSING AND HEALTH CARE MANAGEMENT PRACTICES FOLLOWED BY GIR CATTLE OWNERS FOR CONSERVATION OF GIR CATTLE IN AJMER DISTRICT OF RAJASTHAN

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The study was conducted in Ajmer district of Rajasthan, out of 10 tehsils of Ajmer district two tehsils i.e. Bhinay and Bijainagar were selected purposively. Further, four villages from each selected tehsil were identified. From each village 20 respondents were selected randomly. Thus, the entire sample consists of 160 respondents. The field survey was conducted to collect the first hand information on existing housing and health care management practices followed by Gir cattle owners in Ajmer district of Rajasthan. All the cattle keepers had kuccha floor in shed and 55 percent kept their cattle inside dwelling house. About 64.37 percent of the cattle owners used bedding material during winter season. About 68.13% of the respondents had less ventilation provision in animal shed. Results indicated that 90.62 per cent of respondents vaccinate their animal against diseases. Majority 97.50 percent controlled flies by smoke of waste grasses. Only 20.13 percent of respondents practiced deworming measures. About 25 percent of the owners isolate the sick animals from healthy ones.

Keywords: Management practice, Gir cattle, Conservation, Ajmer, Rajasthan

SP-135

LIVESTOCK SERVICE DELIVERY FOR ENHANCING LIVESTOCK PRODUCTION

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Delivery of quality and affordable veterinary services is one of the effective means of enhancing livestock productivity. The extent to which growth in livestock production can be accelerated would depend on how technology, institutions and policies address constraints facing the livestock sector. Livestock services are critical for enhancing productivity and competitiveness. The plethora of studies has indicated that State Department of Animal Husbandry and Veterinary Services are the main and primary provider of livestock services apart from other private and cooperative service providers. A major challenge for delivery of livestock services in India is the provision of adequate services of an acceptable standard or quality. As per the 19th livestock census the state has 6.98% of cattle, 11.94% of buffalo, 13.95% sheep, 16.03% of goat and 2.31% of pig population of the country. In 2015-16, Rajasthan produced 18,500 thousand tons of milk, 1385.30 million eggs, 13415 thousand kg wool and livestock contributed 8% of GDP. The health of the animals of state is being taken care of by 4696 veterinary institutions comprising of 34 Polyclinics (VPC), 775 First Grade Veterinary Hospitals (VHF), 1518 Veterinary Hospitals (VH), 198 Veterinary Dispensaries, 2171 Sub-Centres (SC). Apart from the state government, some private organisations, NGOs, dairy cooperatives, private vendors etc. are also playing important role in delivering the livestock services to the farmers. Technical intervation include control and prevention of major disease which are the major causes of mortality and morbidity affecting off-take rates. Livestock service delivery system improve fertility and reproductive rates. Development of feed resources and improved feeding practices are the key to increase per capita animal output. The major impact of the livestock service delivery is undoubtedly increased access to promote the development of sustainable and profitable production system.

Keywords: Competitiveness, Cooperative, Per capita, Sustainable, Veterinary Institutions, Veterinary Services.

SP-136

REDUCING THE LIVESTOCK RELATED GREEN HOUSE GASES EMISSION BY BALANCED RATION

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Livestock production contributes to climate change when the green house gases methane, nitrous oxide and carbon dioxide are produced and released into the atmosphere. Ruminants are major culprits of the production of methane. It is therefore important for livestock farmers to try and find ways of reducing these emissions. Green house gas emissions may be reduced by improving feeding practices, increasing productivity through breeding or by reducing earth's temperature. Methane emission from livestock are mainly a result of enteric fermentation and eructation of methane represents a loss of energy to the animal. Mitigation options for enteric fermentation may either be aimed at an increased animal productivity such as increasing number of lambs produced or aimed to effect rumen functioning like increased levels of starch or the use of additives. To reduce these green house gas emission through the adjustment of feed the main focus is on the balance between proteins, starch and fibre in the diet. Methane emission may be reduced by feeding morec oncentrate and reducing the intake of forage. Forage quality may be improved by feeding forage that has lower fibre and higher soluble carbohydrates. Cellulose and hemicelluloses ferment more slowly than non structured carbohydrates thereby yielding more methane per unit of substrate digested. There are a number of additives that have been proposed for the reduction of methane emission such as ionophores, antibodies, halogenated compounds (condensed tannins, saponins or essential oils) and propionate precursors (fumarate and malate).

SP-137

UTILISATION OF WHEY: AS READY TO SERVE (RTS) BEVERAGES

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Whey is the largest by-product of huge dairy industry and is one of the most troublesome byproduct produced which in Biological Oxygen Demand (BOD) value of waste water making the disposal costly and problematic. A value added functional beverage is formulated utilizing unprocessed liquid whey. Whey based beverages with different concentrations of fruit juices and standard ingredients of Ready to Serve (RTS) beverage were prepared. Ready-to-drink beverages

offer the advantages of convenience and portability to today's busy consumers. Utilization of whey for the conversion into best beverage would be one of the important ways to utilize it. Nutritive value of whey may be increased by the addition of some simple ingredients. Whey proteins are often the preferred source for ready-to-drink protein beverages because of their excellent nutritional qualities, bland flavor, ease of digestibility, and unique functionality in beverage systems.

Keywords: Whey, BOD, RTS.

SP-138

EFFECT OF DIETARY SUPPLEMENTATION OF AJWAIN ON THE HEMATOLOGICAL PARAMETERS AND BENEFIT COST RATIO OF PRATAPDHAN CHICKENS

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The present study was conducted to investigate the effect of dietary supplementation of Ajwain on the hematological response and benefit cost ratio of Pratapdhan chickens. Day old unsexed Pratapdhan chicks (n=120) were randomly design in 4 treatment groups with 3 replicates, each consisting of 10 chicks. Three treatment groups were as follows – T_1 : Basal diet as per BIS standards; T_2 : Basal diet supplemented with 0.1% Ajwain; T_3: Basal diet supplemented with 0.2% Ajwain; and T_4 : Basal diet supplemented with 0.3% Ajwain. The chicks were kept under uniform managemental conditions on deep litter system from day 0 up to 8th weeks of age. Among the hematological parameters, Hb found highest in T_3 (11.9 ±0.57) followed by T_2 (11.47±0.38), T_4 (11.37±0.21) and T_1 (10.50±0.36), PCV found highest in T_4 (40.45±0.11) followed by T_3 (40.18±0.07), T_2 (39.40±0.13) and T_1 (37.63±0.54), TEC found better in T_3 (11.9 ±0.57) followed by T_2 (11.47±0.38), T_4 (11.37±0.21) and T_1 (2.0±0.36), TLC found better in T_3 (28.02 ±0.03) followed by T_4 (28.01±0.04), T_2 (27.66±0.10) and T_1 (26.08±0.06). The highest Benefit cost ratio (1.85) was observed in T_3 groups followed by T_2 (1.78), T_1 (1.70), and T_4 (1.67). Thus, it can also be concluded that, the supplementation of Ajwain at 0.2% level was found beneficial in improving hematological profile. It can also beconcluded that Ajwain can be used as efficient, effective and economical alternative to chemical growth promoters in poultry industry.

SP-139

CHARACTERIZATION AND EVALUATION OF MILK COLOSTRUM DERIVED LACTOFERRIN OF SAHIWAL COWS FOR ITS ANTI-CANCEROUS POTENTIAL

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Lactoferrin (Lf), a bioactive glycoprotein is a member of transferrin family and plays an important role in immune defense, iron homeostasis, antioxidant and regulation of cell growth. The present investigation was undertaken to sequence characterize the Lf gene in Sahiwal cattle and further evaluate its anti-cancerous potential against breast cancer cells. Sequence information was generated for complete coding (17 exons) and 5’ and 3’- untranslated regions. The analysis has shown an ORF of 2127 bp with 780 amino acids. Comparative data analysis of Sahiwal and *Bos taurus* revealed a total of 15 SNPs with distribution of 2 SNPs in 5’-flanking region, 1 in 5’-UTR, 10 in CDS region. Out of 10 SNPs in CDS region, 7 were non-synonymous - I145V, S538T, T546N, T596S, D621E, K627E, and H632R. Further analysis of nsSNPs by SIFT, PROVEAN, I-Mutant and PloyPhen-2 tools revealed their non-deleterious nature. On molecular docking with lipopolysaccharide ligand different docking scores were obtained for these nsSNPs indicating their potential effect on anti-bacterial activity. To evaluate anticancer potential, Lf was purified from colostrum of Sahiwal and Karan Fries cow using HPLC and its high purity was further confirmed by LC-MS. A protocol was standardized successfully to purify Lf protein from cow colostrum milk. The results indicated sufficient quantity of Lf purified from colostrum of Sahiwal cows (6.0 mg/ml) using HPLC-AKTA-prime plus in SP-Sepharose prefilled beads. The protein fraction collected from HPLC were analyzed by SDS-PAGE and LC-MS techniques to confirm the purity of Lf protein. The Mascot analysis revealed a molecular mass of 80.12kDa of purified protein. Different concentration of Lf ranging from 125-2000 µg/ml were used to evaluate the dosage and time points (24h, 48h, and 72h) for cell culture studies. A dosage of 750 µg/ml of Lf and time point of 48h and 72h was selected for further experimentation. Both MDA-MB-231 and MCF-7 cells were treated with 750µg/ml of Lf from three different sources; Sahiwal Lf (SAC-Lf), Karan Fries-Lf (KFC-Lf) and Commercial-Lf (C-Lf) for 48h and 72h and parameters like LDH based cytotoxicity assay, cell viability, Annexin V based apoptotic and cell proliferation assays were measured. All three sources of Lf showed a significant ($p<0.05$) increase in cytotoxicity level in both the cancerous cell types compared to untreated cells. Comparatively, Lf from commercial source (C-Lf) had maximum effect on cytotoxicity, cell viability, cell proliferation and induction of apoptosis in MDA-MD-231 and MCF-7 cells followed by SAC-Lf and KFC-Lf. Further, the effect of Lf treatment was also evaluated through changes in expression of genes associated with apoptosis (*Bax, Bcl-2*), tumor progression (*p53, p21, CD44, NF-κβ*) and cell survival (*survivin*) in cancerous cells. The overall results strongly emphasized to the fact that Lf purified from cow colostrum has the capacity to inhibit the growth of cancerous cells albeit to a varied extent. The findings of the present study have indicated the therapeutic potential of lactoferrin as an anti-tumor agent which should be further validated using *in vivo* models.

SP-140

EVALUATION OF PHYSIOLOGICAL, HEMATOLOGICAL AND TRANSCRIPTOMIC CHANGES IN RESPONSE TO ENDURANCE EXERCISE OF ZANSKAR PONIES ADAPTED TO HIGH ALTITUDE OF LADAKH REGION

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NATIONAL SYMPOSIUM: Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income &
XV Annual Convention of Society for Conservation of Domestic Animal Biodiversity (SOCDAB)
8-10 February 2018 at College of Veterinary & Animal Science, Rajasthan University of Veterinary & Animal Sciences, Bikaner (Rajasthan)

Zanskar pony, a native breed of Ladakh mainly used for transportation in Trans-Himalayan region of India, is well adapted to high altitude hypobaric hypoxia environment. Due to extreme conditions of Ladakh, better endurance of these ponies under hypoxic and extreme cold conditions is of utmost concern for their recruitment in Indian Army. In the present study, a total of 12 Zanskar animals and 6 GS mules maintained at Zanskar Ponies Breeding Unit located inside Siachen Vets of Remount Veterinary Services (RVS), Partapur, Leh were subjected to endurance exercise. The animals were made to travel for about 45-50 min on a hilly track of 6-7 Km (track meant for exercise) with 70 Kg loads. Various physiological parameters like heart rate, pulse rate, rectal temperature, and body temperature were recorded and blood samples were collected from each of Zanskar ponies and GS mules during pre-exercise (T_0), post- exercise (T_1) and post recovery (T_2, 2 hours post resting) stages. The results revealed that, GS ponies had significantly higher PR, DBT, VBT and HT than Zanskar ponies. The RR, PR, HR and RT increased significantly during T1 period and come down to almost normal level during T2 period in both the species. The increase in RR, PR, HR and RT was 1.25, 1.26, 1.18 and 1.01 times in Zanskar ponies and 1.47, 1.44, 1.4 and 1.03 times in GS mules. The SaO_2 did not change significantly after the exercise in both the species. Hence, the physiological data indicated that the exercise regimen carried out during the experimentation resulted in modulation of various physiological responses in the Zanskar ponies and GS mules. Complete blood count (CBC) parameters revealed that, Hb%, PCV%, TEC and TLC were slightly higher in GS mules than Zanskar ponies. Regarding the effect of resting intervals, all the blood parameters related to RBCs such as Hb%, TEC and PCV% decreased during the post-stress period (T1) and again come to normal level during the post-recovery period (T2), although the differences were not statistically significant. The decrease in Hb%, TEC and PCV was 4, 2 and 4 per cent, respectively in Zanskar ponies and 6, 7 and 6 per cent, respectively in GS mules. On the other hand parameters except neutrophils % related to WBCs such as TLC and DLC increased during the post stress period and the differences were significant in TLC, neutrophils%, lymphocytes%, neutrophils count and lymphocytes count. The decrease in neutrophils% was 2 and 25 per cent in Zanskar ponies and GS mules, respectively. Hence, the CBC data indicated that the exercise regimen carried out during the experimentation resulted in modulation of various haematological parameters in Zanskar ponies and GS mules. RNA seq based transciptome data of 9 PBMCs samples, 3 each from pre-exercise (T_0), post- exercise (T_1) and post recovery period (T_2) groups of Znskar ponies were generated to identify genes and pathways associated with endurance exercise at high altitude. The obtained reads were mapped to the Equs caballus genome (Equcab 2.0) using TopHat and Bowtie programmes. To get the FPKM values for each transcript, cufflinks software was used. The analysis of RNA seq data has helped to understand the modulation in transcriptome of Zanskar ponies PBMCs and identify the genes up-or down-regulated in before and after endurance exercise at high altitude. At FDR <0.05, a total of 115 transcripts were found to be differentially expressed across three time points. Several genes related to stress, abiotic stimulus, biotic stimulus, inflammatory response, chemokines, cyclin dependent protein kinase, cell-cell adhesion molecules were shown to be differentially expressed across three time points. Further analysis of RNA seq data is in progress to identify pathways and genes networks. In future, some of these physiological, hematological parameters and molecular parameters could be evaluated as potential biomarkers in selecting ponies with superior endurance trait specifically under hypoxic conditions.

SP-141

A SURVEY ON HYDROFLUOROSIS IN CATTLE AND BUFFALOES IN FLUOROSIS ENDEMIC AREAS OF RAJASTHAN

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Drinking water samples were collected from village Girwar and its adjoining areas, Abu road, district Sirohi (n=16) and village Garudvasi, district Jaipur (n=12) for estimation of fluoride concentrations. Cattle and buffaloes reared in these areas were examined for lesions suggestive of hydrofluorosis *i.e.* lesions in teeth, bony exostosis in metacarpal, metatarsal, ribs and frontal bones and lameness. Dental lesions were scored on a 0 to 5 point scale as suggested by Swarup and Dwivedi (2002). Lameness was scored on a 4 point scale (0: no lameness; 1: mild lameness; 2: moderate lameness and 3: severe lameness). Physical condition of the animal, reproductive status and milk production were also recorded. Mean (±S.E.) fluoride concentration in drinking water in village Girwar and its adjoining areas was found 1.41±0.06 ppm, while it was 1.44± 0.08 ppm in village Garudvasi, Jaipur. Dental lesions were the most common, followed by bony exostosis and lameness in cattle and buffaloes reared in two villages. Poor body condition, hoof deformities, hypogalactia, repeat breeding and anoestrus were other clinical problems recorded in those animals. Dental lesions suggestive of hydrofluorosis were also noticed in human population in those villages.

Keywords: Dental lesions; Exostosis; Fluoride; Hydrofluorosis; Lameness

SP-142

BREEDING AND FEEDING MANAGEMENT PRACTICES FOLLOWED BY GIR CATTLE OWNERS FOR CONSERVATION OF GIR CATTLE IN AJMER DISTRICT OF RAJASTHAN

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The study was conducted in Ajmer district of Rajasthan, out of 10 tehsils of Ajmer district two tehsils i.e. Bhinay and Bijainagar were selected purposively. Further, four villages from each selected tehsil were identified. From each village 20 respondents were selected randomly. Thus, the entire sample consists of 160 respondents. The field survey was conducted to collect the first hand information on existing breeding and feeding management practices followed by Gir cattle owners in Ajmer district of Rajasthan. It was observed that only 37.50% of respondents adopted natural service, 31.25% used indigenous (purebred) under quality of breeding bull. Majority 96.87% can detect heat, 68.75% inseminate their cows at an early heat stage. 65% Gir cattle keepers followed pregnancy diagnosis. Regarding feeding practices, most (58.75%) of the farmers followed group feeding and grazed in fallow/harvested field. 85% of Gir cattle keeper soaked concentrate mixture before feeding, 90% of cattle keepers fed concentrate mixture to cattle in advance pregnancy.

Keywords: Management practice, breeding, feeding, indigenous, soaked concentrate.

SP-143

IMPORTANCE OF COLOSTRUM FEEDING TO NEW BORN CALVES

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The calf must receive the first milk which the cow gives after calving and is called colostrum. The calf should be feed colostrum between 2 to 2.5 liters daily for the first 3 days following its birth. If possible where a cow is milked before calving, freeze some of the colostrum for later feeding to the calf. The digestibility of colostrum increases when it is given at a temperature between 99°F and 102°F. The protein of colostrum consists of a much higher proportion of globulin than doe's normal milk. The globulins are presumed to be the source of antibodies which aid in protecting the animal from many infections liable to affect it after birth. Gamma- globulin level in

blood serum of neonatal calves is only 0.97 mg/ml at birth. It increase to 16.55 mg/ml level after first colostrum feeding at 12 hr and subsequently on the second day shows a peak of 28.18 mg/ml. This level more or less persists till the reticulo-endothelial system of the calf starts functioning to produce antibodies. The protein content of colostrum is 3 to 5 times as that of normal milk. It is also rich in some of the materials, of which copper, iron, magnesium and manganese are important. Colostrum contains 5-15 times the amount of Vitamin-A found in normal milk, depending upon the character of the ration given to the mother during the rest period. Colostrum is also superior to milk in having a considerably greater amount of several other vitamins which have been found essential in the growth of dairy calves, including riboflavin, choline, thiamine and pantothenic acid. Colostrum act as a laxative to free the digestive tract of faecal material. So the feeding of colostrum is mandatory to new born calves.

SP-144

FEEDING STRATEGIES FOR SUSTAINABLE LIVESTOCK PRODUCTION IN ARID REGION OF RAJASTHAN

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Rajasthan is spread over 3.42 lakh Km^2 area, which is 10.41% of total area of India. About 60% area of state is dry arid zone, which spreads in 12 districts of western Rajasthan. Nearly 1/3rd area of arid zone of Rajasthan are wastelands, of which 50% are grazing lands and 45% are sandy wastes (Balak Ram, *et al,* 2005). The occurrence of droughts is common in arid regions which affects agricultural and forage production. Grazing of livestock is a common practice in arid zone of Rajasthan, however, the availability of green fodder is restricted to monsoon and post monsoon months only and during rest of the period livestock graze on dry grasses and crop residues available in cultivated, wastelands and other grazing lands. The availability of fodder is not only less but the quality of fodder is also very poor. The fodder deficit of western Rajasthan is estimated to be as high as 60% of the demand. This situation is further aggravated during drought years. Since the state is facing shortage of dry roughages, concentrates and green fodder, we have to look for alternate feed resources like fibrous crop residues, non-conventional feed resources (NCFR), monsoonal weeds to cope up with the feed requirement in arid zone. High fibre crop residues and NCFR may be subjected to various processing methods such as physical, chemical and biological treatments for their effective utilization. Supplementation of mineral mixtures and common salt is also essential for proper utilization of feeds. Feeding strategies like reallocation of a given amount of feed in the herd, purchase of feed from surplus location, establishment of fodder banks, densification of feeds, Urea treatment of straw, Urea molasses mineral blocks (UMMB), Complete Feed Block (CFB), Multi Nutrient Block (MNB) and Multi Nutrient Mixture (MNM) to supplement nutrients to the livestock for maintaining their health and productivity at sustained levels.

Keywords: Grazing, arid zone, fodder shortage, drought and feeding strategies.

SP-145

EFFECT OF COPPER AND ZINC SUPPLEMENTATION ON BLOOD NEUTROPHILS AND TOTAL LEUKOCYTE COUNT IN KANKREJ CATTLE

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Twenty pregnant Kankrej cows at 30 days before the expected date of calving were selected and grouped into 4 homogenous groups of 5 each as control, supplemented Copper, supplemented Zinc and supplemented combination. Control group fed normal basal diet. Blood sample was collected day of 30th, 15th at pre partum, at day of calving and day of 15th, 30th, 45th at post partum to study neutrophils percentage and total leukocyte count in blood. Maximum increase in blood neutrophils percentage was found in control cows as compared to the supplemented cows followed by Zinc and Copper supplemented cows, respectively. Maximum increase in Total Leukocyte Count Percentage was found in control cows as compared to the supplemented cows. While, minimum increase was found in combination cows. Blood neutrophils percentage and total leukocyte count differed significantly ($P \leq 0.01$) between groups between different days of peripartum period, day of calving and post partum days. There was no significant effect on blood neutrophlis and total leukocyte count due to the interaction of group x days on cows of various group. There was significant difference found in copper, zinc and combination group with the control group. For Copper and Zinc supplemented groups no significant difference was observed in total leukocyte count in blood. Thus micronutrient supplementation improves immunity of an animal.

Keywords: blood neutrophlis, total leukocyte count, Zinc, Copper, Kankrej.

SP-146

STUDY OF EFFECT OF VITAMIN *E'* AND SELENIUM ON FAT PERCENTAGE IN MILK OF KANKREJ CATTLE

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In an attempt to assess the possibilities of improvement in production performance of Kankrej cattle by supplementation of vitamin E and Selenium, an experiment was conducted to investigate the effect of vitamin E and Selenium during transition period in Kankrej cows. A total of 24 cows were selected on the basis of their milk yield, parity and body weight are grouped into

four homogenous treatment groups of 6 each. Out of these, one group served as control, fed as per NRC (2001) wherein no supplementation was given. Cows in treatment groups, Group-1 vitamin E, Group-2 selenium and Group-3, vitamin E + Selenium supplementation were given daily along with control diet. Milk quality in terms of milk fat percentage was determined up to 30 days of lactation. For this purpose, quarter foremilk samples were collected on day of calving and 3rd 7th 15th and 30th day postpartum. Milk fat percentage was calculated by Milkometer. Milk fat percentage of milk differed significantly ($P<0.01$) between groups but milk fat percentage among groups differed non-significantly between different days of lactation period. The interaction effect including group x days was found non- significant. Economics of milk production indicates that return (Rs./cow/day) from sale of milk over expenditure (supplementation and feeding cost) was highest in combination group followed by selenium, control and vitamin E supplementation. Therefore it can be inferred that vitamin E and Selenium supplementation is economically viable and beneficial and it can be adopted to improve milk health and net return from lactating Kankrej cows.

Key word: vitamin E and Selenium. Milk quality. Milk fat percentage.

SP-147

INTEGRATED FARMING SYSTEM FOR RESOURCES CONSERVATION AND ENVIRONMENTAL SUSTAINABILITY

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Conventional agriculture is known to cause soil and pasture degradation because it involves intensive tillage, in particular if practised in areas of marginal productivity. An integrated crop-livestock farming system represents a key solution for enhancing livestock production and safeguarding the environment through prudent and efficient resource use. The increasing pressure on land and the growing demand for livestock products makes it more and more important to ensure the effective use of feed resources, including crop residues. An integrated farming system consists of a range of resource-saving practices that aim to achieve acceptable profits and high and sustained production levels, while minimizing the negative effects of intensive farming and preserving the environment. Based on the principle of enhancing natural biological processes above and below the ground, the integrated system is the combination that (a) reduces erosion; (b) increases crop yields, soil biological activity and nutrient recycling; (c) intensifies land use, improving profits; and (d) can therefore help to reduce poverty and malnutrition and strengthen environmental sustainability. The waste products of one component serve as a resource for the other. For example, manure is used to enhance crop production; crop residues and by-products feed the animals, supplementing often inadequate feed supplies, thus contributing to improved animal nutrition and productivity. Thus a high integration of crops and livestock is often considered as a step forward, but small farmers need to have sufficient access to knowledge, assets and inputs to manage this system in a way that is economically and environmentally sustainable over the long term.

Keywords: Integrated farming system; Crop-livestock; Environmental sustainability; Resource conservation;

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EFFECT OF LACTATION CORRECTION FACTOR ON REPEATABILITY IN SAHIWAL COWS

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A total of 1266 lactation records of 412 Sahiwal cows maintained at Bull Mother Experimental Farm and Government Cattle Farm, Anjora, Durg were used to standarized lactation milk yield for parity. Correction factor was developed by converting entire lactation milk yield on first lactation basis upto three lactations by ratio method. For conversion of total milk yield of a particular lactation on first lactation basis, total milk yield of that particular lactation was multiplied by its corresponding correction factor.The multiplicative correction factors obtained were 1.00, 0.98 and 0.90 for parity-1, parity-2 and parity-3, respectively. Repeatability was estimated taking first two lactation records and first three lactation records, separately by intra-cow correlation method. The repeatability estimate was 0.647±0.054 taking first two lactation records and 0.474±0.058 taking first three lactation records but estimates were more accurate after adjusting the data by the suitable correction factors for parity and thus the repeatability obtained was 0.654±0.05 for first two lactation records and 0.53±0.05 taking first three lactation records. It was concluded in this study that the repeatability after adjustment for parity increases.

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FUTURE NEEDS IN ANIMAL BREEDING FOR IMPROVEMENT OF CATTLE IN INDIA

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The demand for milk, meat and dairy products will increase in coming decades as India's population will reach to 1.9 billion by 2050. Cattle are going to play the most significant role because of its huge and unexplored population with tremendous scope for improvement. There are 41 acknowledged breeds constituting only 20-25 per cent of the total population while the rest as non-descript. The genetic up gradation of these indigenous non-descript cattle with high yielding indigenous breeds even if brings a small increase in productivity, the total milk production will increase tremendously. Crossbred genetic potential for milk production can be fully exploited in the commercial herds so steps must be taken to reduce the crossbred population under the small

holding system. Sire evaluation can be done using MOET and Full sib information for faster genetic improvement. The high producing indigenous cattle population may be increased by replacing the crossbred and non-descript population at the rate of 15-25 per cent per decade as per the model proposed by CIRC, Meerut. The bull mother farm and bull rearing unit for each of the significant breeds of the country need to be established and strengthened. There is need to bring 70% of entire cattle population under genetic improvement program by including all the farmer herd, using AI, reliable field data recording and good implementation of recommended breeding policies. Application of genomics, proteomics, ONBS, MAS, and nanotechnology will lead to development of markers/diagnostics for fertility, pregnancy and associated traits to be used in selection of superior bulls and dams.

SP-150

EFFECT OF NON-GENETIC FACTORS ON MILK YIELD AND MILK CONSTITUENTS OF SAHIWAL CATTLE

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The present study pertained to records on milk production and milk constituents of 100 Sahiwal cattle over a period of 13 years from 2004 to 2016, collected from Animal Genetics and Breeding division of ICAR-National Dairy Research Institute, Karnal, Haryana. To study the effect of various genetic and non-genetic factors on milk yield and milk constituent's traits mixed model least-squares analysis was used for analysis of data. Overall least-squares mean for all lactation traits revealed that overall least-squares mean in the present study of the first lactation 305 days milk yield, first lactation total milk yield, first lactation 305 days fat yield, first lactation 305 days SNF yield, first lactation 305 days protein yield in Sahiwal cattle was found to be 2034.99 ± 111.14, 2314.56 ± 155.89, 95.28 ± 5.19, 172.72 ± 9.80, and 45.19 ± 3.95, respectively. In the present study non significant effect of season of calving, period of calving and age at first calving were found on first lactation 305 days milk yield in Sahiwal cattle. Period of calving and age at first calving had significant effect on FLTMY while, season of calving had non-significant effect on FLTMY in Sahiwal. In this study effect of period of calving was found to be significant on first lactation 305 days fat yield and season of calving and age at first calving had non-significant effect on first lactation 305 days fat yield. The period of calving, Season of calving and age at first calving had non significant effect on FL305 DSNFY. In this study period of calving had significant effect on and FL305DPY.

Keywords: Sahiwal Cattle Non-genetic factors, Milk Yield, Milk Constituents traits.

SP-151

CONSTRAINT PERCEIVED BY RATHI CATTLE BREEDERS IN CONSERVATION OF RATHI CATTLE IN THE BIKANER DISTRICT OF RAJASTHAN

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The study was conducted in Bikaner district of Rajasthan, out of 8 tehsils of Bikaner district two tehsils *i.e.* Bikaner, and Lunkaransar were selected purposively. Further, four villages from each selected tehsil were identified. From each village 20 respondents were selected randomly. Thus, the entire sample consists of 160 respondents. The data was collected through the personal interview. The field survey was conducted to collect the first hand information on constraint perceived by Rathi cattle breeders in conservation of Rathi cattle in Bikaner district of Rajasthan. It was observed that the constraints mostly faced by the respondents were abundance of stray animal (92.5 percent and 90 percent). Lack of good breed-able Rathi cattle bulls (88.75 percent and 91.25 percent). Distant location of veterinary hospital (87.5 percent and 83.75 percent), Repeat breeder (82.5 percent and 86.25 percent), Lack of Gosala's, NGO and conservation society in area for livestock conservation (76.25 percent and 70 percent), Lack of A.I. centers, ill equipped and poor service at A.I. center (68.75 percent and 72.50 percent), Lack of knowledge about importance of animal biodiversity (61.25 percent and 65 percent), Lack of knowledge about concentrate feeding according to milk production (56.25 percent and 62.50 percent), Lack of health care awareness and livestock production improvement program in area (48.75 percent and 55 percent), lack of knowledge about proper sanitation and hygiene (43.75 percent and 50 percent) in both Lunkaransar and Bikaner tehsil, respectively.

Keywords: Constraint, Rathi cattle, conservation, livestock owner.

SP-152

EFFECT OF GENETIC GROUPS ON PERSISTENCY OF MILK YIELD IN (HF×SAHIWAL) CATTLE IN NORTHERN INDIA

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The present study was undertaken with the objective of investigating the effect of genetic groups based on the level of exotic inheritance on persistency of milk yield in crossbred cattle.

The data was subjected to assess the effect of genetic groups on persistency indices by Johansson and Hanson method (P1), Gengler method (P2), Khmel'Nit skii method (P3) and Sturtevent method (P4). The 577 first lactation daily milk yield records of crossbred cattle maintained at GADVASU dairy farm over a period of 25 years from 1991-2015 were utilized to study the effect of genetic groups on persistency indices. Animals were grouped on the basis of exotic inheritance into four groups *viz* <75%, =75%, >75≤87.5% and >87.5%. Data was analyzed by the SAS 9.3 using Least squares analysis as described by Harvey (1987) to study the effect of genetic groups on persistency indices. The genetic groups had non-significant effect on all the four persistency indices because most of animals in the herd had exotic inheritance of 75% or more than 75%.

SP-153

CHEMICAL COMPOSITION OF CERTAIN STRAWS USED AS LIVESTOCK'S FEED IN AND AROUND PALI DISTRICT OF RAJASTHAN

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Different kind of straws viz. *Triticum asetivum* (wheat), *Hordeum vulgare* (barley), *Pennisetum typhoides* (bajra), *Zea mays* (maize), *Cicer arietinum* (gram), *Sorghum bicolor* (jowar), *Cyamopsis tetragonoloba* (guar), *Arachis hypogaea* (groundnut), *Vigna radiate* (moong), *Vigna aconitifolia* (moth) were collected from in and around Pali district of Rajasthan to ascertain their chemical composition. The proximate compositions of these straws were analyzed by standard methods described by AOAC (1999). The DM content ranged from 90.05 to 93.44%. Out of the straws analysed groundnut straw contained the highest % CP of 10.24 which was followed by moth 9.27, moong 8.47, guar 7.8, gram 6.27, jowar 5.83, barley 5.73, wheat 4.04, bajra 3.47 and maize 3.12% CP. The straws of, bajra, jowar, guar, moong, moth, maize, groundnut and gram contained crude fibre 38.78, 30.11, 36.41, 33.20, 27.12, 32.26, 37.59, 26.81, 39.43%, respectively. However, barley contained maximum percentage (45.60) of crude fibre. The average ether extracts content of wheat, barley, bajra, jowar, guar, moong, moth, maize, groundnut and gram was 0.92, 1.63, 1.45, 1.9, 1.12, 2.22, 0.80, 0.95, 1.95, 1.87%, respectively. The percentage of ash was highest in barley (12.86) and lowest in bajra (5.77). The chemical composition of various straws suggested that these could be used to develop a database of straws, which is available in and around Pali district of Rajasthan.

SP-154

DPPH FREE RADICAL SCAVENGING PROPERTIES OF CERTAIN PHYTOGENIC FEED ADDITIVES

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Free radical scavenging properties of ethanolic extracts from different phytogenic feed additives were evaluated for comparison with standard ascorbic acid. Ethanolic extracts of 5 and 10 percent solutions of *Aloe Barbadensis* (aloe vera), *Ocimum tenuiflorum* (tulsi), *Murraya koenigii* (curry leaves), *Moringa oleifera* (drumstick), *Azadirachta indica* (neem), *Trigonella foenum-graecum* (methi) and *Linum usitatissimum* (linseed) were compared for their scavenging against the 2,2-diphenyl-1-picryhydrazyl (DPPH) free radical using colorimetric method. The extracts were capable of neutralizing the DPPH free radical via hydrogen donating activity by 86.75 and 85.99 percent for aloe vera, 86.59 and 89.08 percent for tulsi, 85.98 and 85.42 percent for curry leaves, 87.82 and 87.39 percent for drumstick, 89.81 and 88.04 for neem, 86.04 and 88.34 percent for methi and 86.35 and 86.97 percent for linseed at concentration of 100 and 50 µg/ml, respectively. Highest free radical scavenging properties was found in neem and lowest in curry leaves at 100µg/ml and at 50µg/ml highest free radical scavenging properties was found in tulsi and lowest in curry leaves. These results suggest that these all phytogenic feed additives have a potent radical-scavenging activity against DPPH radical and can be used as a source of antioxidant in livestock and poultry feeding.

SP-155

CHEMICAL COMPOSITION OF NATURAL FEED ADDITIVE FENUGREEK (*TRIGONELLA FOENUM-GRAECUM*) COMMONLY USED IN RUMINANTS IN JAIPUR DISTRICT OF RAJASTHAN

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Natural feed additives have been used all over the world to benefit animals as well as animal production. The use of fenugreek natural feed additive can help to improve animal productivity and increase milk production. Fenugreek is such a feed additive and is derived from a plant that belongs the leguminous family. Fenugreek has been shown to have a positive effect on lactation performance in ruminants such as dairy cow, buffaloes and goats. Fenugreek seed was collected

from in and around Jaipur district of Rajasthan to ascertain chemical composition. The proximate compositions of these straws were analyzed by standard methods described by AOAC (1999). DM content of the fenugreek seed was 91.12. Chemical analysis of different samples revealed that the mean contents (% DM basis) of different nutrients were CP: 24.05, CF: 7.03, EE: 4.08, NFE: 60.66, and ash: 4.18, respectively in fenugreek (*Trigonella foenum- graecum*) seed.

SP-156

CHEMICAL COMPOSITION OF SOME TREE LEAVES AS FODDER FOR RUMINANTS IN JAIPUR DISTRICT OF RAJASTHAN

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Some tree leaves used as fodder in ruminants in jaipur district of Rajasthan such as- Moringa (*Moringa oleifera*), Neem (*Azadirachta indica*) and curry leaves (*Murraya koenigii*) were collected and analyzed for proximate composition for determining their nutritive value. The proximate compositions of these tree leaves were analysed by standard method described by AOAC (1999). DM content of the tree leaves ranged from 33.14 to 39.53%. Out of these tree leaves analysed curry leaves contained the highest % CP of 14.93 which was followed by moringa leaves 14.88% and lowest value was found in 13.77% CP. Neem leaves has the highest crude fibre value that is 21.13% which was followed by moringa leaves 12.70% and curry leaves has the lowest CF that is 7.06%. Moringa leaves has the highest ether extract value 8.93% that is followed by curry leaves 7.45% and lowest in neem leaves that is 2.66%. The highest ash content was found in curry leaves that is 11.96% which was followed by moringa leaves 10.70% and lowest ash content was found in neem leaves 7.78%.

SP-157

FIRST LACTATION TRAITS ARE NOT INDICATIVE OF MATURE LACTATION MILK YIELD IN FRIESWAL COWS

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Frieswal is one of the crossbred cattle strain developed by Central Institute for Research on Cattle, Meerut, India having 5/8 Holstein Friesian and 3/8 Sahiwal inheritance in collaboration with Ministry of Defence. It is essential to assess the genetic potential of animals based on mature age as the milk yield increases with age. So, in the present study, an attempt has been made to predict the mature lactation milk yield based on the first lactation traits. First lactation traits considered under the study were age at first calving, 305 days milk yield, peak yield, service period, dry period and calving interval. The lactation records of 1766 Frieswal animals born between 2001 to 2013 were considered for prediction of mature lactation milk yield from first lactation traits. Out of the total animals used in the study, 78.14 percent had attained mature lactation milk yield within age of fourth lactation itself. The correlation of mature lactation milk yield and peak yield were 0.31 and 0.21, respectively. The correlation of mature lactation milk yield with other first lactation milk yield was very low and it varied from -0.005 to 0.024. Step wise regression model was used to find out the best prediction model and only the 305 day milk yield qualified for inclusion. The equation derived was $Y= 3113.16+0.41\ (MY)$. The R^2 and root mean square error values of the model were 9.4% and 780.84, respectively. Other curvilinear models like algorithmic, quadratic , cubic and exponential models also developed. Quadratic and cubic models indicated that the first lactation traits cannot be used for predictive mature lactation milk yield.

SP-158

SUSTAINABLE PRODUCTION PERFORMANCE OF JERSEY CROSSBRED CATTLE IN EASTERN INDIA

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Sustainability of farm incomes can be maintained by optimizing the balance between maximum production while minimizing cost of production. This could be achieved by maximizing the rate of genetic improvement under breeding programmes. In the present study, data on 305 days milk yield (305MY), total milk yield (TMY), lactation length (LL), average daily milk yield (305 days milk yield/lactation length (305MY/LL)), peak yield (PY) and days to attain peak yield (DPY) up to 6th lactation were analyzed in Jersey crossbred cattle maintained at Eastern Regional Station, ICAR-National Dairy Research Institute, India. Lactation records were edited and the percentage of crossbred cattle completed different lactations was 100, 79.68, 58.39, 38.06, 26.77 and 18.39% in consecutive six lactations. Mixed model least-squares analysis of 996 lactation records (1981-2014) showed that overall least-squares means for 305MY, TMY, LL, 305MY/LL, PY and DPY were 2085.26 ± 63.15 kg, 2327.04 ± 88.76 kg, 345.56 ± 7.48 days, 7.29 ± 0.21 kg/day, 12.06 ± 0.25 kg and 23.49 ± 1.21 days, respectively. Random effect of sire and fixed effect of period of calving, season of calving, genetic group and parity of animals were found to be significant on all the traits except effects of season and genetic group on LL and effect of genetic group on DPY. Heritabilities for 305MY, TMY, LL, 305MY/LL, PY and DPY were estimated as 0.376, 0.369, 0.176, 0.484, 0.398 and 0.148, respectively. Genetic gain as a result of selection for 305MY, 305MY/LL and PY was 67.187, 0.303 and 0.617 kg from first to second lactation; 5.229, 0.064 and 0.00 kg from second to third lactation; 33.899, 0.099 and 0.215 kg from third to fourth lactation. However, the effect of selection declined in subsequent lactations and the genetic gain was observed as -52.603, -0.196 and -0.127 kg from fourth to fifth lactation and -85.791, -0.174 and -0.420 kg from fifth to sixth lactation for the corresponding traits. It was found that Jersey crossbred cattle is more sustainable up to fourth lactation under sub-tropical agro-climatic Eastern region of India.

SP-159

LIFETIME PERFORMANCE OF THARPARKAR CATTLE AND ITS CROSSES WITH HOLSTEIN FRIESIAN (KARAN FRIES CATTLE)

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The present study was conducted on 1991 Karan Fries cows (daughters of 189 sires) and 531 Tharparkar cows (daughters of 75 sires) over a period of 36 years (1979-2014) and 57 years (1958-2014), respectively, maintained at ICAR-NDRI, Karnal. The influence of non-genetic factors on different traits was estimated using least-squares analysis. The overall least squares means of lifetime traits including ALTMY, HL, PL, NC, BE-Wilcox (%), DO (%), DD (%), LTMY-4L, NC-6Y, NC-8Y, NC-10Y, LTMY-6Y , LTMY-8Y, LTMY-10Y, LTFY-6Y, LTFY-8Y, LTFY-10Y, LTSNFY-6Y, LTSNFY-8Y and LTSNFY-10Y in Tharparkar cattle were observed as 8013.07 ± 322.08 kg, 2884.86 ± 49.67 days, 1700.03 ± 49.73 days, 4.63 ± 0.20, 87.07 ± 0.6 percent, 26.03 ± 0.78 percent, 19.82 ± 0.71 percent, 8595.55 ± 220.68 kg, 2.78 ± 0.05, 4.40 ± 0.08, 6.22 ± 0.14, 5337.27 ± 148.48 kg, 9366.257 ± 226.15 kg, 13105.12 ± 448.40 kg, 272.08 ± 17.57 kg, 435.99 ± 24.10 kg, 617.71 ± 51.48 kg, 479.35 ± 30.19 kg, 767.05 ± 41.32 kg and 1093.61 ± 91.41 kg, respectively. The performance across periods did not show a definite pattern, although, a slight decreasing trend was observed in some traits. The animals having optimum age at first calving (around 1200 days) were found with better lifetime performances. Similarly for Karan Fries cattle, the least squares means of these traits were found as 15048.04 ± 338.04 kg, 2526.04 ± 27.89 days, 1509.74 ± 27.82 days, 3.97 ± 0.10, 84.47 ± 0.82 percent, 26.91 ± 0.69 percent, 14.80 ± 0.48 percent, 17403.53 ± 322.13 kg, 3.12 ± 0.04, 4.63 ± 0.07, 6.20 ± 0.14, 13002.46 ± 199.52 kg, 20938.81 ± 405.55 kg, 27956.05 ± 848.52 kg, 556.39 ± 10.91 kg, 883.29 ± 21.56 kg, 1124.44 ± 51.27 kg, 1163.47 ± 23.13 kg, 1841.14 ± 45.69 kg and 2350.74 ± 110.05 kg, respectively. The performance of production traits was observed in positive direction whereas declining trends were observed in fertility traits from earlier to recent periods. The F1 cow was found superior over interbred (KF×KF) and higher crosses (HF×KF). It was also observed that the animals having age at first calving around 900 days (mean AFC of herd) were found to show better lifetime performances. The present investigation concludes that the lifetime fertility of Tharparkar cattle was found comparable with Karan Fries cattle whereas lifetime production of Tharparkar cattle was lower to a great extent as compared to Karan Fries cattle. These findings may be useful in development of sustainable breeding strategies for the cattle in the country.

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EVALUATION OF EFFECT OF NON GENETIC FACTORS ON PRODUCTION TRAITS OF RATHI CATTLE

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This study was based upon 768 lactation records of 177 Rathi cattle maintained a Livestock Research Station, Nohar over a period of 34 years from 1974 to 2008 were analyzed by least-squares technique of fitting constants, described by Harvey (1987).

The averages for different production traits on the basis of overall lactation were 194.58±5.75 days (dry period), 289.01±3.05 (lactation length), 1431.81±78.4 litres (milk yield), 1791.50±18.30 litres (three hundred days yield), 3.83±0.06 litres (milk yield per day of calving interval), 5.97±0.06 litres (milk yield per day lactation length) and 10.48±0.18 litres (peak yield). The effect of season on different production traits were found to be significant except milk yield, milk yield per day of lactation length and peak yield which were found to be non-significant in the present investigation. Dry period and lactation length were significantly lower during winter season as compared to other seasons. However, milk yield in 300 days and milk yield per day of calving interval were significantly higher during winter season and lower during monsoon season.

The effect of period of calving on all the production traits except on milk yield and milk yield per lactation length was highly significant. On the contrary milk yield in 300 days and milk yield per day calving interval were significantly higher in fourth period. The highest peak yield was observed in third period. Regression of lactation length on all production traits was recorded highly significant except on milk yield.

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ASSESSMENT OF LEVEL OF ADOPTION OF IMPROVED ANIMAL HUSBANDRY PRACTICES AMONG LIVESTOCK FARMERS OF VILLAGES OF LADPURA TEHSIL OF KOTA DISTRICT

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Livestock production plays an important role in socio-economic transformation in the rural areas. In the present context rural economy is agriculture based and animal husbandry plays an important role. Livestock farming is one of the most important aspects in rural areas as a continuous source of income. The present study was conducted to assess the level of adoption of improved animal husbandry practices among the livestock farmers of three villages of Ladpura tehsil of Kota district namely Rangpur, Gawdi and Gangaicha. Total of 90 livestock farmers were randomly selected, 30 from each village, having at least one milch cattle/buffalo. Three important practices i.e. Health (vaccination), Nutritional (concentrate feeding) and Reproductive Practices (artificial insemination) were selected to ascertain the level of adoption of these practices among the livestock farmers. The study regarding heath practices revealed that, adoption level of health practices (FMD and H.S. vaccination) 1.8% of livestock farmers had not adopted, 4.44% were in rarely adopted, 10% in sometimes adopted and only 16.66% frequently adopted and 66.66% of them fully adopted the vaccination to their animals. Study about nutritional parameter (Concentrate feeding to livestock), 5.55% of them had not adopted, 7.77% were sometimes adopted, 13.33% were frequently adopted and 73.33% were fully adopted these practices. Study about reproductive practices revealed that use of superior germplasm as insemination to bred their female livestock, 13.33% had not adopted, 8.88% were rarely adopted, 18.88% were sometimes adopted, 27.77% only frequently adopted and 31.11% fully adopted the artificial insemination to bred their female animals. Study revealed that as far as level of adoption is concerned a remarkable proportion of livestock farmers had adopted the Health (vaccination) followed by nutritional (feeding of concentrate) and reproductive practices (artificial insemination).

Keywords: Adoption level, Improved Animal Husbandry Practices, Livestock farmers

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RELATIONSHIP BETWEEN THE SELECTED TRAITS OF THE RATHI CATTLE BREEDERS AND THEIR KNOWLEDGE ABOUT CONSERVATIONAL PRACTICES

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The study was conducted in Bikaner district of Rajasthan. It comprised of 8 tehsil, out of which two tehsil were selected randomly. The selected tehsil were Bikaner and Lunkaransar. Further, four villages from each selected tehsil was identified. From each village 20 respondents were selected randomly. Thus, the entire sample consisted 160 respondents from selected eight villages in two tehsil of the district. Knowledge about conservational practices of Rathi cattle was measured with the help of researcher made knowledge test based on the scale developed by Jha and Singh (1970) and was administrated with slight modifications to suit the present study. The characteristics namely education, mass media exposures, extension contact, training were positively and highly significantly correlated with knowledge, Age and family size had negative correlation and non significant with the knowledge level of the Rathi cattle breeders about Rathi cattle conservational practices in study area. The variables like land holding, herd size, occupation and annual income were positively and highly significantly correlated with knowledge about Rathi cattle conservational practices. Family size had positive and non-significant correlation with knowledge about Rathi cattle conservational practices in study area.

Keywords: Rathi, Conservation, Knowledge.

SP-163

BIOCHEMICAL PARAMETERS AS AN INDICATOR OF KETOSIS STATUS IN DAIRY CATTLE: A PRELIMINARY STUDY

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Ketosis is a major metabolic disorder caused by negative energy balance, characterized by relatively high concentrations of ketone bodies with a concurrent decrease in blood glucose levels. In this study a total of 350 post parturient cows having a history of anorexia and drop in milk yield were included. These cows were screened for ketosis using modified Rothera's test. Based upon test results 40 cows were diagnosed as ketotic. The overall prevalence of clinical ketosis was 11.42 per cent. It was concluded that the maximum cases of ketosis were recorded during 8 to 9 year of age, 3rd and 4th parity, 0 to 2 month post-partum and during winter month. The major findings of the biochemical studies were that there was highly significant increase in ketones (acetone and acetoacetic acid) levels in both serum and urine of affected cows when compared with healthy cows. Hypoglycemia was another major finding recorded in ketotic cows. There was no significant but decreased level of serum insulin in some animals. There was highly significant decrease level of serum cortisol and serum calcium recorded. There were significantly higher urine ketones, serum total protein, serum albumin and serum globulin, serum cholesterol, serum triglycerids, serum total lipids, serum aspartate aminotransferase (AST) and serum alanine aminotransferase (ALT).

SP-164

MANAGEMENT OF PICA IN HOLSTEIN FRIESIAN CATTLE

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Pica is a metabolic disease found amongst livestock, especially in cattle. It usually occurs in a place where there is a deficiency of minerals such as phosphorous and magnesium in soil so the vegetation is lacking in these minerals. Instinctively the cattle seem to seek mineral rich sources of different kinds, for example licks, or eating soil, but also dead animal matter.

When rotting dead animal matter is consumed they can pick up botulism, which causes semi paralysis which can lead to death. A 5 year old Holstein Friesian cross breed cattle turned in to college clinic with history of persistent and compulsive cravings, eating and licking of non-food objects such as soil, stones and licking of wall. Clinical examination revealed pale mucus membrane, tachycardia, emaciated and having appearance of turgid skin. The case was diagnosed as pica in cattle by history and clinical examination. The case was successfully managed by giving of intra muscular injection of Tonophosphan® Vet (Sodium salt of 4-dimethylamino-2 methylphenyl-phosphinic acid 0.2 gm) for 5 days and mineral mixture was advised to fed for 1 month. The sign disappeared gradually after 7 days.

Keywords: Pica, phosphorous, metabolic disease, mineral mixture.

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STUDIES ON THE STORAGE AND ACCESSIBILITY OF BIOACTIVE PEPTIDE RICH BUFFALO MILK YOGHURT

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In the study, anti oxidant potential, physicochemical and microbiological attributes before and after storage for different periods of time (3, 5 and 7 days) of buffalo milk yoghurt fermented with Lactobacillus helveticus were analyzed. Evaluation of fermented buffalo milk product have been done during 7 days of storage period at 4ºC and it were analyzed for change in pH, TA, anti oxidant activity (ABTS and DPPH activity), lipid peroxidation (TBA value) and microbiological study (Plate count, Coliform count, Yeast-Mold count and MRS count for Lactobacillus). Lactobacillus helveticus was the main fermentative organisms in the buffalo milk yogurt. The load of lactic acid bacteria, found in yoghurt at day 7 of storage, which showed that yoghurt have probiotic nature. The study reveals that buffalo milk yoghurt fermented with Lactobacillus helveticus, showed its highest functional properties in fresh conditions, and during storage, it diminished in terms of its antioxidant potential.

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MODELING LACTATION CURVE FOR GENETIC EVALUATION OF MURRAH BUFFALOES

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A study was conducted on first lactation 39059 weekly test-day milk yield (WTDMY) records of 961 Murrah buffaloes sired by 101 bulls during 1977 - 2012 (36 years) maintained at Livestock Farm, ICAR-NDRI, Karnal. A total of four different lactation curve models viz., Gamma Function

(GF), Exponential Function (EF), Polynomial Regression Function (PRF) and Mixed Log Function (MLF) were used for predicting weekly test day milk yields. The adjusted R^2-values for GF, EF, PRF and MLF were 92.78, 88.50, 99.30 and 95.60%; whereas the RMSE with these functions were 0.94, 1.26, 0.30 and 0.78%, respectively. The PRF was the best fit with highest R^2 and lowest RMSE values which was used subsequently to estimate the first lactation 305-day or less milk yield (FL305DMY) from its predicted records of weekly test-day milk yields. The sires are evaluated using four linear models viz. Least Squares(LSQ), Simple Regressed Least Squares (SRLS), Sire (BLUP-SM) and animal (BLUP-AM) models from actual as well as PRF predicted FL305DMYs. BLUP-AM was the most efficient, among the sire evaluation models, in predicting the breeding values. Sire evaluation on the basis of predicted data (using PRF) was similar to that on the basis of actual data indicating that the best fitted lactation curve function can be used as an alternative for early animal evaluation and reduction of generation interval. It was concluded that this method should be applied for estimation of breeding values of Murrah sires for better accuracy, efficiency and stability.

Keywords: WTDMY, lactation curve, sire evaluation, Murrah buffalo.

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ESTIMATION OF GENETIC PARAMETERS FOR PRODUCTION AND REPRODUCTION TRAITS IN MEHSANA BUFFALOES UNDER FIELD CONDITION

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The present investigation was carried out to estimate genetic parameters of various first lactation production and reproduction traits of 8072 of Mehsana buffaloes, spread over a period of 25 years under field progeny testing programme of Dudhsagar Research and Development Association, Mehsana, Gujarat. The data were grouped into three clusters, five periods and three seasons. The heritability was estimated by paternal half-sib correlation method. The genetic and phenotypic correlations and their standard errors were obtained using the formula given by Becker (1975) and Robertson (1959), respectively. The heritability estimates for first production and reproduction traits viz., first lactation 305-days milk yield (FL305MY), total milk yield (TMY), first lactation length (FLL), first dry period (FDP), first service period (FSP), first calving interval (FCI) and age at first calving (AFC) were 0.18 ± 0.03, 0.16 ± 0.03, 0.05 ± 0.01, 0.03 ± 0.03, 0.09 ± 0.03, 0.04 ± 0.03 and 0.15 ± 0.02, respectively. The genetic correlations of AFC with FL305MY and TMY found to be 0.46 ± 0.11 and 0.61 ± 0.11 which were high and significant. However, the genetic correlations of FDP, FSP and FCI with FL305MY, TMYand FLL ranged from -0.11 ± 0.30 to -0.37 ± 0.26 which were moderate but negative and non significant except for FLL and FDP. The phenotypic correlations of FCI with FDP and of TMY with FL305MYand FDP were very high, positive and significant. Further, the estimates of phenotypic correlations among other traits such

as TMY with FSP, FSP with AFC and FCI with FSP, were all substantially high and significant. However, the phenotypic correlations among other traits were low to moderate but not significant. The moderate estimates of heritability for the first production traits indicated that there is further scope for improvement of these traits through selection.

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EFFECT OF NON-GENETIC FACTORS ON VARIOUS REPRODUCTION TRAITS IN MEHSANA BUFFALOES

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The present investigation was carried out on the data of first lactation reproduction records of 7838 of Mehsana buffaloes, spread over a period of 24 years (1989–2012) under field progeny testing programme of Dudhsagar Research and Development Association, Mehsana, Gujarat, with objective to study non-genetic factors affecting various reproduction traits in Mehsana buffaloes under field condition. The data available for the study were grouped into four periods, two seasons and three age at first calving (AFC) groups. The data were analysed by least squares analysis of variance (Harvey, 1990) and the differences between means of different factors for a given trait were tested for their significance using Duncan's multiple range test as modified by Kramer (1957). The least squares means for first reproduction traits *viz* service period (SP), voluntary waiting periods (VWP), daughter pregnancy rate (DPR), calving interval (CI), first to successful service period (FTSS) and age at first calving (AFC) were 214.36 ± 6.19 days, 119.46 ± 4.84 days, 0.54 ± 0.11, 540.03 ± 7.73 days, 42.85 ± 1.34 days and 1437.64 ± 2.59 days, respectively. The effect of period was non-significant for all the traits except for DPR and AFC. However, season of calving and AFC group had significant effects on all the reproduction traits in Mehsana buffaloes. Significant effect of most of the non-genetic factors justifies the correction of records for these sources of variation for estimation of genetic parameters.

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MINERAL STATUS OF DIFFERENT CATEGORIES OF BUFFALOES IN DAUSA DISTRICT OF RAJASTHAN

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A survey was conducted to assess the mineral status of buffaloes and feed and fodder of Baswa block of district Dausa of Rajasthan. The blood samples were collected randomly from buffaloes in three categories *viz* growing, lactating and animals with reproductive problems. Each category was further divided into two sub-categories viz. murrah and native. The serum calcium content of different sub-categories of buffaloes was found to be below the critical range i.e. 7.17±0.69 in murrah and 6.89±0.58 % in native in the growing category, 6.09±0.74 % in murrah and 5.76±0.44% in native in the lactating category and 5.42±0.64 % in murrah and 5.41±1.08 % in native in the reproductive problems category. Low levels of phosphorus were observed in the entire categories *i.e.* growing, lactating and reproductive problems category. Magnesium was found to be within the normal range. Among micro minerals Cu, Zn, Mn and Fe were found to be within the critical range. Survey of the area revealed that the main problems found in animals of the area include retarded growth in young ones, pica and reproductive problems like anoestrus, repeat breeding and retention of placenta. Calcium, phosphorus and protein deficiency in animals could be the underlying cause of these problems. It was concluded from the study that the animals of this block need dietary supplementation of Ca and Ps to overcome the reproductive problems and production and health losses.

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MILK COMPOSITION ESTIMATES IN PURNATHADI BUFFLAO

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Purnathadi buffalo is population found in the Akola and Amravati District of Maharashtra and reared by the rural farmers. Purnathadi is preferred because of its high milk fat content, good reproductive efficiency and low cost of rearing, however till date no systematic documentation is available about its milk composition. In view of this, the research was carried out in 57 lactating buffaloes of different stages of lactation in its breeding tract. Fresh milk samples were collected and milk composition traits were estimated using automatic lactoscan machine. Data generated was analyzed using statistical software SPSS (version 24). Results revealed that milk constituents ranged between 7.66±0.28 to 8.79±0.43 percent milk fat, 4.23±0.07 to 4.36±0.07 lactose, 3.55±0.09 to 3.93±0.10 percent proteins, and 8.78±0.12 to 9.27±0.17 percent SNF. Density of milk, freezing point and salt varied from 28.01±0.49 to 29.92±0.86, -0.522±0.010 to -0.538±0.013 and 0.62±0.02 to 0.67±0.02, respectively. Analysis of variance revealed significantly higher values of solid not fat and salt in first lactation milk as compare to pooled lactations at 5% level of significance. The early, mid and late stages of lactation had shown non- significant effects on all the traits studied. However, higher values for all the constituents except salts content were found during late lactation. From these results, it may be inferred that the Purnathadi buffalo milk contains comparatively higher fat percentage in milk, which makes it preferred buffalo for milk.

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A SOCIO-ECONOMIC PROFILE OF PURNATHADI BUFFALO STAKEHOLDERS IN MAHARASHTRA

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Livestock keeping is an integral part of agriculture and plays a pivotal role in social and economic livelihood of small farmers and landless laborers. Purnathadi, an excellent buffalo genetic resource is being maintained by the farmers of Vidarbha region and its native breeding tract includes Akot and Akola tehsils of Akola district and Daryapur and Anjangaon tehsils of Amravati district of Maharashtra. This germplasm receives its name from River Purna, originating in Satpuda hills and passing through Akola and Amravati district of Vidarbha region, and has evolved along its bank. Planning genetic improvement for any germplasm includes the knowledge about socio- economic status of the stakeholders, besides management practices and utility. With this view a survey was conducted in 35 villages of four tehsil of Akola and Amravati districts. About 98 famers maintaining Purnathadi buffaloes were interviewed. Survey revealed Purnathadi buffaloes are maintained by all the communities especially of Muslims, Bari, Kumbi, Mali, Gaowli and Dhangar. The stakeholders preferred Purnathadi buffaloes due to low animal cost, high fat% in milk, disease resistance, good reproductive performance and low maintenance cost on feeding and management. The average family size of Purnathadi keepers was seven. About 35.42, 50 and 14.58% respondents had small (<=5), Medium (>5 to 10) and Large (>10) family sizes, respectively. Around 90% buffalo keepers were literate and among educated group 16.67% were graduates. None of them received training on animal husbandry practices nor received any loan or grant for maintaining buffaloes. Females have larger participation (80%) in maintaining buffaloes and in dairy operations. About 73% farmers have well-constructed residential house and 100% farmers were found having electricity and sanitation in their homes. The average number of buffaloes per household studies was 4.01 with average total number of livestock was 6.54. The average farm land holding was recorded as 7.27 acre whereas 25% of the keepers were landless, 20.83% marginal, 16.67% small, 10.41% semi-medium, and 22.91% medium. About 4.16% were large farmers based on land holding capacity. About 18.75% farmers were solely involved in the buffalo farming and 67.71% were allied to agriculture while 13.54% were having some additional jobs or businesses along with supplementary buffalo farming. The buffalo sheds were not well constructed *i.e.* 'Kaccha' in 52.09%, 'Pakka' in 39.58% cases where 8.33% had no sheds. In more than 50% cases the buffalo shed is either a part of residential house or inside the house boundary, 48% farmer had separate buffalo sheds. 54.17% farmers offer the farm grown green fodder along with some purchased feed whereas 25% famers totally dependent on purchased green fodder. The average price of Purnathadi buffalo ranges between rupees 25,000 to 40,000 for female and Rs. 20,000 to 35,000 for breeding bulls. Shortage of greens during half of the year and increasing cost of dry forage and concentrate is a prime reason to force livestock keepers to shift from buffalo keeping to other occupations.

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GENETIC EVALUATION OF SURTI BUFFALO FOR PRODUCTION TRAITS

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The present investigation was carried out on 621 lactation records of 178 surti Buffalo maintained at Livestock Research Station, Vallabhnagar (Rajasthan) to assess the influence of non genetic factors on production traits. The least squares means for total lactation milk yield (TLMY), lactation length (LL), 305 days or less milk yield (305DMY) and peak yield (PY) were 1610.92 ± 15.47 kg , 296.80 ± 2.30 days, 1559.41 ± 13.58 kg and 9.42 ±0.08 kg, respectively. Season, period and parity of calving showed significant effect on total and 305 days milk yield and peak yield. Calving during winter season showed highest milk yield than other season. Production performance in winter calvers was observed as 1679.24 ± 29.65 kg for TLMY, 301.84 ±4.85 days for LL, 1624.97 ± 24.88 kg for 305 DMY and 9.81 ±0.14 kg for PY. The heritability estimate was 0.39±0.04 for first lactation 305 days milk yield.

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COPPER POISONING IN SHEEP

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Sheep are unique among farm animals in the way they utilize copper. Copper nutrition in sheep is quite complicated. It is a required mineral for sheep, yet highly toxic. Copper is an essential trace element for animals needed for bone formation, wool growth, pigmentation, collagen formation, elastin formation, white blood cell function and as a part of many metalloenzymes. Copper status of sheep is influenced by breed, age of animal, health status of animal and levels of other minerals consumed such as molybdenum and sulfur which act as antagonist of copper. Sheep are more likely to get copper poisoning than other species because sheep have a greater difficulty disposing of excess copper than other species of animals. If there is an excess of copper in a sheep's diet, it is stored in the liver. When the animal is stressed, the copper is released all at ones into the blood stream. This is called chronic copper poisoning and is more common than acute copper poisoning. Death is certain when a sheep shows symptoms. The acute form of copper toxicity occurs quickly, shortly after ingestion of high amounts of copper. The chronic form occurs when sheep are fed diets over a period of time that are higher in copper content. This could be over a period of weeks or months, depending on actual copper intake by the sheep. Prevention of copper toxicity is the most practical method of dealing with this problem because treatment options are not much feasible. However the usual treatment consists of drenching or feeding ammonium molybdate, sodium sulfate and penicillamine over a period of weeks.

Keywords: Metalloenzymes, Poisoning.

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ESTIMATION OF GENETIC PARAMETERS FOR REPRODUCTIVE TRAITS IN CHOKLA SHEEP

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Six reproductive traits of Chokla sheep were analysed *viz*. Age at first service (AFS), Weight at first service (WFS), Total lambs born (TLB), Total lambs weaned (TLW), Total weight weaned (TLWW) and Mean weight per lamb weaned (MLWW) over the ewe's lifetime. Data were collected for 1172 ewes born over a period of 20 years (1995-2014), maintained at Central Sheep & Wool Research Institute, Avikanagar and Bikaner, Rajasthan, India. Genetic and non-genetic factors significantly influencing the traits were included in the analysis. Six animal models were fit to obtain the REML estimates of the parameters, taking into account the direct and maternal genetic effects, maternal permanent environmental effects and their covariance. The most appropriate model was selected on the basis of log-likelihood ratio test and included in bivariate analysis. Heritability estimates for AFS, WFS, TLB, TLW, TLWW and MLWW were 0.083±0.046, 0.161±0.055, 0.077±0.062, 0.103±0.066, 0.141±0.071 and 0.065±0.047, respectively. No evidence of maternal genetic effects was found suggesting no role of maternal effects while selecting for these traits. Low - moderate genetic progress is possible in the flock by selection. Genetic correlation of AFS with WFS was high and negative (-0.82) which is suggestive of heavier ewes attaining earlier sexual maturity. Similarly, AFS had highly negative genetic correlation with TLB, TLW and TLWW (-0.99, -0.89, -0.79), which demonstrated the higher productivity of the ewes attaining earlier maturity. However, the offspring of such ewes tended to be lighter at weaning as signified by a moderately positive genetic correlation between AFS and MLWW (0.46). Efforts should be directed to optimize the weight of pre-pubertal ewes to hasten the sexual maturity and in turn, increase the lifetime productivity.

Keywords: Chokla sheep, Reproduction traits, Genetic parameters, Heritability, Correlations.

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PREFERENCE FOR TWINNING AMONG KENGURI SHEEP REARERS IN ITS HOME-TRACT

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Kenguri is a meat purpose sheep breed of Karnataka also popular in adjoining districts of Telangana and Andhra Pradesh. Increasing demand for mutton has started a new trend of Kenguri ram lamb fattening. Also, there were many experiments in India with regard to introgression of FecB gene, known for high fecundity. In this backdrop, a field survey was conducted to know the farmers' preference towards multiple births in Kenguri sheep. Data was collected by a structured interview schedule framed in consultation with experts and field visits. Raichur and Koppal districts were selected purposively being the home tract of Kenguri sheep breed. Deodurg taluk from Raichur district and Koppal taluk from Koppal district were selected randomly. Forty Kenguri sheep rearers with flock size of more than 50 and with a rearing experience of 10 years and above were randomly selected from each selected taluk. Analysis of survey data revealed that none of the rearers gave extra supplements for ewes during pregnancy. Among the farmers interviewed, only two per cent of them reported incidence of twinning. However, the survey was conducted in lambing season and it was found that, out of 80 flocks there was only one twinning noticed. The average birth weight of male and female lamb when born as single was 3.1 and 2.8 kg, respectively. The lambs when born as twins were weak and their weight was 2.1 kg and 2 kg. Majority of the farmers (93%) even though desired multiple births did not prefer twinning, as they felt that lack of milk for the young ones is the primary difficulty in rearing the twins. Also they indicated that most of the twins were born weaklings and rarely survived beyond 2 months. The survey showed that twinning per cent was very low in Kenguri sheep and Kenguri sheep farmers did not prefer twinning in their flocks.

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(CO) VARIANCE COMPONENTS AND GENETIC PARAMETERS FOR GROWTH TRAITS IN AVIKALIN SHEEP

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"Avikalin"is a synthetic dual type sheep evolved for carpet wool and mutton production at ICAR-CSWRI, Avikanagar by stabilizing the crossbred population of Rambouilliet and Malpura at 50% exotic inheritance. (Co) variance components and genetic parameters for birth weight (BWT), weaning weight (WWT), 6-month weight (6WT), 12-month weight (12WT), average daily gains from birth to weaning (ADG1), weaning to 6 months (ADG2), 6 months to 12 months (ADG3), Kleiber ratio (KR) from birth to weaning (KR1), weaning to 6 months (KR2) and 6 months to 12 months for Avikalin sheep were estimated by Restricted Maximum Likelihood, fitting six animal models with various combinations of direct additive and maternal effects. Records of 7274 animals descended from 398 sires and 2163 dams were taken for this study over a period of 41 years (1976–2016). Total heritability estimates (from best model as per likelihood ratio test) for BWT, WWT, 6WT, 12WT, ADG1, ADG2, ADG3, KR1, KR2 and KR3 were 0.15, 0.20, 0.17, 0.13, 0.14, 0.18, 0.11, 0.18, 0.13 and 0.14, respectively. Maternal permanent environmental effects contributed 15.5% of the total phenotypic variation for BWT and thereafter declined significantly for all the traits. Maternal permanent environmental effect (c^2) declined significantly with advancement of age of animal. A small effect of c^2 on post-weaning weights was probably a carryover effect of pre-weaning maternal influence. A significant large negative genetic correlation was observed between direct and maternal genetic effects for all the traits, indicating antagonistic pleiotropy, which needs special care while formulating breeding plans.

Keywords: Genetic parameters, heritability, maternal effects, Avikalin sheep.

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ESTIMATION OF GENETIC PARAMETERS AND TREND FOR FERTILITY AND LITTER TRAITS IN NILAGIRI SHEEP

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The Nilagiri sheep, well adapted to the Nilgiri hills are **endangered** in numbers. Therefore it is necessary for **periodical evaluation** of reproduction and fitness traits. Understanding the trend and identification of environmental factors affecting the traits will be useful in suggesting suitable managemental interventions and **formulate breeding plans for conservation** as well. The data comprised of 6321 ewes records on fertility and litter size over a period of 27 years (1989 to 2015) collected from Sheep Breeding Research Station, Sandynallah. The traits studied here are fertility, litter size at birth and litter size at weaning based on lambing. (Co) variance components and corresponding genetic parameters were estimated under Restricted Maximum Likelihood (REML) method by fitting of most appropriate animal model including additive genetic and permanent environmental effects. Bivariate analysis was performed to estimate the genetic covariances and correlations among different traits. Age of the dam at breeding, contemporary group of dam at breeding and birth, level of inbreeding and ewe weight at mating showed significant effect on fertility trait while, age of the dam at breeding and contemporary group of breeding showed significant effect on litter traits. Direct heritability estimates for fertility, litter size at birth and litter size at weaning based on lambing were 0.024±0.017, 0.203 ± 0.035 and 0.131 ± 0.029, respectively. The repeatability estimates were low to moderate, with 0.106±0.015 for fertility and 0.321 ± 0.020 and 0.229 ± 0.019, respectively for litter size at birth and litter size at weaning. The direct genetic and phenotypic correlation between litter size at birth and weaning were positive and high with values of 1.00 ± 0.077 and corresponding phenotypic correlation were also positive 0.89 ± 0.007. High positive genetic and phenotypic correlation between litter size at birth and weaning indicates scope for **indirect selection**. Genetic trends for fertility and litter traits were not different from zero. Genetic trends estimated as average breeding value over year of birth showed negligible values for all the traits studied.

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FARMER PERCEIVED REASONS FOR REARING KENGURI SHEEP IN ITS HOME-TRACT

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Sheep rearing till recent times has been a traditional/ancestral or caste based job. With changing times, the people involved in sheep rearing and the purpose of rearing has also changed. An opinion survey was undertaken to identify and rank the perceived reasons for rearing sheep and to know the utility of sheep rearing towards their livelihood. Raichur and Koppal districts being the home tract of Kenguri sheep breed were selected purposively. Deodurg taluk from Raichur district and Koppal taluk from Koppal district were selected randomly. Forty Kenguri sheep rearers with flock size of more than 50 and with a rearing experience of 10 years and above were randomly selected from each selected taluk. A semi-structured interview schedule was used to record reasons for sheep rearing as perceived, and their ranking as expressed by the farmers. Garrett's ranking technique was adopted to analyse the reasons perceived by farmers for sheep rearing. Top five reasons for rearing sheep were, for liquidation during emergencies and necessities, as a source of employment, for multiplying and creating assets, manure for own use and sale, to generate income from sale or trade of animals. Next five farmer perceived reasons for rearing Kenguri sheep or its utility were, milk for shepherds and watchdogs, religious sentiments, as a status symbol, use breeding rams for natural service for other flocks and lastly to earn income from direct sale of meat.

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EFFECT OF NON GENETIC FACTORS ON GROWTH PERFORMANCE TRAITS OF SONADI SHEEP

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Data pertaining to 519 Sonadi sheep maintained at Mega Sheep Seed Project (Sonadi Unit) College of Veterinary Science, Navania (Rajasthan) were analyzed to assess the effect of non-

genetic factors (sex, season and period of lambing) on growth traits birth (BW), three (3MW), six (6MW), nine (9MW) and twelve (12MW) months weights. The estimated least-squares means for BW, 3MW, 6MW, 9MW, 12 MW were 3.07±0.03 kg , 11.32±0.30 kg, 15.94± 0.56 kg, 19.12 ±0.53kg, 22.73±0.56 kg, respectively. Sex of lambing had significant influence on all growth traits. Male at six months of age had higher (17.24± 0.48 kg) weight than female lambs (15.59 ± 0.48 kg). Lambs born during the month from February to April had higher (16.89 ± 0.40 kg) body weight at six months of age than lambs born during July to November (15.94 ±0.56 kg).

Keywords: Sonadi Sheep, Non genetic factors, Growth traits.

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NECESSITY OF FEEDING MULTI-NUTRIENT-MIXTURE IN GOATS FOR ENHANCING PRODUCTION IN ARID REGION OF RAJASTHAN

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Goats are reared mainly by extensive, semi-intensive and intensive system of rearing. Goats are having fastidious eating and browsing habit. The feed requirement of goats is mainly met by extensive grazing on common lands, degraded pasture and road side vegetation in arid regions, which often causes deficiency of certain nutrients like energy and protein especially in the scarcity period. In semi-intensive rearing, small flock of goats are fed with top feeds of tree like Khejri leaves (*Prosopis cineraria*), Pala (*Ziziphus nummularia*) and other concentrate feed available at farmer's home. But in case of large flock size, the supplementation of concentrate and top feeds are not given to the goats due to high cost of conventional concentrate feeds (cereal grain, bran, oil cakes etc.) and top feeds like khejri leaves. Therefore, there is need to seek alternative supplements to improve the nutrition during scarcity period to sustain the productivity of goats. The multi-nutrient-mixture (MNM) powder can be formulated using molasses, urea, common salt, vitamin-mineral mixture, dolomite, wheat bran, clusterbean meal and organic binder. Use of high energy MNM feed as an alternative supplement containing high energy ingredients, non-protein nitrogen substance and vitamin mineral mixture results in a significant improvement in dry matter intake from grazing, water intake and consequently improved growth, milk yield and overall health of the animals. Thus MNM is a suitable economically viable option to supplement deficient nutrients in goats and sustain the productivity during feed scarcity period.

Keywords: grazing, scarcity period, multi-nutrient-mixture and productivity.

SP-181

STUDY OF INDUCED HYPOTHYROIDISM BY THIOUREA FEEDING SUPPLEMENTATION IN MARWARI GOATS (*CAPRA HIRCUS*)

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Thyroid hormones are the major regulators of basal metabolism increasing oxygen consumption and therefore heat production. Other effects of thyroid hormones are evident during growth and development. Thus it is evident that the thyroid endocrine gland has an important role for control of animal production and adaptation for cold environmental conditions.The investigation was carried out to study the effects of thiourea supplementation on Triiodothyronine (T3), Thyroxine (T4) and Thyroid stimulating hormone (TSH), some enzyme (AST & ALT) and some important blood biochemical parameters (glucose, cholesterol, urea, total protein, albumin, globulin and A:G ratio) in Marwari goats.

Six male goats (bucks) below 8 months to 1 year age group were subjected to thiourea supplementation in increasing doses for 6 days (@20 mg/kg body weight, weight for first two days , 40 mg/kg body weight for next two days, 40 mg/kg body weight for next two days and 60mg/kg body weight for last two days. The blood samples were collected and analyzed on 1st and 2nd day (control phase) and different sub sequent phases of thiourea supplementation.ANOVA revealed a highly significant ($P \leq 0.01$) decrease in serum thyroxine (T4), where - as serum Triiodothyronine (T3) and thyroid stimulating hormone (TSH) showed a non-significant ($P > 0.05$) effect. Serum glucose and total protein showed a significant ($P < 0.05$) decline effect, temperature, pulse rate and respiration rate showed highly significant ($P < 0.01$) decrease and cholesterol, urea, SGOT (AST), SGPT (ALT) showed highly significant, whereas non – significant ($P > 0.05$) effect was observed in albumin, globulin and A:G ratio. It is concluded from the present study that thiourea supplementation in goats alters the blood hormonal, enzymatic, biochemical and physiological parameters.

SP-182

STUDY OF POTASSIUM IODIDE SUPPLEMENTATION ON THE BLOOD THYROID HORMONE PROFILE IN MARWARI GOATS (*CAPRA HIRCUS*)

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Thyroid gland secretes Triiodothyronine (T_3) and thyroxyne (T_4), which are essential for normal metabolism, production, and growth performance of domestic animals. The critical elements required for thyroid hormone synthesis are amino acid tyrosine and iodine. Thyroid hormones are the major regulators of basal metabolism increasing oxygen consumption and therefore heat production, because they stimulate oxidative phosphorilation. Other effects of thyroid hormones are evident during growth and development. The investigation was carried out to study the effects of KI supplementation on Triiodothyronine (T_3), Thyroxine (T_4) and Thyroid stimulating hormone (TSH), some enzymes (AST & ALT) and some important blood biochemical parameters (glucose, cholesterol, urea, total protein, albumin, globulin & A:G ratio) in Marwari goats.

Six male goats (bucks) below 1 year age were subjected to KI supplementation in increasing doses for 6 days (i.e. @ 13mg/kg b.wt for 1st two days, 20mg/kg b.wt for next 2 days and 26mg/kg b.wt for last 2 days). The blood samples were collected and analyzed on 1st and 2nd day (control phase) and different subsequent phases (treatment phases i.e. T_1, T_2 and T_3) of KI supplementation. ANOVA revealed a highly significant ($p \leq 0.01$) decrease in serum TSH at phase T_3 whereas serum T_4 showed a significant ($p \leq 0.05$) increase in phase T_2 and serum T_3 showed a non-significant effect. In serum glucose, urea, albumin, SGOT, SGPT, temperature, pulse rate, respiration rate a highly significant effect ($p \leq 0.01$) with overall increasing trend was observed, whereas serum cholesterol, globulin and A:G ratio indicated a non-significant effect.

From the present study, it is concluded that dietary iodine should be limited to nutritional requirements and that prolonged use of prophylactic or therapeutic amounts should be avoided.

SP-183

MORBIDITY AND MORTALITY INCIDENCE IN GADDI FLOCKS UNDER TRANSHUMANCE PRODUCTION SYSTEM

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Transhumance production system is very common across Himalayas involving Gaddi tribe of nomadic pastoralists of Himachal Pradesh, who rear sheep and goats of *Gaddi* breed. In summers, their flocks (commonly known as *Dhan*) climb to high altitude alpine Himalayan pastures and during winters they are grazed in the foot hills. The *Gaddis* might have derived their name from their native land, the *Gadheran*, which lies on both sides of the Dhauladhar ranges. The present study was conducted on *Gaddi* goats maintained by the *Gaddi* shepherds under transhumance production system. The data pertains to the animals belonging to four field units (2011-2017) associated under AICRP on Goat Improvement. All the animals were identified by ear tagging. The overall incidence of morbidity and mortality (2011-17) was 16.87 and 7.38%, respectively. The major causes of morbidity recorded were diarrhoea (21.17%), cough (16.12%), weakness/debility (12.38%) and plant poisoning (10.92%). Similarly major causes of mortality observed were collibacilosis (29.37%), pneomonia (22.22%), predation (17.86%), general weakness (17.46%) and toxaemia (8.33%). The findings of the present study suggest that under transhumance production system a variety of predisposing factors like poor housing, less mothering care and low nutrition are responsible for morbidity and mortality. Some of the factors especially those associated with sub optimal management can be resolved by developing suitable and effective extension interventions for this type of production system.

SP-184

EVALUATION OF GROWTH PERFORMANCE AND REALIZED HERITABILITY THROUGH THE USE OF ELITE MARWARI BUCKS IN FARMER'S FLOCK

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The body weight at different stages of life especially at earlier age may provide suitable selection criteria for higher body weight at slaughter age. It also determines the post-natal growth and survivability. Studies on the evaluation of growth performance through use of elite Marwari bucks in farmer's flock was carried out on a total of 3366 and 2877 records at birth and six month age, respectively. The data were obtained from records of All India Co-ordinated Research Project on Goats entitled "Genetic Improvement of Marwari goat for meat production in farmer's flock. The overall least square means for body weights at birth and six months of age were estimated as 2.91±0.007 and 17.49±0.078 kg, respectively. The body weight of progenies of elite sire group was observed to be highly significant ($P \leq 0.01$) heavier than progenies of local sire group at birth and six months of age. The effect of centre was observed to be highly significant ($P \leq 0.01$) on body weights at six months of age, but on birth weight which was non-significant. The estimate of realized heritability was observed as low to medium of six months body weight. The overall realized heritability for six months body weights was estimated as 0.17, 0.26 and 0.15 at Deshnok, Kalyansar and Moondsar centre, respectively. The use of elite Marwari bucks in farmer's flock increases the body weight at slaughter age which is significant economic gain to a poor shepherd.

SP-185

STAR-GAZING IN GUINEA FOWL: A CASE REPORT

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Vitamins are a group of organic compounds that poultry only require in small quantities, but they are essential for normal body functions. Vitamins are divided into two categories: fat-soluble and water-soluble. The fat-soluble vitamins are A, D, E, and K. The water-soluble vitamins include vitamin C and the B vitamins. The B vitamins include vitamin thiamin, riboflavin, niacin, pantothenic acid, pyridoxine, biotin, folic acid, and cyanocobalamin. The B vitamins are involved in many metabolic functions, including energy metabolism. Thiamine (Vitamin B_1) is necessary for proper carbohydrate metabolism. The objective of the present study was to diagnose and treat Star-gazing condition or Thiamine deficiency on the basis of clinical sign and symptoms. A 1.5 year old Guinea fowl turned into college clinic with characteristic signs, birds sitting on flexed legs and drawing back the head in a 'star-gazing' position, with history of wheat bran and cereal grains feeding. This Case responded successfully by thiamine treatment.

SP-186

EFFECT ON FEED INTAKE BY ADDING DIFFERENT LEVELS OF AMBADI (*HIBISCUS CANNABINUS L*) CAKE IN BROILER RATION

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The present study was conducted to estimate the effect of incorporation of Ambadi (*Hibiscus cannabinus L.*) cake (AC) in broiler chicks ration @ 0, 10, 20 and 30 per cent levels in T_1, T_2, T_3 and T_4, respectively. To determine the body weight and weight gain, feed intake, feed conversion ratio, mortality percentage and cost per unit of gain on different levels of Ambadi cake rations. Three hundred day old commercial broiler chicks of same hatch were taken for this study. There were randomly divided into four equal groups of seventy five chicks each and reared on feed without Ambadi cake (control) and three feed mixtures with 10, 20 and 30 per cent Ambadi cake at eight weeks. The average feed consumption per chick in eight weeks ranged from 2498.18g (T_4) to 3119.45g (T_2). The average CP intake and ME was found to be maximum in T_2. The highest feed conversion ratio 2.82 and best performance index 380.14 were observed in T_2 and performance index in T_3, respectively.

SP-187

EFFECT OF AGE AND SEX ON HAEMATOLOGICAL PROFILE OF KADAKNATH FOWL REARED UNDER INTENSIVE SYSTEM

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The study was designed to investigate the haematological parameters at different age groups of male and female Kadaknath fowl, maintained in the poultry unit of College of Veterinary Science & Animal Husbandry, Anjora, Durg Chhattisgarh, reared under intensive farming system using standard feeding and management practices. For this study the blood samples were taken from 15 male and 15 female birds at 8, 12, 24, 40 and 48 weeks of age. The values for packed cell volume (PCV), erythrocyte sedimentation rate (ESR), total erythrocyte count (TEC), total leucocytes count (TLC), Haemoglobin (Hb), mean corpuscular volume (MCV), mean corpuscular haemoglobin (MCH), mean corpuscular haemoglobin concentration (MCHC) and differential leukocyte count (DLC) were assessed. Effect of age in PCV, TEC, TLC, Lymphocyte, Heterophil, Monocyte, Eosinophil, Hb, MCV, MCH and MCHC were significant ($p<0.05$). However, no significant ($p>0.05$) age difference was observed in basophil. In general in all the haematological parameters there is an increasing trend with advancement of age. Effect of sex was found significant for Eosinophil, lymphocyte, Hb, MCHC, PCV and Heterophil. In general, these values are higher in males than in females.

Keywords: Male, Female, Haematological, Age.

SP-188

GROWTH PERFORMANCE OF PRATAPDHAN CHICKEN WITH AJWAIN (*TRACHYSPERMUM AMMIL.*) FEED SUPPLEMENT IN DIET

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The present study was conducted to observe the effect of supplementation of Ajwain on the growth of Pratapdhan chicken. One hundred twenty unsexed Pratapdhan chicks (day old) were used on a completely randomized design in 4 treatments with 3 replicates, each consisting of 10 chicks. The treatments included the control group (T_1) fed with standered chick ration as BIS standards 2007 and other groups were kept on standered chick ration mixed with Ajwain powder @ 0.1%, 0.2% and 0.3% in T_2, T_3 and T_4, respectively. All other management practices were followed as per recommendation during the experimental period of 56 days. The feed intake and body weight of chicks was recorded weekly for further analysis. The body weight (g) of the chicks at 8 weeks of age was the highest in T_3 chicks (1203±42.24), followed by T_2 (1158.39±45.10), T_4 (1140.46±36.35) and T_1 (1130.88±), respectively. The weekly body weight gain (215.26± 2.88) was highest in T_3 the difference was significant over control group. The total feed intake (g) was lowest in T_3 (3017) followed T_2 (3073), T_1 (3206) and T_2 (3234). The increase in the feed intake of T_4 group may be due to the laxative and purgative effect of Ajwain. The feed conversion ratio (3.28±0.02) of T_3 group was also found better over the control group. Performance index of T_3 (65.54±1.76) group was significantly higher than the other groups. Similar trend was also found in protein efficiency (1.51±0.02) and energy efficiency (10.87±0.28). Results revealed that Ajwain is a potential feed ingredient in broiler feeding and it can be incorporated into broiler rations up to 0.2% without any adverse effects.

SP-189

SURRA IN CAMEL

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Camel trypanosomosis which is also known as surra caused by *Trypanosoma evansi*, is the most important cause of morbidity and mortality in camels. Trypanosoma evansi is transmitted mechanically by haematophagous biting flies. Surra can attack camels at any age, even foetuses. There is a particularly high incidence of infection in juvenile camels shortly after weaning. Numerous environmental and host factors influence the course of the disease, such as other infections, nutritional status, age, pregnancy, previous exposure or immunosuppression by other diseases, and stress.

As the disease develops camel loses weight, develops a drooping hump, is unable to walk long distances, and may or may not develop oedema of the feet, brisket, underbelly and eyelids. The coat becomes rough. In the initial attack of fever there may be lacrimation, shivering, reduced appetite and mild diarrhoea. The animal always shows progressive anaemia and fluctuating body temperature with initial peaks of fever up to 41°C the net effect associated with above changes is immunosuppression which later develops and predisposes the animals to other infections and death if untreated. Later the appetite is relatively unimpaired and the temperature may become normal or slightly elevated. The mucous membranes are pale and the packed cell volume (PCV) drops to below 25% (v/v), sometimes as low as 10% (v/v). The herders may notice a characteristic odour of the camel's urine. Abortion in all stages of pregnancy is common. Trypanosomiasis is diagnosed by demonstrating the parasite.

A tentative diagnosis can be reached without microscopy, by taking into account the owner's observations and clinical examination of camels in the field. Two drugs are recommended for the treatment of *evansi* infections in camel one is suramin and another is quinapyramine. No vaccines are available for the disease. To control the disease accurate diagnosis and treatment with effective drugs is necessary. Control of surra can be difficult as there is no vector specificity and a wide range of hosts. Drugs such as suramin, prothridium and isometamidium chloride (as a prophylactic) and diminazene aceturate (curative) can be used although drug resistance has been reported.

SP-190

FEEDING MANAGEMENT OF CAMEL IN SIKAR DISTRICT OF RAJASTHAN

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Rajasthan is ranked first in total camel population of India. Camel is the state animal of Rajasthan. Camels are reared on semi-intensive system or on total stall feeding in Sikar district of Rajasthan. Extensive feeding management system is rare there. The efficient adaptable digestive system allows camels to maintain themselves on poor quality roughage and scanty vegetation of desert. This is partly attributed to anatomical features of digestive tract and partly to its digestive physiology. Camel is called as the ship of desert. In rainy season shrubs, bushes and trees provide maximum nutrients to the camel but in winter season only tree leaves are available for grazing so, supplementary ration is essential. While in summer season camel has to roam around even for tree leaves. Generally camel prefers to browse rather than to graze. The common tree leaves available for camel to browse are khejri, neem, sissoo, shahtoot, peepal, banyan, khimp, and phog. Camels are able to browse thorny plants like acacia and zizyphus which other animals cannot utilise. In semi-intensive system, camel rearers graze their camel for 5-6 hours/day and give wheat straw, moth straw, jowar, maize and jaggery etc. Moong straw, barley straw, guar straw, taramira and mustard is offered as roughage to the camel in stall feeding. Concentrate mixture contains bajra grains, barley, wheat bran, gram churi, common salt and alum. So the camel is fit for the prevailing conditions of the desert and hence is liable to be conserved.

Keywords: Semi intensive, Top feeds, Roughage.

SP-191

EFFECT OF FEEDING OF PELLETED COMPLETE FEED CONTAINING *AZOLLA PINNATA* IN CAMEL CALVES ON PERFORMANCE

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Dromedary camels are semi-domesticated animals, freely ranging, but under herdsman control. In fact, dromedary camel's census sizes has severely declined over the past 20 years and also have been "extinct" from the wild for the past 2000 years. To conserve camel population and use of locally available non-conventional feed resources, present investigation was carried out on 15 healthy camel calves distributed randomly in three treatment groups having 5 calves in each. Treatment group T_1 fed pelleted complete feed without Azolla incorporated while T_2 and T_3 groups fed pelleted complete feed containing Azolla at the levels of 2% and 4%, respectively. Results indicated that camel calves grow at faster rate and significantly improvement on feed conversion efficiency and average daily gain. It concluded that inclusion of Azolla (*Azolla pinnata*) at 4 per cent level in pelleted complete feed could be viable proportion to keep pace with scarcity of feed and fodder to some extent and to have profitable camel rearing.

Keywords: Azolla, Camel, Extinct, Scarcity.

SP-192

HAIR FIBRE QUALITY AND QUANTITY IN MEWARI AND JALORI CAMEL

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The camel hair is traditionally used in making carpets, blankets, ropes and other items of day to day use by the camel owners. Fine quality hair is utilized for blanket making whereas coarse quality hair is used for carpet and rope making. These carpets and blankets are very cheap and durable. The life of a carpet is approximately 50 years and that of a blanket is 15 years. The rope made of camel hair is used for tying the animals and in making cots. In the present study, the annual hair production from an adult camel was observed to be 700 gm in Mewari and Jalori camels. Fifty samples each were collected from the breeding tract of Mewari and Jalori camel and analysed for the fibre quality parameters. The average fibre length was measured as 5.62±0.10 cm in Mewari camel and 6.69±0.14 cm in Jalori camel, and it ranged from 3.00 to 10.20 cm in Mewari camel and 4.0 to 12.40 cm in Jalori camel. The average fibre diameter was measured as 40.44±2.14 µ in Mewari camel and 42.49±2.31 µ in Jalori camel. The average fibre diameter ranged from 19.25 to 89.79 µ in Mewari camel and 19.53 to 100 µ in Jalori camel. The pure, hetero and hairy fibres were 4.87±0.73, 25.46±2.21 and 69.67±2.81 % in Mewari camel and 5.25±0.00, 38.37±2.95 and 56.39±3.32 % in Jalori camel, respectively. Total medullation was 95.13±0.73% in Mewari camel and 94.75±1.08 % in Jalori camel. Thus, the fibre quality was almost comparable in the two breeds of camel. The handicraft industry has already started using the camel hairs and is making the decorative and daily use items fetching good price, this may further be diversified and strengthened to increase the economic returns to the farmers.

SP-193

SUBCLINICAL MASTITIS PATHOGENS AND THEIR ANTIMICROBIAL DRUG RESISTANCE IN ORGANIZED DAIRY FARM, MAHARASHTRA, INDIA

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The purpose of this study was to investigate sub-clinical mastitis in organized dairy farm and various pathogens associated with subclinical mastitis with antimicrobial resistance in organized dairy farm, Maharashtra. Randomly, milk samples found positive for subclinical mastitis by California mastitis test were investigated for presence of various bacterial pathogens at Research Cum Development Project on Cattle, Mahatma Phule Krishi Vidyapeeth, Rahuri, and Maharashtra. A total of 10 lactating crossbred cows found positive for sub-clinical mastitis were subjected for isolation and biochemical characterization. From ten samples, 2 were found positive for *E. coli* and 8 were found positive for *S. aureus*. Antibiotic resistance pattern revealed that the highest resistance to the antimicrobials used was to observed in Penicillin G (90.0%), followed by Amoxyclav, Co-trimoxazole, Tetracycline (80.0% each); Ampicillin, Chloramphenicol, Cephalexin, Cefoperazone (70.0% each); Ciprifloxacin (60.0%); Ceftriaxone (50.0%); Gentamicin, Levofloxacin (40.0% each). The lowest drug resistance was observed in Enrofloxacin, Cefotaxime and Cefachlor (30.0% each). Multiple antimicrobial resistances was observed in all the 10 isolates from subclinically positive milk samples. This study confirms the importance of *S. aureus* as a one of the major subclinical mastitis causing bacterium and existence of alarming level of resistance to frequently used antimicrobials by *S. aureus* and *E. coli* a potential risk for human health from nearly possible transmission of the both bacteria as milk borne pathogen.

Keywords: Cattle, Subclinical mastitis, organized dairy farm, S. aureus, *E. coli,* Antimicrobial Drug resistance.

NATIONAL SYMPOSIUM: Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' Income &
XV Annual Convention of Society for Conservation of Domestic Animal Biodiversity (SOCDAB)
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SP-194

PRODUCTION OF FERMENTED BUFFALO MILK PRODUCT BY USING OF *Lactococcus lactis ssp. Cremoris* AND FORTIFIED WITH JUJUBE (*Ziziphus jujuba*) SYRUP#

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The dried fruit of the jujube (Ber) *Ziziphus jujuba* is a fruit similar to dates and figs. It is a small deciduous tree or shrub grown in arid and semi-arid regions of India. Jujube is rich in biological components and various secondary metabolites, which are related to both nutritional values and biological activities. In view of this, an effort was made to utilize jujube in form of jujube syrup @ 5% W/W and sugar @ 5% W/W basis incorporated in the buffalo milk fermented with *Lactococcus lactis ssp. cremoris* and then fermented buffalo milk products was produced at the time period of fermentation, where it show highest antioxidant activity (both ABTS and DPPH basis) (8 hours of fermentation of buffalo milk) to develop fiber rich product i.e. yogurt. to "A yogurt was evaluated for sensory quality by the group of 10 panelists using 8 point hedonic scale". Thus the Proximate analysis and sensory evaluation data shows that the yogurt made up of fermented buffalo milk had acceptable flavor, texture, colour and overall acceptability.

Keywords: Buffalo milk product, jujube, sensory evaluation, and yogurt.

SP-195

STUDY OF EFFECT OF VITAMIN E AND SELENIUM ON MILK FAT PERCENTAGE IN MILK OF KANKREJ CATTLE

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In an attempt to assess the possibilities of improvement in production performance of Kankrej cattle by supplementation of vitamin E and Selenium, an experiment was conducted to investigate the effect of vitamin E and Selenium during transition period in Kankrej cows. A total of 24 cows were selected on the basis of their milk yield, parity and body weight are grouped into four homogenous treatment groups of 6 each. Out of these, one group served as control fed as per NRC (2001) wherein no supplementation was given. Cows in treatment groups, Group-1 vitamin E, Group-2 Selenium and Group-3, vitamin E + Selenium supplementation were given daily along with control diet. Milk quality in terms of milk fat percentage was determined up to 30 days of lactation. For this purpose, quarter foremilk samples were collected on day of calving and 3rd 7th 15th and 30th day postpartum. Milk fat percentage was calculated by Milkometer. Milk fat percentage of milk differed significantly ($P<0.01$) between groups but milk fat percentage among groups differed non- significantly between different days of lactation period. The interaction effect including group x days was found non- significant. Economics of milk production indicates that return (Rs./cow/day) from sale of milk over expenditure (supplementation and feeding cost) was highest in combination group followed by selenium, control and vitamin E supplementation. Therefore it can be inferred that vitamin E and Selenium supplementation is economically viable and beneficial and it can be adopted to improve milk health and net return from lactating Kankrej cows.

Keyword: vitamin E and Selenium, Milk quality, Milk fat percentage

Technical Session-IV

Young Scientist Award Presentations.

SP-196

COMPARATIVE ANALYSIS OF TWO BOVINE BEADCHIP DENSITIES FOR GENOMIC CLUSTERING BASED STUDIES

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The study was planned to seek out the efficiency of genomic breed clustering and admixture related studies across two densities (i.e., 50K and HD), besides working out the evidence of bias(es) (if any) along the different aspects of whole genome SNP based studies. The SNP genotypic data of the two densities, based on Illumina Bovine SNP Bead Chip, was collated for different breed combinations and ordered into three datasets (A, B, and C). Genotypic datasets were processed for different inclusion thresholds and quality control filters. The research methods included the Bioinformatics' analysis via ADMIXTURE program and statistical analysis in terms of cross-validation errors and PCA. The genotypic data in three datasets was used to compute the individual- and population-wise exclusive genomic breed clustering levels by applying model-based approach in ADMIXTURE program. There was no significant increase in accuracy of clustering levels of different breeds upon an increase in density levels (from 50K to HD), as evaluated by statistical analysis. The results from ADMIXTURE program for different datasets showed evidence of bias towards breeds of *taurine* lineage and against *indicine* breeds. Further affirmation came from the comparison of variance proportions explained by principal component analysis. The proportion of markers polymorphic at 5% and 1% levels were consistently higher for breeds of *taurine* lineage of dataset C when compared with breeds from *indicine* group. A similar view was found with average minor allele frequency (MAF) values for breeds of *taurine* lineage. In conclusion, there were definite evidence of bias(es) of Bovine SNP chip towards breeds of *taurine* lineage used in the study and it may be attributed to a rare allele frequency of markers in *indicine* breeds or to ascertainment bias.

Keywords: Admixture, Ascertainment bias, Clustering, HD, *indicine*, PCA, *taurine*, 50K.

SP-197

STR MARKERS AND MITOCHONDRIAL D-LOOP SEQUENCE BASED GENETIC DIVERSITY ANALYSIS INDICATES UNIQUE POPULATION STRUCTURES AMONG BUFFALOES OF ODISHA STATE

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Odisha state is rich in livestock biodiversity flourished from its ancient anthropological activities and geographical richness. This state possesses diverse buffalo populations including two recently registered breeds i.e. Chilika and Kalahandi apart from other three minor populations of Paralakhemundi, Sambalpuri and Manda. In this study, we used the mitochondrial D-loop sequencing to analyze the evolutionary relationships of Odisha buffaloes with other riverine and swamp buffaloes of India along with simple tandem repeats (STR) marker based genetic diversity evaluation. The samples were procured from different breeding tracts of Chilika, Kalahandi and Paralakhemundi buffaloes. Mitochondrial D-loop sequencing and haplotype sharing of buffaloes of Odisha showed a close phylogenetic relationship with other riverine and Assamese buffaloes but grouping in different sub cluster. Total 66 haplotypes were found, resulting from 84 variable sites, with an overall 0.94 haplotype diversity. Out of all the breeds of Odisha, Chilika showed haplotype sharing with pure bred swamp buffaloes of Northeast. More than 130 animals of these Odisha buffaloes were studied for the assessment of genetic variability using 23 fluorescently-labelled microsatellite markers. The Mean Fixation Index (F_{IS}) values and the Mean polymorphic Information Content (PIC) values of Chilika, Paralakhemundi and Kalahandi breeds were found to be 0.21 and 0.686, 0.281 and 0.776, 0.215 and 0.680, respectively. Allelic diversity based mode shift analysis revealed none of the population experiencing any recent bottle neck. Multivariate correspondence analysis indicates Odisha buffaloes grouping into separate cluster. Additionally, cytogenetic analysis of 30 animals each of these breeds showed few riverine-swamp hybrids among Chilika having 49 chromosomes and the remaining two populations with 50 chromosome showing typical riverine status. Conclusively, the mitochondrial haplotype sharing along with cytogenetic analysis of Odisha buffaloes indicates close evolution of Chilika buffaloes with swamp types and possessing unique population structure.

SP-198

GENETIC DIVERSITY ANALYSIS OF CHOKLA SHEEP BREED OF RAJASTHAN

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The Genetic diversity of Chokla sheep was studied using 18 microsatellite markers, proposed by the Food and Agriculture Organization and the International Society for Animal Genetics

(FAOISAG). A total of 150 alleles ranging from 4 to 13 were found across 18 microsatellite loci. The most polymorphic marker was OarFCB48 with a total of 13 alleles detected. The high genetic variation (MNA=8.3) was observed in Chokla sheep compare to other reported breed in Rajasthan. All studied loci contained high PIC value (>0.5) in the present study, where mean PIC value (0.751) is higher than the earlier reported study on sheep in India, which indicates highly informativeness of markers to characterize Chokla sheep breed population and showed abundant genetic diversity in this population. Further, the mean expected gene diversity (Hexp) and observed heterozygosity estimated as 0.783 and 0.576, respectively. In spite of high genetic variability in chokla sheep, the present study revealed the differences between expected heterozygosity (H_e) and observed heterozygosity (H_o), suggesting departure from Hardy-Weinberg equilibrium (HWE) and the possibility of inbreeding. This was also reflected by a high inbreeding coefficient (F_{is}) value 0.256±0.079. The Mode shift analysis revealed a normal "L" shaped curve indicating this sheep breed is non-bottlenecked. Hence, we can conclude after thoroughly analysis of results that there is a demand to change existing breeding strategies for further improvements of this breed.

Keywords: Genetic Diversity, Chokla, Polymorphic Information Content (PIC), Microsatellite markers, Inbreeding coefficient (F_{is}), Heterozygosity.

SP-199

SINGLE NUCLEOTIDE POLYMORPHISMS IN EXON-I AND PARTIAL INTRON-I OF GROWTH HORMONE GENE AND ITS ASSOCIATION WITH BODY WEIGHT TRAITS IN INDIAN BROILER STRAIN (VENCOBB-400)

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In this study chicken growth hormone (*cGH*) gene polymorphism has been investigated in broiler strain (Vencobb-400) by PCR-RFLP. The genomic DNA was extracted from 150 samples by using modified spin column technique. The DNA fragment of the growth hormone gene with 776 bp was amplified by PCR using specific primers. Then the PCR products were digested with *Msp*I restriction enzyme and analyzed on 8% polyacrylamide gel. The partial gene is amplified by one pairs of primers and single nucleotide polymorphism (SNPs) is detected by the bioinformatics tools such as Chromas and Bioedit then confirmed by DNA sequencing. The PCR products were sequenced. Sequencing was compared and aligned with the sequence obtained from the gene bank (accession number MG586896, MG586897 and MG586900). Six SNPs were identified in this study. This analysis showed that the SNPs present at position 148 A/G, 314 T/G, 414 T/C, 434 C/M (A or C, Heterozygosity), 452 A/G and 654 G/R (A or G, Heterozygosity). The allelic frequency of exon-I and partial intron-I locus for A and B allele were 0.39 and 0.61, respectively. The genotypic frequency for AA, AB and BB in Broilers were 0.22, 0.28 and 0.50, respectively. The result showed that the exon-I and partial intron-I of *cGH* is polymorphic in broiler and mutations are found.

Keywords: Chicken Growth hormone, polymorphism, sequence.

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 151 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 lifespan.
- Dissemination of knowledge and technologies about sustainable management and economic utilization 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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SOCDAB EVENTS- AT A GLANCE

SN	Type of Event	Theme	Date & Year	Host Institute	Organizing Secretary
1	1st National Symposium	**Livestock Biodiversity vis-à-vis Resources Exploitation: An Introspection**	Feb 11-12 2004	NBAGR, Karnal- 132001 Haryana	Dr. R.K. Pundir
2	2nd National Symposium	**Domestic Animal Diversity: Status, Opportunities and Challenge**	Feb 10-11 2005	NBAGR, Karnal- 132001 Haryana	Dr. B. Prakash
3	Workshop	**Crossbreeding at the Cross-roads**	Oct 22, 2005	Veterinary College, Banglore-560024 (K.V.A.F.S. University, Bidar)	Prof. 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- 132001 Haryana	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 834006 (Jharkhand)	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-560024 (KVAFS University, Bidar)	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- 132001 Haryana	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 388001, Gujarat	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, Orissa	Dr. Sanat Mishra
10	9th National Symposium	**Role of Indigenous Animal Genetic Resources in Rural Food Security vis-à-vis Climate Change**	Feb 24-25 2012	BAIF Development Research Foundation, Pune (Maharashtra)	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 (Uttarakhand)	Dr. C.V. Singh
12	National Seminar	**Technological and Policy Interventions for Sustainable Cattle Breeding in India**	March 14 2013	PDC, Meerut (U.P.)	Dr. Umesh Singh
13	11th National Symposium	**Harmonizing Phenomics & Genomics for sustainable management of livestock vis-à-vis upliftment of rural masses**	Feb. 6-7 2014	NBAGR, Karnal	Dr. N.K. Verma
14	12th International Symposium	**Sustainable management of animal genetic resources for livelihood security in developing countries**	Feb 13-14 2015	TANUVAS, Chennai	Dr. Peria G Kumarasamy
15	13th National Symposium	**Policy planning for livestock security through domestic animal biodiverisaty**	Feb 11-12 2015	SKAUST-J, Jammu	Dr. R.K. Taggar
16	14th National Symposium	**Biodynamic Animal Farming for The Management of Livestock Diversity Under Changing Global Scenario (SOCDAB Compendium 2017)**	Feb 8-10 2017	COVAS, Mannuthy, Thrissur, Kerala	Dr. K. Anil Kumar

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(Recognized by Veterinary Council of India)
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First Veterinary College in Rajasthan under Private Sector for providing rich experience of Veterinary Education in India

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Features:

- Campus with salubrious milieu.
- Vast infrastructure with well maintained laboratories
- Well experienced and highly qualified faculties
- Innovative teaching and Assessment methods
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- Fully Wi-Fi campus with high speed internet connectivity.
- Separate blocks of hostels for boys' and girls' including AC hostels
- Playgrounds for volley ball, badminton, basket ball and cricket for students and staff

Clinical Facilities:

- Modernized facilities for both outdoor and indoor patients.
- 24 x 7 OPD in TVCC for large and small animals.
- Well equipped TVCC with facilities like c-arm X-ray machine, ultrasonography, biochemical analysers, otoscope, laryngoscope, etc. for better diagnosis and treatment of diseases.
- 24x7 emergency mobile veterinary services.
- Facilities in small and large animal services include specialty in dermatology, internal medicine, ophthalmology, orthopedic surgery, immunization, general surgery gynaecology and obstetrics.
- Well equipped veterinary investigation laboratory is available in the college. The lab provides a full range of animal disease diagnostic services to veterinarians, livestock producers and pet owners in and around Sikar.
- Drug Store at TVCC. This saves the hassle for the livestock and pet owner to procure medicines from outside. Besides, high quality drugs and medicines are provided free of cost.
- ILFC with Various small and large species of animals and ultramodern milk shed with automatic milking machines.

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