# वार्षिक प्रतिवेदन
# ANNUAL REPORT
# 2016-17

भाकृअनुप–राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो
करनाल–132001 (हरियाणा) भारत

**ICAR-NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES**
Karnal-132 001 (Haryana ) INDIA

*With Best Compliments*

*from*

*Director, ICAR-NBAGR*

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रा.प.आ.सं.ब्यूरो

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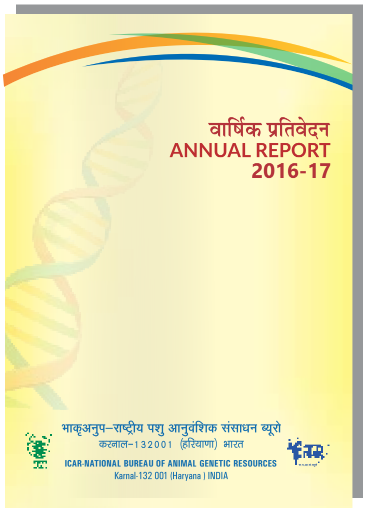

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## Contents

**History and Profile**

**Research Accomplishments**

**Research Projects and Publications**

**Training and Capacity Building**

**Other Activities**

**Personnel**

**हिन्दी खण्ड**

# From Director's Desk ....

*I am pleased to present the major activities and achievements of ICAR- National Bureau of Animal Genetic Resources in the form of this annual report for the period 2016-17. Since its inception in 1984, the institute has been constantly putting sincere efforts to meet the objectives under its mandated activities of identification, characterization, evaluation and conservation of domestic animal genetic resources of the country.*

*I am happy to inform that during the last one year, bureau scientists have identified and characterized new cattle germplasm of Ladakh region which is well adapted to harsh climatic and hypoxic conditions and also yields A2 type milk under extensive management system. Besides this, cattle populations of north-east and Konkan regions, Bargur buffaloes of Tamilnadu and buffaloes of Odisha state have also been characterized and found suitable for registration as new germplasm. Among small ruminants and other livestock, our scientists have characterized Mouli and Yelga sheep populations of Karnataka, Chitarangi and Dumba sheep of Rajasthan and Punjab, Long hair goat of Nagaland and local donkeys of Andhra Pradesh. In situ conservation of Hariana and Sahiwal cows has been taken in gaushalas where 17 calves were produced through AI. Germplasm repository of Gene Bank was strengthened by preserving more semen doses, embryos, epididymal sperms, DNA and somatic cells as ex situ activity. New initiative for developing and preserving the fibroblast cell line of Bactrian camel has been taken. Y-chromosomal microsatellite based diversity analysis has also been accomplished in 18 native cattle breeds. We established that grazing cows have higher MUFA and PUFA as well as essential amino acid contents as compared to stall fed animals. Work on analysis of meat quality parameters in Bandur and local sheep was also carried out which indicated higher tenderness in Bandur sheep meat. Being the nodal agency, bureau registered nine new breeds of livestock and poultry which increased the total registered breeds in the country as 160.*

*Milestones have also been achieved under externally funded projects with the sincere efforts of bureau scientists. Ten populations of seven different species of livestock and poultry have been genetically characterized under Network Project on AnGR. A de-novo transcriptome assembly representing ten different tissues of Dromedarian and Bactrian camel was constructed. Databases have been developed for SNPs identified in these two species as well as for candidate genes related to milk production, disease resistance and adaptive traits of cattle and buffalo. In buffalo, data generated through genotyping by sequencing helped in the identification of QTLs for milk fat and milk protein percentage, age at first calving, somatic cell score. Besides using the SNP data generated on 15 buffalo populations, a medium density SNP chip, represented by 98346 genome wide SNPs is also being developed. Under National Fellow scheme, transcriptome data was generated which helped in the identification of several genes and pathways responsible for thermo-tolerance in cattle and* *buffalo. Work carried out under DRDO funded project on Zanskari horses identified the genes responsible for hypoxic endurance. Under NASF project on health implications of A1/A2 beta casein variants, sequence characterization of beta casein gene identified a number of nucleotide variations between Bos indicus and Bos taurus cattle.*

*Institute has currently 20 research projects, five externally funded and one National Fellow project. During last one year our scientists published 48 research articles and several technical and popular articles. Six training programs were organized on capacity building under HRD program. To review the progress under different research projects, IRC and RAC meetings were held in time. Awareness among masses on utility of AnGR was generated by holding exhibitions, brain storming sessions and lectures. Apart from the individual awards fetched by the scientists, Institute received Ganesh Shankar Vidyarthi Krishi Patrika Puruskar (2nd) of ICAR for its publication 'Pashudhan Prakash'. Bureau attracted a number of distinguished persons which included Dr. James M. Reecy, Director of the Office of Biotechnology, Iowa State University, Ames, Iowa, USA, DG and DDG (AS), ICAR, Secretary (ADF), Min. of Agri. & Farmers Welfare, Govt. of India, Additional Secretary, DARE& Secretary (ICAR).*

*I convey my heartfelt thanks to Dr T. Mohapatra, Secretary (DARE) & DG, ICAR, Dr H Rahman and Dr J.K. Jena, DDGs (AS), Dr R S Gandhi, ADG (AP&B) and Dr Vineet Bhasin, PS for their constant support and guidance. I appreciate all the scientists, technical, administrative officers and other staff members as well as research scholars of the bureau for their contribution in the progress of the institute. At the same time, I congratulate the editorial team for compiling the bureau's achievements in the shape of this document and publishing it in time.*

*Looking forward to suggestions for improvement.*

*(ARJAVA SHARMA)*
*DIRECTOR*

# Executive summary

National Bureau of Animal Genetic Resources has been the nodal organization in India with the mandate "Identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country and coordination and capacity building in animal genetic resources management and policy issues". Three divisions namely Animal Genetic Resources Division, Animal Genetics Division and Animal Biotechnology Division along with Livestock Information Unit and Network Project Unit were created in 2013 to achieve the objectives under institute's mandate. Total expenditure of Rs. 990.49 lakh was made under Non-plan and Plan budget against the total receipt of Rs. 1014.00 Lakhs during financial year 2016-17. Under Network project, total expenditure was Rs. 100.93 Lakhs, against Receipt of Rs. 101.00 Lakhs. A Revenue to the tune of Rs. 34.70 Lakhs was generated against the target of Rs. 24.81 Lakhs assigned by the council for the year 2016-17.

ICAR- NBAGR has also been anodal agency for registering the breeds. The breed registration Committee approved registration of nine new indigenous breeds of livestock and poultry. This included Badri cattle, Teressa and KodiAdu goats, Chevaadu and Kendrapada sheep, Tenyi Vo, Nicobari and Doom pigs, and Kaunayen chicken. With these additions total number of registered indigenous breeds reached 160 consisting of 40 for cattle, 13 for buffalo, 26 for goat, 42 for sheep, 6 for horses & ponies, 9 for camel, 6 for pig, 1 for donkey and 17 for chicken.

Indigenous cattle (Ladakhi) of Ladakh region of Jammu & Kashmir state was characterized through survey. It is a short stature and docile cattle with coat of black and brown colors with long and shiny curly hair. Hump and dewlap are not well developed. Horns are medium and curved pointing forward. Daily milk yield ranged from 2 to 5 litres with 5.24% fat. Ladakhi cattle revealed the higher frequency (0.90) of A2 allele.

Indigenous cattle of North East states of India were characterized and documented. Here cattle are reared for milk, meat, bullock power and manure. Animals were small to moderate in size. Brown coat colour predominated except Siri cattle of Sikkim. Daily milk yield ranged from 1.0 to 5.0 kg. Indigenous cattle of Nagaland and Sikkim were slightly bigger than that of Meghalaya. Height at wither was the most differentiating trait in these cattle populations. Canonical discriminate analysis showed maximum distance (15.04) between Sikkim and Tripura cattle, whereas, Meghalaya and Tripura cattle had the lowest (2.51). Siri of Sikkim and Tho-Tho of Nagaland were found different from other cattle.

Cattle of Konkan region of Maharashtra were surveyed and characterized in their native tract. The animals are small in size with small to medium hump and dewlap in cows and medium to large in bulls.The average daily milk is 2.23 kg. Few elite animals with milk production of 5-6 litres were also present.

Bargur buffalo of Tamil Nadu was surveyed for phenotypic characterization. The animals are maintained under zero input system and are mainly reared for manure, milk and meat. The milk yield of the animals ranges from 1.5 to 2.0 liters per day. The animals are about 102.10±1.23 cm in height and are able to graze in the hilly terrain.

Phenotypic and genetic characterization of Mouli and Yalaga sheep populations of Karnataka was accomplished under field conditions. Mouli sheep are tall with deep body and long legs. Coat colour is white with or without brown spots/patches. A brown ring is present around the eyes. Nose line is roman. Yalaga animals are medium to large sized.Coat colour is white and consisted of small thick hair. Face is white, with black or brown patches of varying size.

Chitarangi sheep was surveyed in Fazilka and Muktsar of Punjab, Sri Ganga Nagar of Rajasthan. 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.

Dumba sheep was characterized through breed survey. The coat colour is white and brown mostly. Ears are large in size. The deposition of fat in the tail is a distinct characteristics. Average adult body weights of male and female were 90.92 and 66.33 kg, respectively.

Eight sheep populations (Kolhapuri, Lonand, Marwari, Munjal, Muzaffarnagri, Madgyal, Sangamneri and Solapuri) profiled on seven morphometric traits were classified using Classical Discriminant Function Analysis and Artificial Neural Network (ANN) models. Discriminant analysis results showed that all the measured traits were significant ($p<0.0001$) indiscriminating the eight sheep breeds. The ANN model gave more than 99% assignment accuracy between various breed combinations.

Long hair goat of Nagaland was characterized and evaluated in their native tract. Different colour variants viz. white with black patches, black, brown with grey hair were recorded. Animals possessed proportionate body, straight nose line, medium size, erected, horizontally placed ears. Long hair was present in the adult males. The average body weight was 31.48 Kg in adult males and 25.79 Kg in females. Hair obtained from the Nagaland goats has commercial utility for the tribal people.

Phenotypic and genetic variations associated with tick infestation were studied in Indian cattle populations. Females were more susceptible than male (60.82%). Animals less than one year of age group were more infected (73.33%).

Under the project on conservation of Sahiwal and Hariana cattle at Gaushalas, Hariana and Sahiwal cows were selected in four Gaushalas of Karnal (Haryana). A total of 90 Hariana and 26 Sahiwal cows were inseminated artificially. A total of 17 calves were born. In Sahiwal, daily milk yield ranged from 4.0 to 10.0 kg, whereas in Hariana ranged from 1.0 to 4.0 kg.

An appropriate extender has been developed for freezing epididymal sperms of indigenous sheep for ex situ conservation utilizing cauda epididymal spermatozoa. *In vitro* fertilization revealed that frozen epididymal spermatozoa retain the fertility potential. Germplasm repository at Gene Bank NBAGR is being strengthened by preserving diversified form of germplasm (semen, embryos, DNA,epididymal sperms and somatic cells).

Microsatellite based diversity analysis of Ladakhi cattle revealed 9.79 mean number of alleles and 0.749 observed heterozygosity, reflecting sufficient genetic diversity. The phylogenetic analysis revealed genetic distinctness of Ladakhi population with respect to other analyzed Indigenous breeds of cattle. Haplotypic diversity based on mtDNA was 0.942. A high proportion of haplotypes (67%) were scored indicating the existence of sufficient mtDNA haplotypic diversity in Ladakhi cattle.

Haplotype diversity based on seven Y chromosomal microsatellites was explored in 202 bulls representing 18 native cattle breeds. A total of 19 *Bos indicus* specific haplotypes were identified. The six most common haplotypes had a total frequency of 94%.

In Bargur buffalo, a total of 40 haplotypes were observed with an overall haplotype diversity of 0.9524 and nucleotide diversity 0.03894 during mtDNA D loop analysis. At microsatellite level, overall average number of alleles was 8 with observed heterozygosity of 0.66. FIS value was found to be 0.056±0.037.

Biochemical tests run on sera samples collected from 10 animals each of Chilika, Paralakhemundi and Murrah buffaloes showed relatively higher urea/creatinine ratio in Chilika compared to Paralakhemundi and Murrah, indicated better adaptation of Chilika to dehydrated conditions. Microsatellite data generated for 23 markers on Chilika, Kalahandi and Paralakhemundi after comparison with other riverine and swamp buffaloes revealed considerable diversity across populations. Mode shift analysis divulged absence of bottleneck.

The diversity analysis of sheep populations of Karnataka revealed 5.23, 0.637 and 0.783 effective number of alleles, mean observed heterozygosity and gene diversity respectively in Mouli sheep and 4.865, 0.596 and0.757 respectively in Yalaga sheep. Absence of a recent reduction in the effective population size or a genetic bottleneck was observed.

A study was conducted on HSPgene polymorphism and expression profiles and its association with hemato-physio-biochemical parameters in Chokla, Magra, Marwari, and Madras Red sheep. Gene expression analysis revealed higher expression in less adapted animals with Madras Red <Magra<Chokla< Marwari expression pattern.

Genetic characterisation of Nagaland goat by microsatellite markers showed 0.347 observed heterozygosity.The population tested for HW equilibrium indicated departure from Hardy-Weinberg Equilibrium. Polymorphic information content value was 0.494, revealing its usefulness in determining the genetic diversity. Mode shift test suggested the absence of bottleneck.

Microsatellite based genetic characterization of local donkeys of Andhra Pradesh revealed 12 scorable loci of the horse origin. Observed number of alleles was 6.92 with mean heterozygosity of 0.57. Genetic diversity estimate (FIS) was 0.21 indicating a moderately high level of inbreeding. The cumulative exclusion probability of these loci was 0.999892 indicating their suitability for parentage testing in these donkeys.

Comparative profile of milk metabolites of grazing indigenous cattle (Sahiwal), exotic (Holstein Friesian) and crossbred (Sahiwal x Holstein Friesian) cows maintained in intensive system of management was studied. The milk of grazing cow was richest in protein and fat percentage. Milk of grazing indigenous cow has more than two fold level of β-carotene as compared to Indigenous, exotic and cross bred cows. Milk of grazing cows was richest in UFA (35%) followed by indigenous cow (31.46%). Milk of grazing cows was richer in MUFA and PUFA both. Major ω6 (Linoleic acid) and ω3 (Linolenic acid) fatty acids were significantly higher in grazing cows. Milk of grazing cows was the richest source of essential amino acids (1.2314 g/100g milk) among the group.

The tenderness of different muscles of the Bandur sheep had lower values (12.74N-22.65N) as compared to those of local sheep (16.44N-26.19N). The lower shear force values in Bandur sheep indicated greater tenderness which is a desirable trait. Sensory evaluation of the mutton revealed slightly higher juiciness and flavour in Bandur sheep meat but the difference between the two groups was not significant.

The pooled samples of Ladakhi and Sikkimi yaks were sequenced on a single lane of HiSEQ 2000. The number of reads ranged from 1227316 to 1126501. The average GC content of Ladakhi and Sikkimi yaks is 46.52 and 45.80 respectively. The mean read quality Phred score in Ladakhi and Sikkimi yaks ranged from 34.28 to 34.59 respectively.

Cytogenetic screening of 286 bulls of cattle and buffalo and 8 cows belonging to different government agencies was carried out for detecting any chromosomal abnormality/ aberration. Two bulls (Sahiwal and Red Sindhi) were found to carry the chromosomal defects. Total 92 bulls (73 cattle,10 buffalo) were also DNA tested for genetic diseases (Bovine leukocyteadhesion deficiency, Deficiency of uridine monophosphate synthase, Citrullinemia and Factor XIdeficiency). All the animals were found to carry normal genotype.

Under the network project, microsatellite based genetic characterization was done for the populations being characterized under XII plan. Measures of diversity which forms the basis for planning their utilization and/or conservation were calculated for ten populations of seven different species.All the populations except Tibetan sheep exhibited fair genetic variation. The diversity indices pointed towards diminished genetic diversity in the Tibetan, a valuable

Himalayan sheep breed classified as endangered. Indications of loss in the variability was also depicted by the higher heterozygote deficiency recorded for the Dharwadi buffalo (FIS = 19%), Hazra chicken (22%) and Arunachali Yak (14%). FST values of breed differentiation for Jalori and Mewari camel indicated that only 3.7% of the total genetic variation was due to unique allelic differences between the breeds, with the remaining 96.3% corresponding to differences among individuals within the breed.

DNA samples of Sahiwal, Tharparkar, Gir and Vechur cattle were genotyped using 777K SNP chip. Total 1000 markers, accounting 39 % of the genetic variation between the breeds were identified. The breeds were clearly classified into small and large sized indicating shared ancestry of large sized milch breeds. The highest linkage disequilibrium was observed in Gir and the lowest in Sahiwal. A number of genes were found under selective sweeps in different breed pairs, which may be helpful to map the QTL of economic important traits.

A database has been developed to store the information on genomic variations and sequences in candidate genes related to milk, disease resistance and adaptive traits on cattle and buffalo breeds.

NGS data of ten tissues of dromedarian and bactrian camel were *de novo* assembled using five different *denovo* algorithms. In addition to *de novo* assembly tissue wise the raw reads of the transcriptome of various tissues were separately mapped on the draft genomes available for camel and their relatives. The isoform analysis of the transcriptome using annotation procedures revealed a number of genes having 2 or more isoforms.

The database for Bactrian camel and dromedarian camel have been developed and are at present accessible through http://14.139.252.118/Dcamel/index.php (for Dromedarian camel) http://14.139.252.118/Bcamel/index.php (for Bactrian Camel). To tal 392179 and 277435 identified SNP can be visualized in dromedarian and Bactrian camels, respectively.

For Somatic cell banking, double humped camel (*Camelusbactrianus*) fibroblast cell line was successfully established by using primary explant technique.

GBS data was analysed for different chromosomes to Identify markers for economic traits in buffalo. QTLs on each of the 24 autosomes for milk fat, milk protein percentage, total fat yield, total protein yield, Age at first calving, Age at first heat and somatic cell score were prepared. All the QTLS were found distributed across the buffalo chromosomes. All the identified QTL in buffaloes have been compiled in the form of a buffalo QTL database at http:// 14.139.252.118:8084/BuffaloQTL/.

A Medium Density SNP chip with 15 populations of buffalo distributed throughout the country was developed. A total of 98346 SNPs have been identified which are genome wide and have passed the quality control parameters for development into an SNP Array. The mean distance among the SNPs is 27.9 Kb. This medium density SNP array can be used for Genomic selection in buffaloes.

Genome data mining was carried out in native cattle and buffaloes to unravel molecular basis of thermo-tolerance and adaptation to diverse environments. Local native cattle of Ladakh from high altitude and Sahiwal cattle from low altitude resulted in identification of several hundred differentially expressed genes, biological processes, molecular functions and pathways. The data revealed distinct transcriptome signature of PBMCs in Sahiwal and Ladakhi cows as revealed by hierarchical, k-means clustering and distinct heat maps. qPCR revealed significant increase in expression of hypoxia associated genes like HIF-1 and its regulated genes in high altitude cattle in Ladakhi cows suggesting their pivotal role in high altitude adaptation.

Tissue specific expression of isoforms of Na/K ATPase genes in riverine buffaloes was studied. Expression of ATP1A pointed towards the critical role of Isoforms in maintaining the ionic concentration in the cells and tissues.

Effect of heat stress on cellular parameters was assessed in Sahiwal, HF and Murrah buffaloes. Viability of heat stressed PBMCs was lower than unstressed, significantly more in HF at time points 4 hr, 16 hr and 24 hr post heat stress. The cytotoxicity was significantly ($p<0.05$) higher in HF cows than others. Cytotoxic levels, apoptosis was highest in PBMCs of HF cows and reached maximum level at 16 hr and 24 hr post heat stress showing higher rate of cell death. The study indicated superior cellular tolerance of Sahiwal cows than HF and Murrah buffaloes. microRNAs associated with stress and immune response showed significant ($p<0.05$) induction in their expression after heat stress in Sahiwal.

A study was conducted for identification of genes and molecular pathways associated with endurance trait in Zanskari ponies. 12 Zanskari horses and 6 GS mules were put on trial for endurance at high altitude of Ladakh region. Results revealed that, GS mules had significantly higher values of various physiological parameters than Zanskari ponies after endurance test. Transcriptomic analysis of Zanskari ponies PBMCs resulted in identifying the genes up-or down-regulated before and after endurance exercise at high altitude. 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 during pre and post exercise and resting periods.

Under NASF project on health implication of A1/A2 milk of cattle, sequence characterization of beta casein gene was carried out to determine the variants/ haplotypes across Indian native breeds, crossbred and exotic cattle. A number of nucleotide variations identified between *Bos indicus* and *Bos taurus* cattle. In Indian cattle, frequency of all known variations was low. Six haplotypes were observed where A2 type occurred with maximum frequency of 0.86.

A total of 11 research projects, including one externally funded were completed during the year. At present 20 research projects including five externally funded and one National Fellow projects are on-going.

Total 48 research papers were published in National and International Journals of high impact factor. Ten technical/popular articles , 5 books, 4 monographs and training manuals were also published by the institute. Four patents were filed to the Indian Patent Office,New Delhi.

Six training programmes and two brain storming sessions were organized by the Institute. Short training course on "Advanced tools for conservation of domestic livestock diversity"and Model training course on "Strategies for characterization and conservation of animal and poultry genetic resources" were organized for scientific and academic staff. Other important trainings included Awareness and skill up gradation program on "Intellectual Property Rights and related aspects in the area of agriculture and livestock sector", Training cum awareness Programme on "IP Protection and Technology Transfer in Indian Perspective", Training on "Skill upgradation in laboratory methods".

Scientists of the Bureau participated actively in Mera Gaon Mera Gaurav programme where they visited various villages and created awareness among farmers. Five exhibitions on AnGR were organized at various places to showcase institute's activities and sensitize farmers about the benefits of indigenous animals.

Foundation Day of Bureau, Biodiversity day, Republic Day and Independence Day, Rashtriya Swachhta Abhiyan, Vigilance Week, Hindi Pakhwada were celebrated at NBAGR campus.

Library was enriched by adding 20 new books and 30 journals during the period.

The meetings of Research Advisory Committee (RAC) and Institute Research Committee (IRC) were held on time. The progress of research projects was reviewed during these meetings.

Bureau staff participated in the various events of Annual Sports Meet-2017 organized on the occasion of Republic day. NBAGR basketball team won silver medal (runner-up) in ICAR North Zone Sports Meet, held at NDRI, Karnal.

A number of distinguished persons including DG, DDG (AS), ICAR visited the institute and interacted with scientists.

Scientists were also deputed for training and attending the workshops, symposia and conferences within the country

Being the NDRI faculty, NBAGR scientists taught various courses of Animal Genetics & Breeding, Animal Biotechnology and Animal Biochemistry disciplines to NDRI post-graduate students. They also guided the students of different institutes and universities for their thesis of masters and PhD degrees.

Apart form the individuals awards won by the scientists, the institute also received ICAR's Ganesh Shankar Vidhyarthi Krishi Patrika Purshkar (second prize) for the best publication of Pashudhan Prakash, Pancham Ank (2014).

During the period 2016-17 manpower of bureau included 28 scientific, 16 technical, 16 administrative and 5 skilled supporting staff persons. Two scientists and one technical one administrative staff got promotions to the next higher grade. One skilled supporting staff member was superannuated.

Sh. Sopal, Upper Divisional Clerk left for heavenly abode on 13 April, 2016.

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Certificate No.: VNBAGR070815Q2913
Date of Issue : 07/08/2015
Date of Expiry: 06/07/2018
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2nd Surveillance on or before: 06/07/2017

*Authorized by*
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*The approval is subject to the company maintaining its system to the required standards, which will be monitored by VRC Services Inc. The above audited accredited scope shall be monitored by KAN rules & regulations and unaccredited scope shall be monitored by VRC Services Inc. management scheme regulations.*

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# HISTORY AND PROFILE

- About Bureau
- Divisional Profile
- Organogram
- Financial Outaly

# HISTORY AND PROFILE

## About Bureau

The need for the establishment of National Institute of Animal Genetics was accepted in principle during 4th Five Year Plan. During 5th and 6th Five Year Plan, various government agencies coordinated the efforts for the establishment of this Institute. Therefore, National Bureau of Animal Genetic Resources (NBAGR) and National Institute of Animal Genetics (NIAG) were set up on 21st September, 1984. These institutes started at Regional Station of National Dairy Research Institute, Bangalore. Bureau and the institute were then shifted to Karnal in 1985 and temporarily housed in NDRI main Campus before shifting to its own campus at Makrampur, Karnal in 1994. Both Institute and the Bureau were merged to function as a single unit as National Bureau of Animal Genetic Resources in 1995. National Bureau of Animal Genetic Resources has been the nodal organization in India with the mandate and objectives as given below:

### MANDATE

- ☞ Identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country.
- ☞ Coordination and capacity building in animal genetic resources management and policy issues.

### OBJECTIVES

- To conduct systematic surveys to characterize, evaluate and catalogue farm livestock and poultry genetic resources and to establish their National Data Base.
- To design methodologies for ex-situ conservation and in-situ management and optimal utilization of farm animal genetic resources.
- To undertake studies on genetic characterization using modern techniques of molecular biology.
- To conduct training programmes as related to evaluation, characterization and utilization of animal genetic resources.

## Divisional Profile

Following divisions have been created in 2013 to achieve the institute's mandate and objectives:

1. Animal Genetic Resources Division
2. Animal Genetics Division
3. Animal Biotechnology Division

In addition to this two units namely- Livestock Information Management Unit and Network Project Unit are functioning to support the divisional activities.

### Animal Genetic Resources Division

Animal Genetic Resource (AGR) Division has been engaged in developing formats for breed characteristics, survey strategies and breed description methodologies. The present form of Animal Genetic Resources (AGR) division came into existence after a number of transformations. In 1987, Animal Genetic Resources and Animal Conservation divisions was merged into Animal Genetics Resources and Conservation Section. In 1991 a new section of Animal Gene Bank was created which was reframed as Animal Physiology and Reproduction section during 1991-92. Reorganization continued and in 1992-93 the then NBAGR had one section and two units viz. Livestock Information and Management Section, Animal Genetics Resources Unit and Animal Conservation and Gene Bank Unit. During 1994-95 the sections and units were again reframed as: a) Information and Management Unit/Computer Unit b) Animal Genetic Resources and Conservation Section c) Animal Physiology and Reproduction Section. In 1996, the Animal Physiology and Reproduction Section was merged into Animal Genetic Resources Division and since then the division continues in its present form.

At present Animal Genetic Resources Division along with its 'National Gene Bank' is engaged in phenotypic characterization, which is accomplished through systematic/pilot field surveys to assess flocks/herd structure, population status, practices, phenotypic characteristics, body biometry, reproduction and production performance, and marketing of live animals and products. The production performance of local breeds is evaluated and recorded under agro-climatic conditions of their habitat. The surveyed breeds/populations are documented in the form of breed monographs, breed descriptors and charts in addition to research publications. Based on the information, new strategies have been formulated for improvement and conservation of the breeds under field conditions. The *in situ* conservation has been implemented for breeds of various livestock species. In addition, the division is also working in the frontier areas of long term *ex-situ* conservation of germplasm.

### Animal Genetics Division

The major research thrust in initial years of National Institute of Animal Genetics (NIAG) was on characterization of indigenous genetic resources using cytogenetics and biochemical polymorphism studies. The initial research projects encompassed studies of chromosomal profile of cattle, buffalo, sheep, goat, pigs and camel. Since cattle, buffalo and goats had relatively more information available, so emphasis was laid on species, like camel, pigs, equines and poultry. In the year 1997, a major change in the focus of the divisional research activities was to switch to molecular characterization and biodiversity analysis of native breeds of cattle, buffalo, sheep, goat, other livestock species (camel, horse, yak, mithun, pig, donkey) and poultry using molecular markers especially microsatellites. To understand the nature of mitochondrial DNA diversity, maternal lineages and evolutionary relationships amongst native breeds, efforts were also made using mitochondrial D-loop marker. Significant work was carried out in the field of immunology especially on the MHC and bovine interleukins in Indian cattle. In recent years, sizeable progress has been made in sequence characterization and identification of single nucleotide polymorphism (SNPs) at several candidate gene loci influencing trait of functional importance viz; milk yield/composition, wool, meat, growth and Development, adaptive, thermotolerance, disease resistance in our native breeds from different livestock species. The division has successfully completed the NAIP and several DBT projects.

After the unification of NBAGR and NIAG to National Bureau of Animal Genetic Resources, all the scientists working in the fields of cytogenetics, immunogenetics, and molecular genetics became the part of Animal Genetics Division which was established in the year 1996 and formally approved in 2014 with the objective 'Molecular, immunological, biochemical , cytogenetic characterization and candidate gene analysis of livestock species'. The division has presently five principal scientists, three senior scientists, one scientist Senior Scale, one technical officer, one steno grade III and one skilled supporting staff. During the period under report, scientists from this division completed three IRC and one Cabin project successfully. The results were published in reputed journals of high impact factor. Scientists also fetched several awards. Apart from this, scientists were involved in teaching and guiding the M.Sc and Ph.D students. One of the important activities of the division is to provide consultancies/services for testing the breeding bulls for any inheritable abnormality and thus generate revenue for the institute.

### Animal Biotechnology Division

Animal Biotechnology Division was established at ICAR-NBAGR by the orders of council in 2014, merging erstwhile DNA Fingerprinting Unit into it. At present, six scientists from the discipline of animal biotechnology, supported by three technical and one skilled supporting staff are working in the division in the areas of mandated institutional activities. Work is going on under various institute and externally funded projects on genetic characterization of livestock species with emphasis also on the use of genomic tools for the identification and evaluation of genes and transcripts associated with adaptation, disease resistance and various production traits. In addition to five institutional projects, the work has been carried out on three externally funded collaborative projects also. Under one DRDO funded project in collaboration with Defense Institute of High Altitude Research, the transcriptome analysis of PBMCs in local Zanskar ponies of Ladakh under controlled stress conditions, has helped in identification of transcripts responsible for hypoxia and high altitude adaptation. Considering the important breakthroughs made during previous term, the National Fellow project on heat stress adaptation in cattle has been given extension for next five years. The work is being carried out to understand the molecular basis of thermal adaptation in indigenous cattle and buffalo, generating genome wide SNP and transcriptome profiles. Major achievements of the division during last one year include- STR markers and mitochondrial D-loop sequence based diversity analysis of cattle, buffalo and sheep genetic resources of India has been accomplished. Characterization and polymorphism detection in candidate genes governing milk, meat production, disease resistance in cattle, sheep and buffalo done. Transcriptome data has been generated on sheep skeletal muscle and cattle and equine PBMCs. Under NASF funded project, A1/A2 and other allelic variants identification in beta casein as well as their impact on milk production traits in indigenous and crossbred cattle has been explored. Transcriptome analysis and whole genome scanning has been employed, to help in understanding the molecular mechanism of thermo tolerance in indigenous cattle compared to exotic. Swamp-riverine hybrids have been identified first time among Chilika buffaloes of Odisha using cytogenetic and mitochondrial D-loop sequencing tools. Data has been collected on infertility traits among breeding bulls for association of genetic polymorphism identified in candidate genes. Phenotypic and genetic characterization of Ladakhi cattle, a unique bovine germplasm also completed. Work has also been initiated on understanding the differential tick resistance mechanism among indicus and crossbred/exotic cattle.

Scientists of the division are also involved in teaching and guiding student, being faculty members of biotechnology discipline at National Dairy Research Institute, Karnal. The division has received three Dr. PG Nair best scientific worker awards of the Bureau so far, besides several best poster and oral presentations awards. Most of the scientists of the division are well trained in reputed labs abroad and have received several awards and recognitions in the field of Animal Biotechnology. The division remains top in publishing quality research papers in national & international journals of high repute.

### Livestock Information Management Unit

This Unit is engaged in digitization of information on animal resources and to provide it to the users in an easily retrievable format. This section also provides LAN, Internet and computing facilities to the institute. The section is also looking after registration of livestock and poultry genetic resources.

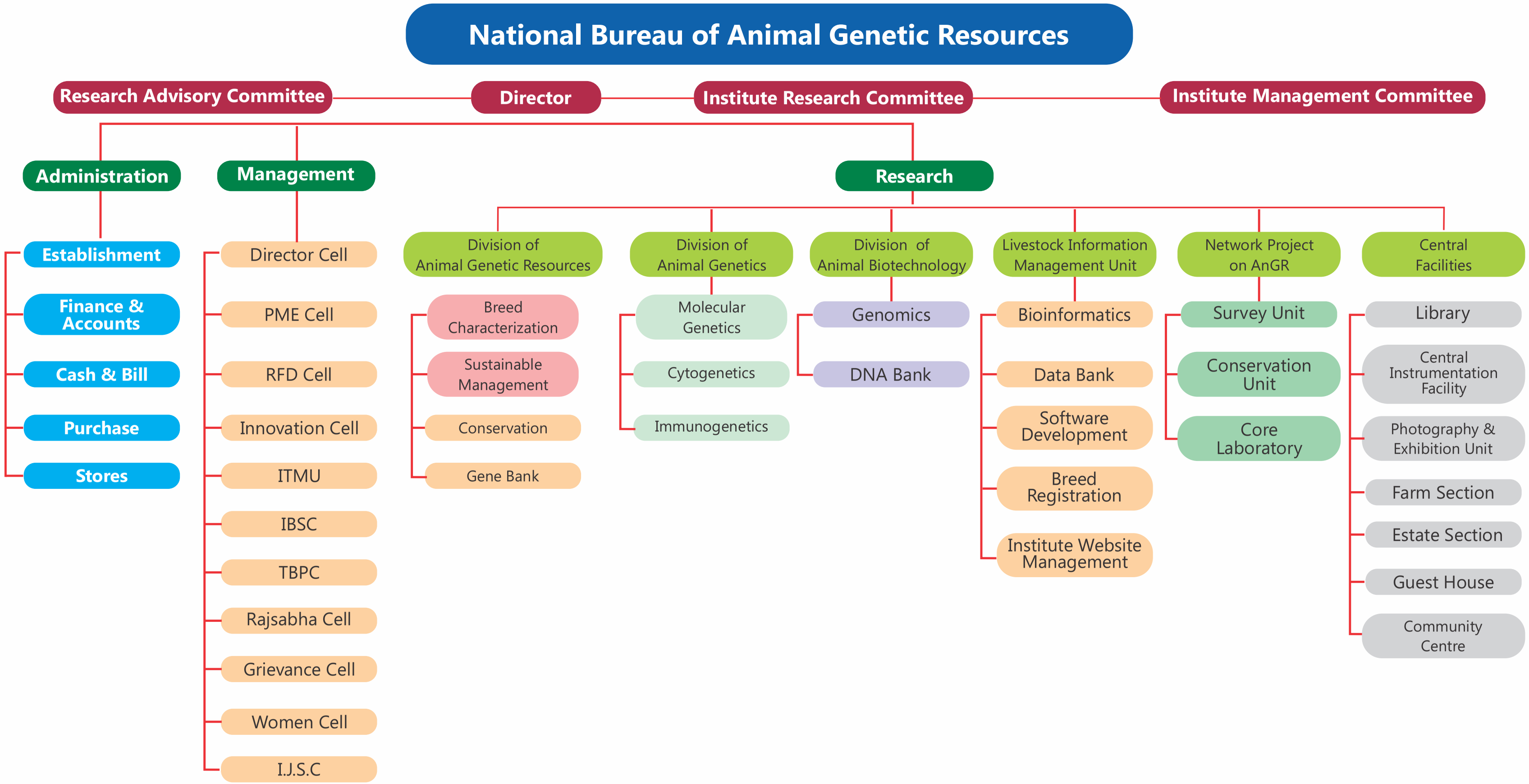
### Network Project Unit

The Network project was initiated in 1996 with the following objectives:

- To characterize the breeds in terms of both qualitative and quantitative traits.
- Molecular genetic characterization and candidate gene studies in indigenous breeds.
- To develop the breed descriptors.
- To conserve the germplasm.

There were 8 centers in VII plan for characterization of breeds. In IX and X plan 12 new centers in each plan were undertaken for characterization of breeds. Genetic characterization and conservation activities were also initiated from IX plan. In XI plan one core lab was established in NEH region and buffalo genomics work was also taken up. During current XII plan 17 new Breeds/populations were undertaken for characterization and 4 at risk breeds for conservation. The updated achievements include phenotypic and genetic characterization and development of breed descriptors of 11 breeds of cattle (Deoni, Ongole, Gir, Umblachery, Bachaur, Dangi Amritmahal. Khillar, Gaolao, Tho Tho, Gangatiri), 3 breeds of buffalo (Jaffarabadi, Nagpuri, Surti), 8 breeds of sheep (Changthangi, Deccani, Mecheri, Mandya, Rampur Bushair, Banpala, Coimbatore, Chhota-Nagpuri), 5 breeds of goat (Osmanabadi, Barbari, Attapady, Ganjam, Mehsana), 2 breeds of chicken (Aseel, Ankleshwar), Kutchi Camel, Spiti horse and Arunchali Mithun. Conservation of AnGR includes 5 cattle breeds (Krishna Valley, Ponwar, Kherigarh, Kangayam, Nagori), 3 buffalo breeds (Pandharpuri, Jaffarabadi, Toda), 3 sheep breeds (Magra, Nilgiri, Kilakarsel), 2 goat breeds (Beetal, Surti) and Spiti horse.

## Organogram


National Bureau of Animal Genetic Resources
Research Advisory Committee
Director
Institute Research Committee
Institute Management Committee
Administration
Establishment
Finance & Accounts
Cash & Bill
Purchase
Stores
Management
Director Cell
PME Cell
RFD Cell
Innovation Cell
ITMU
IBSC
TBPC
Rajsabha Cell
Grievance Cell
Women Cell
I.J.S.C
Research
Division of Animal Genetic Resources
Breed Characterization
Sustainable Management
Conservation
Gene Bank
Division of Animal Genetics
Molecular Genetics
Cytogenetics
Immunogenetics
Division of Animal Biotechnology
Genomics
DNA Bank
Livestock Information Management Unit
Bioinformatics
Data Bank
Software Development
Breed Registration
Institute Website Management
Network Project on AnGR
Survey Unit
Conservation Unit
Core Laboratory
Central Facilities
Library
Central Instrumentation Facility
Photography & Exhibition Unit
Farm Section
Estate Section
Guest House
Community Centre

## Financial Outlay

### Budget estimate under Plan & Non-Plan and Network Project of NBAGR along with expenditure for the financial year 2016-17

Rs. in Lakhs

| Head | Non-Plan | | Plan | | Network Project | |
|---|---|---|---|---|---|---|
| | RE | Exp. | RE | Exp. | RE | Exp. |
| **Capital** | | | | | | |
| i) Works | 0.00 | 0.00 | 10.80 | 10.79 | 0.00 | 0.00 |
| ii) Other capital expenditure | 8.00 | 7.42 | 29.20 | 29.04 | 0.00 | 0.00 |
| **Total Capital** | **8.00** | **7.42** | **40.00** | **39.83** | **0.00** | **0.00** |
| **Revenue** | | | | | **101.00** | **100.93** |
| i) Establishment expenses | 773.50 | 764.26 | 0.00 | 0.00 | 0.00 | 0.00 |
| ii) Traveling Allowance4.00 | 2.89 | 10.00 | 10.00 | 0.00 | 0.00 | |
| iii) Research & Operational expenses | 70.00 | 69.98 | 172.00 | 171.97 | 0.00 | 0.00 |
| iv) Administrative Expenses | 113.00 | 112.97 | 7.80 | 7.80 | 0.00 | 0.00 |
| v) Miscellaneous expenses | 8.50 | 8.36 | 0.20 | 0.19 | 0.00 | 0.00 |
| **Total Revenue** | **969.00** | **958.46** | **190.00** | **189.96** | **101.00** | **100.93** |
| **Pension & Retirement benefits** | **37.00** | **24.61** | **0.00** | **0.00** | **0.00** | **0.00** |
| **Grant Total** | **1014.00** | **990.49** | **230.00** | **229.79** | **101.00** | **100.93*** |

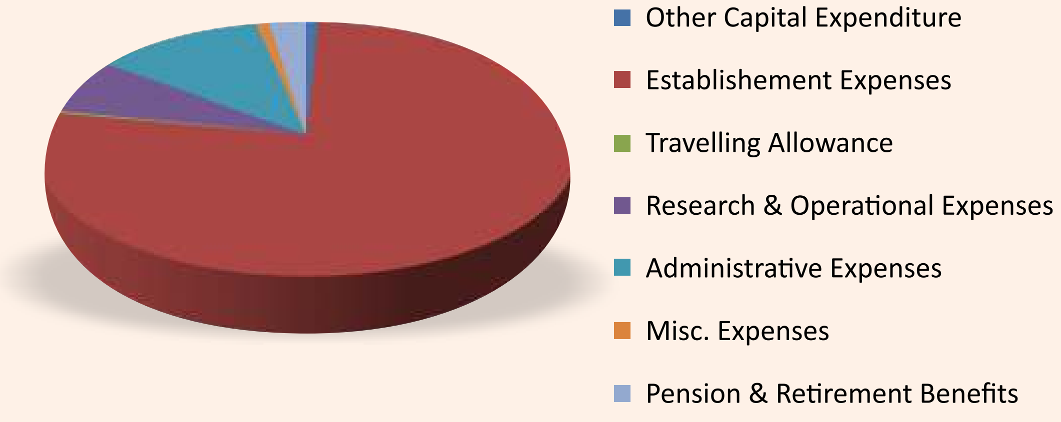
*Includes Releases of Rs.84.93 lakhs

### Revenue Generated

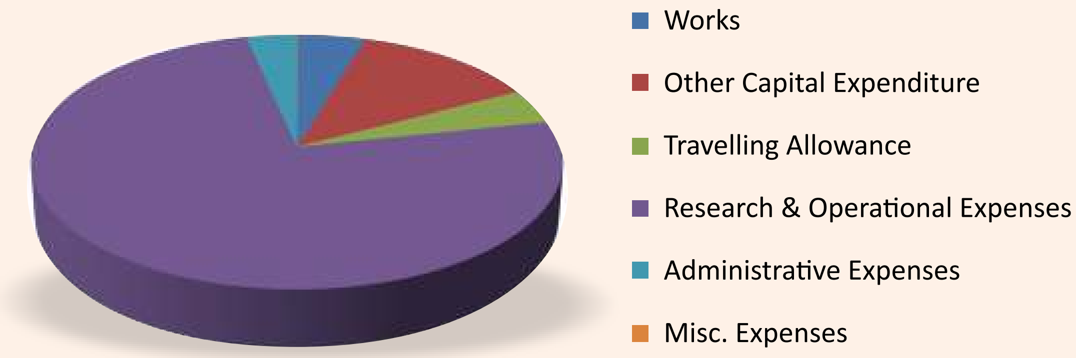
| Sr. No. | Head of Account | Amount (Rs.) |
|---|---|---|
| 1. | Sale of Publication & Advertisement | 33575 |
| 2. | Licence fee | 179204 |
| 3. | Training Programs - Income | 176350 |
| 4. | Hostel and Guest house rent | 298247 |
| 5. | Sale of Technology | 701600 |
| 6. | Sale of farm Produce | 155501 |
| 7. | Others Misc. Revenue Receipts | 1925826 |
| | **Total** | **3470303** |

Revenue Target : 24.81 Lakh
Target Achieved : 34.70 Lakh

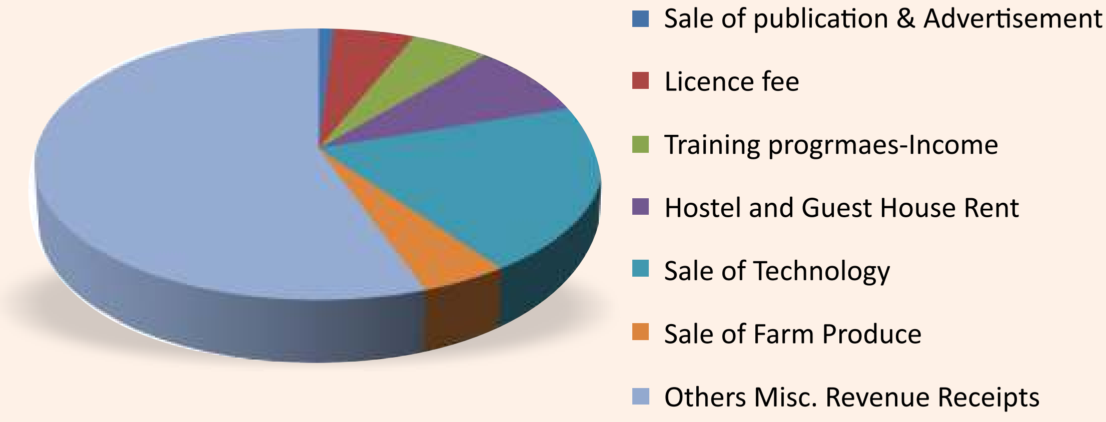
### Funds Utilization under Non-plan



### Funds Utilization under Plan



### Revenue Generation



# RESEARCH ACCOMPLISHMENTS

- Livestock Information Management
- Phenotypic Characterization and Evaluation of AnGR
- Conservation of AnGR
- Genetic Characterization and Genomics
- Network Project on AnGR (Core Lab)
- Externally Funded Projects

## Livestock Information Management

### Registration of Breeds

Breed registration Committee in its meeting on 21st June, 2016 at New Delhi approved registration of nine new breeds of livestock and poultry. This included one breed of cattle, two breeds each of goat and sheep, three breeds of pig and one breed of chicken. After including these, total number of registered indigenous breeds now in the country is 160, which include 40 for cattle, 13 buffalo, 26 goat, 42 sheep, 6 horses & ponies, 9 camel, 6 pig, 1 donkey and 17 chicken.

*Newly registered breeds of livestock and poultry*

| Species | Breed | Home Tract | Accession number |
|---|---|---|---|
| **Cattle** | Badri | Uttarakhand | INDIA_CATTLE_2400_BADRI_03040 |
| **Goat** | Teressa | Andaman & Nicobar | INDIA_GOAT_3300_ TERESSA _06025 |
| | Kodi Adu | Tamil Nadu | INDIA_GOAT_1800_ KODIADU _06026 |
| **Sheep** | Chevaadu | Tamil Nadu | INDIA_SHEEP_1800_ CHEVAADU _ 14041 |
| | Kendrapada | Odisha | INDIA_SHEEP_1500_ KENDRAPADA _ 14042 |
| **Pig** | Tenyi Vo | Nagaland | INDIA_PIG_1400_ TENYIVO _09004 |
| | Nicobari | Andaman & Nicobar | INDIA_PIG_3300_ NICOBARI _09005 |
| | Doom | Assam | INDIA_PIG_0200_ DOOM _09006 |
| **Chicken** | Kaunayen | Manipur | INDIA_CHICKEN_1200_ KAUNAYEN _12017 |

***Badri Cattle:*** Badri cattle are available in hilly areas of Uttarakhand. Badri cattle are small in size having long legs and varied body colours – black, brown, red, white or grey. Hooves and muzzle are black or brown in colour. Hump prominent. Udder is small in size, tucked up with the body. These are well adapted to the hilly terrain and climatic conditions and comparatively more resistant to diseases. Estimated population is approximately 16 lakhs.

***Teressa Goat:*** It is an indigenous goat breed maintained by Nicobari tribal farmers of Nicobar group of islands. These goats are generally tall, sturdy, brownish or dark tan or black or white in colour with white and black patches. The black hair on dorsal midline up to the tail is important feature of this breed. Black colored muzzle, eyelids and hoofs. Peculiar white patch/line starting from inner canthus of both eyes or from eye brows and extending up to nostrils or mouth is also noticed. Tail is medium to long. Large horn with flat base. Erected ears directing downwards. Adult body weight varies from 50 to 79kg. Estimated population is about 7,721.

***Kodi Adu Goat:*** Kodi Adu goats are native to Thoothukudi & Ramanathapuram districts of Tamil Nadu. These are tall, long, lean and leggy animals with compact body. Based on body colour, they are classified into two colour varieties viz. Chem-Porai and Karum-Porai. Chem-Porai goats are white in colour with varying degree of reddish brown colour and intensity, whereas, Karum-Porai goats are white in colour with varying extent of splashes of black colour. They are reared

mainly for meat. Adult body weight varies from 15 to 59kg. Population of these goats is about 1,67,000.

**Chevaadu Sheep:** Chevaadu sheep are found in Tirunelveli district of Tamil Nadu. Animals are small to medium in size. Two colour variant viz. light brown and dark brown or tan are present. Body is covered with brown hair. Head is erected and high in disposition. Horns are curved horizontally outward, backward with blunt conical apex having few thick ridges. Horn is light brown in colour. Adult body weight varies from 18 to 39kg. Estimated population is about 1,58,200

**Kendrapada Sheep:** Breeding tract of Kendrapada sheep comprises of six coastal districts of Odisha viz. Kendrapada, Jagatsingpur, Cuttack, Puri, Jajpur and Bhadrak . These sheep are mostly brown in colour. Head, face, belly and legs are bare. Rest of the body is covered with non-lustrous hair. Animals have horizontal ears; short, straight and drooping tail. Button type horns in few males were also noticed. Adult body weight varies from 24 to 30kg. Estimated population is about 1,23,000.

**Tenyi Vo Pig:** These are indigenous pigs reared in Nagaland mainly for pork production. These are pot bellied animals with sagging back and pendulous belly touching the ground in females, straight tail ending with white switch reaching the hock joint, white stocking, white markings on the forehead and ventral body. Tenyi Vo pigs have strong and long tapering snout, small erect ears and bright alert eyes. Adult body weight varies from 35 to 50kg. Estimated population is about 60,000-70,000

**Nicobari Pig:** Nicobari pigs are indigenous pigs of Nicobar Islands and are reared by Nicobari tribes since time immemorial. They are sturdy and short with long body and red-brown, black, grey, brown, blackish brown and fawn skin colour. Marked bristle crest (mane) on the back extending from mid head/shoulder to base of the tail. Facial profile varied from flat to concave. Neck is short with very large jowl. No curling is the characteristic feature of the tail. They are fast runner. Adult body weight varies from 26 to 61kg. Estimated population is about 35,000.

**Doom pig:** Doom pigs are distributed in Dhubri, Bongaigaon and Kokrajhar districts of Assam state. These are black in colour and have short

concave snout. They are large; flat belly type with short erect ears. Top line is straight with long bristles extending up to thoraco-lumber area. Adult body weight varies from 36 to 50kg. Estimated population is about 3,000.

***Kaunayen Chicken:*** Breeding tract consists of Thoubal, Imphal West, Imphal East and Bishnupur districts in the valley region of Manipur. Some birds are also available in hill region consisting of Chandel, Churachandpur, Senapati, Ukhrul, Tamenglong districts. Kaunayen birds have elongated body with long neck and long legs. The predominant plumage color is black followed by brown (or red) with or without patches. Hens are generally black, grey, blackish grey or whitish grey with few brown feathers on neck, breast and wings. Cocks generally have shinning bluish black feathers on wings, breast, tail and thighs. Comb is red in colour and mainly pea type. Neck, breast and thighs are generally bare, hard and rose red colored in fighting cocks. Spur is long and sharp in cocks. Used for cock fighting. Estimated population is approximately 60,000-80,000.

## Phenotypic Characterization and Evaluation of AnGR

### Ladakhi Cattle of Jammu & Kashmir

Ladakh, land of many high passes, is one of the world's highest inhabited regions. This cold-arid desert at over 3000 meter mean see level has very harsh climate characterized by extreme temperature (-40°C in winter and 35°C in summer); low humidity (25-40%), precipitation (80-300 mm) and oxygen level (nearly 60-70% of the oxygen concentration at sea level); high UV radiations and wind erosion. The local cattle from Leh and Ladakh region, known as "Ladakhi cattle" is a unique germplasm having excellent adaptation potential to hypobaric hypoxic conditions. In spite of extreme climatic conditions, subsistence on poor quality feed and low availability of water, it provides around 2.5-4.5 kg of milk and thus serves as an important protein source for local people, particularly during lean winter period.

The survey of Ladakhi cattle was made by visiting different blocks covering 48 villages in the breeding tract. The data related to physical and morpho-metric traits of ladakhi cattle was generated on 237 animals. The survey revealed that in most of the households in villages of Ladakh, irrespective of land holdings, maintain the Ladakhi cows. Almost all the animals of Ladakhi cattle was observed to be docile and easily manageable. The land holdings of the farmers in Ladakh ranged from 1-40 canals. The family size varied from 3-10 and common occupations of local people are agriculture, farm labour and tourism. Both men and women are involved in animal husbandry practices, however, the women play predominant role in cattle rearing.

The Ladakhi cattle, a short stature cattle is found in two major coat colors namely black and brown. Majority of the Ladakhi cattle have black coat color (62%) followed by brown (36%) and black with white patches in rare cases. The skin color is mostly black (62%) followed by brown (28%) or intermittent of the two colors. Muzzle and eyelids are mostly black. Hair are curly; long (60%) or medium (39%); and shiny. The hump is small in female animals while it is small to medium in males. Dewlap is not well developed. The horns in Ladakhi cattle are grey (53%) to black (39%) in color. In majority of the animals the shape of the horn is curved pointing forward. The forehead is small with slightly long face. Ears are small with horizontal orientation. Udder is small and bowl shaped. Milk veins are not prominent. In majority

Typical Ladakhi Bull

Typical Ladakhi Cow

of the animals the teats are cylindrical shaped with round tip. Hoof and tail switch are mostly black in color. The tail of the Ladakhi cattle is long and almost touches the ground. The average body length, chest girth, height at wither, paunch girth, horn circumference and length; ear length, face length and width; in adult Ladakhi cows (age 5 years and more) were recorded to be 88.48± 0.56, 110.89± 3.09; 91.27± 0.41; 109.39± 3.44; 10.34± 0.18, 14.21± 0.15; 14.21± 0.15; 35.90± 0.38 and 14.89± 0.13 respectively. The tail length with and without switch in adult Ladakhi cows is 85.09± 1.09, 62.55± 0.60 cm, respectively.

The average herd size of Ladakhi cattle amongst households surveyed was 4.3 heads with a range of 1-14 animals including both the sexes. During day time in summer, the animals are generally kept in open type of housing while during night and winter season, the animals are mostly kept in closed houses to provide shelter to the animals from extreme cold and wind. Most often, animal housing is separate from owner's house but in few cases it is also part of owner's dwellings. The closed housing has poor sanitation without proper drainage and also has no ventilation or light facility. The animals are generally left for grazing after morning milking and return to their respective home in evening. As a general feeding practice, one person of the community (in rotation) accompanies all the animals of the village to grazing area for whole of the day. The lactating cows additionally provided with feed called Thuchu that includes left over of the food (rice/raw vegetables/sattu etc.) along with local barley straw.

Under the rural management system of Ladakh, the daily milk yield of Ladakhi cow ranged from 2-5 litres. Average fat percentage, SNF, protein and lactose of Ladakhi cow milk was estimated to be 5.24±0.29, 8.99±0.11, 3.27±0.03, 4.92±0.07, respectively. Lactation length of more than 300 days was recorded in Ladakhi cows without any problem of short lactation. The local farmers informed that Ladakhi cows remain productive for 10-12 lactations during its life span. Milk of Ladakhi cow is consumed as such or converted to ghee, butter or churpi. Allelic profile of A1/A2 allele of beta casein locus ascertained in 85 Ladakhi animals revealed the higher frequency (0.90) of A2 allele. Similar to other Indicine breeds frequency of A2A2 genotype (0.79) was more followed by heterozygous A1A2 (0.21) and none of the Ladakhi animal showed homozygous A1A1 genotype. The data indicated Ladakhi cattle as natural resource for A2 milk. The frequency of B variant of kappa casein (associated with milk protein, fat yield and cheese making properties) and B allele of beta-lactglobulin (associated with fat, protein, total solid content and cheese yield) was also higher in Ladkhi cattle as compared to other indicine breeds.

As a general practice, the farmers keep 2-4 breedable cows and use village bulls for breeding of their cows. Two or three good quality males (lungto) are kept in the village for the breeding purpose. In the entire area surveyed, breeding in Ladakhi cattle is through natural mating while grazing in jungle or hill top. The average age at first calving and age at which bull start serving is round 48 months. The Ladakhi cattle is observed to be a seasonal and regular breeder. Invariably, the females of Ladakhi cattle give birth every year and produce a total of 10-14 calves in its life span.

### Indigenous Cattle of Sikkim, Meghalaya and Nagaland states

The North East states of India (Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura) representing 3.78% of crossbred cattle (0.934 million), 6.57% of Indigenous cattle (10.553 million) and 6.20% of total Indian cattle (11.487 million) of the country. Information on cattle germ plasm from these

*Descriptive statistics of different cattle populations of NE States*

| Trait/State | Tripura | Mizoram | Manipur | Sikkim | Meghalaya | Nagaland |
|---|---|---|---|---|---|---|
| Body length | 98.09±0.54a<br>(136) | 109.03±1.39b<br>(71) | 100.32±0.59a<br>(176) | 106.32±1.40b<br>(25) | 97.64±1.08a<br>(95) | 105.11±0.97b<br>(170) |
| Height at wither | 93.93±0.44a<br>(136) | 106.92±0.84bc<br>(71) | 106.22±0.51b<br>(176) | 114.20±1.55bd<br>(25) | 100.90±0.95b<br>(95) | 107.22±0.60b<br>(170) |
| Heart girth | 122.05±1.09a<br>(136) | 139.52±1.59bc<br>(71) | 137.69±0.78b<br>(174) | 157.80±2.27bd<br>(25) | 128.90±1.58b<br>(94) | 145.45±1.22b<br>(170) |
| Paunch girth | 125.14±1.08a<br>(136) | 146.64±1.80bc<br>(71) | 142.12±0.98b<br>(173) | 162.16±2.61bd<br>(25) | 128.60±1.77a<br>(93) | 146.85±1.25b<br>(170) |
| Horn length | 10.87±0.50a<br>(126) | 11.01±0.42a<br>(67) | 11.85±0.38a<br>(157) | 16.48±0.79b<br>(25) | 9.94±0.63a<br>(95) | 10.75±0.58a<br>(170) |
| Ear length | 19.47±0.24a<br>(136) | 18.02±0.33b<br>(71) | 19.59±0.17ac<br>(176) | 18.24±0.26a<br>(25) | 18.91±0.22a<br>(95) | 20.45±0.23ad<br>(170) |
| Face length | 35.30±0.20a<br>(135) | 36.15±0.37a<br>(71) | 38.06±0.23bc<br>(176) | 40.88±0.75bd<br>(25) | 38.08±0.47b<br>(94) | 38.57±0.28b<br>(170) |
| Tail length without switch | 68.63±0.51a<br>(136) | 68.54±1.07bc<br>(71) | 74.31±0.50bd<br>(173) | 75.56±2.29bd<br>(25) | 68.61±0.97a<br>(90) | 76.14±0.94bd<br>(170) |

states are very scanty in the literature and they are included in non-descript category except Siri cattle of Sikkim. An attempt has been made to record variability available in indigenous cattle of the region. Study incorporated 218 cattle of Meghalaya, 269 of Nagaland and 68 Siri cattle of Sikkim. Number of Siri cattle declined drastically from 79000 to 12171 during the years 2003 to 2012 and breed falls in risk under vulnerable category of risk status. In Meghalaya population of indigenous cattle (8.66 lakhs) is static during the years 2007-12, while it declined in Nagaland (1.06 lakhs) by 50.88% during the same period. Cattle in this region were reared for milk, meat, bullock power and manure. Animals were reared mainly on extensive system of management i.e. mostly grazing, very few farmers provided supplement feeding. Most of the cattle were farm born. Breeding was natural and no indigenous cattle semen was available in veterinary hospitals. Animal houses were made of tin roof and wood stick. There was no wall and drainage system. Animals were smaller to moderate in size with cylindrical type of body. The coat colour varies i.e. brown, grey and black but brown colour predominates except Siri in Sikkim. Birth weight and adult body weight ranged from 10-20 kg and 150-250 kg in cows and 200-350 kg in bull/bullocks,


Siri cattle of Sikkim


Tho-Tho cattle of Nagaland

*Mahalanobis distances between different breeds/populations by Canonical discriminate analysis*

| Tripura | Mizoram | Manipur | Sikkim | Meghalaya | Nagaland | State |
|---|---|---|---|---|---|---|
| 0 | | | | | | Tripura |
| 8.45432 | 0 | | | | | Mizoram |
| 4.47216 | 4.70288 | 0 | | | | Manipur |
| 15.4032 | 6.35477 | 4.88826 | 0 | | | Sikkim |
| 2.51033 | 6.71094 | 2.03087 | 9.51618 | 0 | | Meghalaya |
| 5.40603 | 4.72772 | 0.75504 | 5.11138 | 3.18107 | 0 | Nagaland |

*Individual cows classified into different populations of NE states*

| **State** | **Tripura** | **Mizoram** | **Manipur** | **Sikkim** | **Meghalaya** | **Nagaland** | **Total** |
|---|---|---|---|---|---|---|---|
| Tripara | 93<br>(73.81) | 2<br>(1.59) | 4<br>(3.17) | 0 | 20<br>(15.87) | 7<br>(5.56) | 126 |
| Mizoram | 3<br>(4.48) | 48<br>(71.64) | 3<br>(4.48) | 4<br>(5.97) | 7<br>(10.45) | 2<br>(2.99) | 67 |
| Manipur | 8<br>(5.19) | 8<br>(5.19) | 80<br>(51.95) | 5<br>(3.25) | 13<br>(8.44) | 40<br>(25.97) | 154 |
| Sikkim | 0 | 0 | 1<br>(4.00) | 22<br>(88.00) | 1<br>(4.00) | 1<br>(4.00) | 25 |
| Meghalaya | 13<br>(14.44) | 6<br>(6.67) | 7<br>(7.78) | 4<br>(4.44) | 55<br>(61.11) | 5<br>(5.56) | 90 |
| Nagaland | 2<br>(1.43) | 4<br>(2.86) | 10<br>(5.71) | 2<br>(1.43) | 10<br>(5.71) | 142<br>(82.86) | 170 |
| Total | 119<br>(18.88) | 68<br>(10.75) | 105<br>(16.61) | 37<br>(5.85) | 106<br>(16.77) | 113<br>(31.17) | 632 |
| Error | 0.2619 | 0.2836 | 0.4805 | 0.1200 | 0.3889 | 0.1714 | 0.2844 |

Cattle of Meghalaya

respectively. Daily milk yield ranged from 1.0 to 5.0 kg, while Siri producing more milk and goes up to 10 kg. The age at first calving, lactation length, service period, dry period and calving interval ranged from 28-42 months, 150-210 days, 90-120 days, 120-180 days and 15-20 months, respectively. A pair of bullock may plough around 0.5 acre of land in 5-6 hours. It was observed that indigenous cattle of Nagaland and Sikkkim were slightly bigger than the indigenous cattle of Meghalaya. Multi-Variate discriminate analysis showed that height at wither is the most differentiating trait in these cattle populations of north east states. Mahalanobis distances between different populations by Canonical discriminate analysis showed that cattle of Sikkim and Tripura had maximum distances (15.04) and cattle of Meghalaya and Tripura lowest (2.51). Individual cows classification by cross validation into different cattle populations of NE states showed that indigenous cattle of Sikkim (Siri) assigned correctly by 88% and Tho-Tho of Nagaland by 82%, rest of the populations were assigned their individuals less than 80%. It may be concluded that Siri of Sikkim and Tho-Tho of Nagaland were significantly different than other cattle of the region. Tho-Tho can be registered as a distinct breed. The results were supported by physical characteristics also.

### Konkan cattle of Maharashtra

Konkan cattle are distributed in Thane, Palghar, Raigad, Ratnagiri and Sindhudurg districts of Konkan region of Maharashtra and Goa states. In Konkan region of Maharashtra state, cattle (11.01 lakhs) constitute 60% of the total livestock and 95% of the total cattle are indigenous. Data for phenotypic characterization from three districts of Konkan region of Maharashtra state i.e. Ratnagiri, Sindhudurg and Raigad were collected and analyzed. Physical traits of Konkan cattle were studied on 135 cows and 118 bulls/bullocks and 11 morpho-metric traits were also recorded on 609 animals belonging to different age and sex groups. The average herd size was 6.38 animals, which included 1.83 cows, 0.74 bulls, 1.70 bullocks, 0.93 young stock (1-3 years of

Konkan Cow


Konkan Bull

age) and 0.98 calves. Animals are kept on low input production system. Grazing is the main source of the feeding and 53% farmers put animals on grazing for entire day, however, 72% farmers offer paddy straw and locally available grasses to the animals and 45% farmers also offer 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 is slanting in shape made up of thatched, earthen tiles or sometimes concrete. The breeding of animals was through natural mating with locally available bulls. The coat colour of animals was generally brownish red (45.2% in cows and 44.9% in bulls/bullock) or black (23% in cows and 26% in bulls/bullocks) however, animals of brown, white or mixed coat were also available. The colour of muzzle and tail was generally black but in some animals carroty/mixed muzzle or creamy tail switch were also seen. The forehead was small and straight, sometimes slightly concave. The horns were straight in most of the cases (more than 95%) and orientation of horn was outward, upward and backward. Udders were small in size; teats were small, cylindrical with pointed/ rounded tips. The hump and dewlap were small to medium in size in cows and medium to large in bulls. The animals were small in size with compact body. The animals are hardy and well survived in hot and humid conditions of the coastal area. The average daily milk production was 2.23 kg. 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 months, 17.21±0.35 months, 226.53±6.22 d, respectively. The animals are used for the agricultural operations in area. The population of Konkan cattle is adequate in its breeding tract and deserves for status of a breed.

*Means (cms) along with S.Es for morpho-metric traits of Konkan cattle*

| **Trait** | **Cow** | **Bulls/Bullock** | **Young Male** | **Young Female** | **Calves** |
|---|---|---|---|---|---|
| Body Length | 101.48±0.41<br>(84-117) N=204 | 109.29±0.63<br>(81-132) N=164 | 92.43±1.36<br>(59-117) N=67 | 90.73±1.00<br>(67-110) N=70 | 66.85±1.21<br>(40-95) N=104 |
| Chest Girth | 134.10±0.60<br>(117-162) N=204 | 146.55±0.95<br>(110-179) N=164 | 119.75±1.91<br>(81-150) N=67 | 118.09±1.44<br>(86-140) N=70 | 82.13±1.53<br>(48-120) N=104 |
| Height at withers | 100.78±0.50<br>(88-158) N=204 | 106.54±0.53<br>(85-121) N=164 | 94.60±1.13<br>(56-111) N=67 | 93.06±0.90<br>(74-106) N=70 | 72.91±1.03<br>(52-96) N=104 |
| Paunch Girth | 141.05±0.71<br>(120-170) N=204 | 151.71±1.07<br>(102-186) N=164 | 124.42±1.96<br>(92-159) N=66 | 121.81±1.61<br>(91-146) N=70 | 83.57±1.66<br>(45-122) N=104 |
| Face length | 41.09±0.19<br>(35-49) N=204 | 44.70±0.25<br>(31-50) N=164 | 38.82±0.52<br>(29-49) N=67 | 37.57±0.44<br>(28-48) N=70 | 27.69±0.49<br>(16-39) N=104 |
| Face width | 19.43±0.14<br>(14-28) N=203 | 23.13±0.15<br>(18-28) N=163 | 21.03±0.31<br>(16-27) N=67 | 17.91±0.23<br>(15-25) N=70 | 15.11±0.24<br>(10-26) N=104 |
| Horn Length | 19.82±0.54<br>(4-40) N=199 | 23.91±0.67<br>(4-50) N=161 | 13.60±1.34<br>(2-48) N=52 | 9.95±0.97<br>(1-28) N=44 | 4.00±0.91<br>(2-10) N=10 |
| Horn Circumference | 14.11±0.21<br>(8-24) N=176 | 19.05±0.25<br>(9-28) N=147 | 15.00±0.62<br>(5-22) N=44 | 12.41±0.49<br>(9-19) N=29 | 12.00±1.41<br>(10-14) N=2 |
| Ear Length | 18.30±0.13<br>(14-25) N=204 | 18.45±0.14<br>(13-24) N=164 | 17.54±0.22<br>(14-23) N=67 | 17.39±0.20<br>(14-21) N=70 | 14.52± 0.24<br>(7-19) N=104 |
| Tail With switch | 85.37±0.59<br>(59-108) N=198 | 92.10±0.85<br>(58-115) N=160 | 76.93±1.53<br>(39-105) N=67 | 75.79±1.17<br>(45-98) N=70 | 50.24±1.20<br>(19-84) N=104 |
| Tail without switch | 67.82±0.56<br>(49-98) N=184 | 72.12±0.68<br>(47-92) N=145 | 60.54±1.20<br>(35-83) N=65 | 59.69±0.95<br>(41-85) N=68 | 41.47±0.95<br>(13-68) N=96 |

*Figures in parentheses indicate range and N is number of observations*

### Bargur Buffalo of Tamil Nadu

Bargur buffaloes are being maintained by Burgur Lingayat an indigenous Kanada speaking community in the Bargur villages of Anthiyoor taluk in Erode district of western Tamil Nadu. The buffaloes are good in climbing hills and can graze easily in hill terrain or in slopes. Bargur 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 are housed either in a separate enclosure adjacent to the farmers' house (80%) or 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 farmers (>95%) were practicing natural mating of females with Konans. The animals are mainly reared for manure, milk and the male calves are sold for cara-beef. The milk yield of the animals ranges from 1.5 to 2.0 liters per day and mainly used for house hold consumption in the form of curd and butter milk.

Bargur Buffalo

### Lesser known Sheep Populations of Karnataka State

Phenotypic and genetic characterization of Mouli and Yalaga sheep populations of Karnataka was accomplished under field conditions. Migration was reported in Mouli flocks from October/November to March/May. Yalaga sheep are stationary. Sheep are vaccinated against ET, PPR and FMD. The farmers followed ITK for some common ailments like tympani, fracture, FMD etc.

Mouli Ram

Mouli sheep are tall with deep body and long legs. Average body weight, length, height at wither and chest girth were 41.4±1.43 kg, 77.0±0.8 cm, 79.3±0.5 cm, and 81.3± 0.7 cm in ewes, and 58.6±1.6 kg, 85.4±0.9 cm, 88.4±0.6 cm and 89.7±0.9 cm in rams. Coat colour is white with or without brown spots/patches. A brown ring is present around the eyes. Nose line is roman. About 0.8% ewes and 25% rams were recorded as horned.

Yalaga animals are medium to large sized. Average body weight, length, height at wither and chest girth were 33.9±0.5 kg, 69.2±0.5 cm, 74.0± 0.3 cm and 77.3±0.3 cm in ewes, and 55.0±0.7 kg, 77.8±0.6 cm, 83.2±0.5 cm and 89.9±0.5 cm in rams. Coat colour is white and consisted of small thick hair. Face is white, white with black or brown patches of varying size to complete black. Horns were present in 90% rams and 4 % ewes. Horns are thick, corrugated and curved in rams. Tail is small and thin. Udder is well developed.

In Mouli, age at first lambing was about 13-18 months with a lambing rate of 70 to 80%. In Yalaga, age at first lambing was 18-24 months. The lambing percentage ranged from 70 to 95 % leading to a lambing interval of 12 to 16 months. Average estimated body weight at birth, 3-

Yelga Ram

month, 6-month and 12-month of age were 4.0, 23.8, 34.1 and 48.6 kg in male lambs and 3.5, 21.6, 31.0 and 44.3 kg in female in Mouli whereas, the corresponding body weights were 2.0, 18.2, 28.2 and 43.6 kg in male lambs and 2.5, 15.6, 21.5 and 29.4 kg in female in Yalaga.

### Chitarangi Sheep of Rajasthan

The survey of Chitarangi sheep was conducted in Ghadsana and Anupgarh tehsil of Sriganganagar district of Rajasthan. The villages surveyed were Shamaki, Anupnagar and 18MD of Anupgarh Tehsil and 3MLD, 3GM Jantawali and 3GD of Ghadasana Tehsil. During the survey body biometry, phenotypic characters and performance traits of about 212 animals (121 adults and 91 lambs) were recorded from 18 farmer's flock. Chitarangi is a carpet wool type sheep population, distributed in Fazilka & Muktsar districts of Punjab, Sri Ganga Nagar districts of Rajasthan and nearby areas. The Adult body weight of males and females were 55.25 ± 2.80 and 46.25 ± 1.10 kg, respectively which varies from 40 to 95 kg in males and 26 to 74 kg in females. The overall body length (BL), height, chest girth (CG), paunch girth (PG), face length (FL) , face width (FW), ear length and tail length (TL) were 72.51± 0.38, 72.93 ± 0.35, 86.88 ± 0.58, 88.55 ± 0.69, 20.29 ± 0.10, 9.69 ± 0.10, 17.64 ± 0.13 and 20.56 ± 0.26 cm respectively. Body weight (BW) of lambs in the age groups of 0-1, 1-3, 3-6 and 9-12 months were ranges between 6-13, 10-28, 15-34 and 28-51 kg respectively. The length of ear ranges from 14 to 23 cm. The fleece of Chitarangi is of good carpet quality. The fibre diameter (micron), medulation% and staple length were 42.22 ± 0.10, 56.60 ± 4.22 and 5.90 ± 0.32 respectively.

*Body weight (kg) and biometry (cm) of adult Chitarangi sheep*

| Traits | N | BW | BL | Height | CG | PG | FL | FW | EL | TL |
|---|---|---|---|---|---|---|---|---|---|---|
| Overall | 121 | 48.05 ± 1.10 | 72.51 ±0.38 | 72.93 ± 0.35 | 86.88 ±0.58 | 88.55 ± 0.69 | 20.29 ± 0.10 | 9.69 ± 0.06 | 17.64 ± 0.13 | 20.56 ± 0.26 |
| Sex | | ** | ** | ** | * | NS | ** | ** | NS | ** |
| Male | 24 | 55.25 ± 2.80 | 76.13 ±1.05 | 77.17 ± 0.75 | 89.17 ± 1.32 | 91.17 ± 1.46 | 21.50 ± 0.26 | 10.42 ± 0.16 | 18.04 ± 0.38 | 22.42 ± 0.61 |
| Female | 97 | 46.25 ± 1.10 | 71.62 ± 0.35 | 71.89 ± 0.31 | 83.32 ± 0.63 | 87.91 ± 0.77 | 19.99 ± 0.08 | 9.51 ± 0.06 | 17.55 ± 0.14 | 20.10 ± 0.26 |
| Range M | | 40-95 | 69-90 | 71-85 | 78-102 | 80-108 | 20-24 | 9-12 | 14-23 | 18-30 |
| F | | 26-74 | 63-79 | 66-80 | 73-99 | 73-105 | 18-22 | 8-11 | 15-21 | 12-26 |

### Dumba Sheep of Rajasthan

Dumba is found mainly in Jaipur, Nagour and Ajmer districts of Rajasthan. The animals of Dumba are also available in Delhi, Malerkotla tehsil of Punjab and some parts especially Sitapur and Muzzfarnagar districts of UP. Main objective of rearing Dumba is for Qurbani purpose/ earning of money during the Eid festival as they have great aesthetic and religious value. Fat-tailed sheep breeding is a traditional and an important type of animal production in arid or semi-arid region. The coat colour is white and brown, however, some black animals were also found. The patches of different colors, shapes and sizes were also


Chitrangi Sheep


Dumba Sheep

*Body weight (kg) and biometry (cm) of adult Dumba Sheep*

| Traits | N | BW | BL | Height | CG | PG | FL | FW | EL |
|---|---|---|---|---|---|---|---|---|---|
| Overall | 64 | 73.79<br>± 2.89 | 73.89<br>±0.73 | 77.97<br>± 0.64 | 95.14<br>±0.92 | 96.36<br>± 1.01 | 21.56<br>± 0.24 | 9.56<br>± 0.10 | 18.75<br>± 0.28 |
| Sex | | ** | ** | ** | * | * | ** | ** | NS |
| Male | 15 | 90.80<br>± 5.53 | 78.67<br>±1.44 | 83.80<br>± 1.18 | 101.27<br>± 1.90 | 101.33<br>± 2.28 | 23.27<br>± 0.32 | 10.20<br>± 0.15 | 18.60<br>± 0.41 |
| Female | 49 | 66.06<br>± 2.42 | 72.43<br>± 0.74 | 76.18<br>± 0.53 | 93.27<br>± 0.90 | 94.84<br>± 1.04 | 21.04<br>± 0.25 | 9.37<br>± 0.10 | 18.80<br>± 0.35 |
| Range | M | 54-124 | 70-88 | 77-91 | 88-111 | 84-113 | 22-25 | 9-11 | 15-21 |
| | F | 47--96 | 65-86 | 66-84 | 81-109 | 80-108 | 19-29 | 8-11 | 9-26 |

noticed on body of Dumba sheep. The deposition of fat in the tail is distinct characteristics of this breed. Ears are large in size. The price of these animals is very high as claimed by sheep owners. Adult animals are sold at the rate of Rs 60000 to 125000 and lambs @ Rs 25000-40000.The Adult body weight of males and females were 90.92 ± 6.39 and 66.33 ± 2.50 kg, respectively which varies 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. Body weight of lambs in the age groups of 1-3 and 3-6 months were ranges between 11-32 and 23 -60 kg respectively. The animals are reared under intensive system of feeding.

## Classification of Indigenous Sheep based on Morphometry using Classical and Heuristic Methods

Eight sheep breeds (Kolhapuri, Lonand, Marwari, Munjal, Muzaffarnagri, Madgyal, Sangamneri and Solapuri) were classified using Classical Discriminant Function Analysis and Artificial Neural Network (ANN) model. Sheep aging between 2-8 teeth, having been profiled on seven morphometric traits viz. body weight, body length, height at withers, chest girth, paunch girth, ear length and tail length, were considered for the classification. ANN was tuned on number of hidden layers and number of neurons in each layer to provide better accuracy. The network was designed with two hidden layers. Thirty experiments were conducted for each combination of breeds.

Discriminant analysis results showed that all the measured traits were significant ($p<0.0001$) in discriminating the eight sheep breeds. They were found to have potential discriminatory power. The Mahalanobis distances estimated between the eight sheep breeds were highly significant ($p < 0.0001$). The biggest was between Lonand and Muzaffarnagri (81.0) and the least was between Madgyal and Solapuri (1.3). The discriminant analysis revealed that 453 (24.7%) individuals were misclassified in their source genetic groups. The Marwari breed showed the least assignment error (0%) whilst the Solapuri sheep exhibited maximum error level (44%).

The ANN model gave more than 99% assignment accuracy between various breed combinations of Lonand, Solapuri, Madgyal, Kolhapuri and Sangamneri with Marwari, Munjal and Muzaffarnagri. The assignment accuracy between breed combinations of Lonand, Solapuri, Madgyal, Kolhapuri and Sangamneri varied between 68-97%. Similarly the assignment accuracy of Munjal and Muzaffarnagri breed were 84 and 90% respectively. Overall, the ANN model performed better than classical discriminant analysis.

## Nagaland Long Hair Goat

The study was focused to generate the data on morphological, biometrical traits and management of Nagaland long hair goat. Visits were taken to different parts of Zunheboto, Tuensang, Kiphire, Phek and plain area of Dimapur districts of Nagaland and measurements were recorded from 255 animals consisting of different age groups of both sexes from 42 flocks belonging to different farmers. Information on age at sexual maturity, age at first conception, age at first kidding, kidding interval, gestation length, kidding pattern were

Nagaland long hair buck

Nagaland Long Hair Doe

recorded through interaction with the goat keepers. Different colour variants viz. white with black patches, black, brown with grey hair of long hair goats were seen. Long hair was present in the adult males. Animals were having proportionate body, straight nose line, medium size, erected, horizontally placed ears. The horns in females are shorter, pointed, directed upward and then slightly backward while that of males are thicker, longer, orienting upward and backward. The wattles and beard are present in majority of goats. Muzzle is black/ brown/ pinkish. The belly and legs below knee joint are black. The udder and teats are moderately developed. Udder is bowl shaped and teats are small and cone type. The under belly is black/white. Apart from long hair goats data was recorded on other kinds of goats available in the districts visited. Goats, with stripes on face were seen in Dimapur district. The average measurements for height at withers, body length, Chest/heart girth, paunch girth, face length, horn length, ear length and tail length for adult Nagaland goats irrespective of their sex and colour were 46.12±0.45, 56.94±0.50, 68.49±0.66, 77.77±0.70, 15.81±0.15, 8.44±0.53, 11.64±0.18, 9.50±0.16. The average body weights (kg) in the age groups of 1-3 month, 4-6 month, 7-12 month and adult animals were 7.89±0.42, 12.97±0.39, 16.62±0.26 and 27.69±0.73 respectively. The mean values for height at withers, body length, Chest/heart girth, paunch girth, face length, horn length, ear length and tail length in long hair adult male goats were 48.43±1.52, 58.62±1.73, 71.24±2.21, 75.71±2.20, 16.19±0.45, 13.43±1.74, 10.70±0.38, 9.71±0.29cm respectively whereas for females the average measurements were 45.71±0.61, 56.35±0.81, 68.71±1.03, 77.44±1.40, 15.59±0.28, 7.79±0.71, 11.77±0.35, 9.24± 0.23cm respectively. The overall average measurements irrespective of sex were 46.75±0.71, 57.22±0.83, 69.67±1.06, 76.78±1.20, 15.82±0.24, 9.98±0.88, 11.35±0.27, 9.42±0.18cm respectively. The average body weight for adult males was 31.48±2.45kg and females 25.79±1.05 kg. The overall body weight was 28.22±1.26 kg. Goats are maintained on extensive management by small and marginal farmers. Goat houses are made of mud, concrete, bamboo sticks and wooden logs with no proper arrangement of electric and water supply. Goats depend on the local vegetation available in the jungle while at home they are fed with crushed maize. Goats love salt licking also. The milk yield is 0.3 to 0.5 liters per day. The litter size varies from 1 to 4. Hair obtained from the Nagaland goats has commercial utility for the tribal people. It is used for beautification of garments, ornaments and weaponry. In view of the distinct phenotype and commercial utility, the long hair goat of Nagaland needs further propagation and genetic improvement.

Use of goat hair in ornaments and garments

*Body weight (kg) and biometry (cm) of Nagaland Goats*

| TRAITS | Age Group | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **0 to 3 Months** | | | **4 to 6 Months** | | | **6 to 12 Months** | | | **Adults ( > 18months)** | | |
| | Females (16) | Male(22) | Overall(38) | Females (15) | Male(17) | Overall (32) | Females(9) | Male(12) | Overall (21) | Females (86) | Male (23) | Overall (109) |
| HW | 30.73±1.46 | 33.63±0.89 | 32.44±0.83 | 37.33±1.00 | 37.75±0.84 | 33.75±0.64 | 42.11±1.31 | 41.50±0.60 | 41.76±0.64 | 45.32±0.41 | 48.65±1.40 | 46.12±0.45 |
| BL | 39.45±1.95 | 41.19±0.63 | 40.48±0.87 | 45.53±1.21 | 46.00±0.61 | 45.77±0.66 | 49.78± 1.04 | 49.08±1.17 | 49.38±0.79 | 56.27±0.49 | 58.87±1.52 | 56.94±0.50 |
| CG | 46.09±2.21 | 47.56±0.75 | 46.96±0.99 | 52.87±1.09 | 52.81±1.08 | 52.84±0.75 | 57.22±1.39 | 58.58±0.91 | 58.00±0.78 | 67.52± .62 | 71.61±1.98 | 68.49±0.66 |
| PG | 48.55±2.20 | 54.63±1.19 | 52.15±1.26 | 58.53±1.45 | 57.88±1.59 | 58.19±1.06 | 65.33±0.97 | 65.42±1.12 | 65.38±0.75 | 77.81±0.75 | 75.70±2.07 | 77.77±0.70 |
| FL | 11.36±0.49 | 11.44± 0.22 | 11.41±0.23 | 12.80±0.30 | 12.19±0.26 | 12.48±0.20 | 14.00±0.53 | 13.83±0.53 | 13.90±0.37 | 16.49±0.84 | 16.30±0.43 | 15.81±0.15 |
| HL | 1.68±0.32 | 1.88±0.20 | 1.80±0.17 | 2.80±0.70 | 3.00±0.24 | 2.90±0.35 | 4.56± 0.63 | 5.42±0.65 | 5.05±0.46 | 7.14±0.43 | 13.13±1.60 | 8.44±0.53 |
| EL | 8.91±0.39 | 8.73±0.47 | 8.81±0.31 | 9.79±0.21 | 9.75±0.31 | 9.77±0.19 | 11.75±0.49 | 9.75±0.49 | 10.55±0.41 | 11.96±0.30 | 11.05±0.40 | 11.64±0.18 |
| TL | 6.82± 0.44 | 7.13±0.31 | 7.00±0.26 | 7.27±0.33 | 8.38±0.52 | 7.84±0.32 | 8.78±0.46 | 8.92±0.36 | 8.86±0.28 | 9.48± 0.19 | 9.65±0.34 | 9.50±0.16 |
| B.wt | 7.31±0.77 | 8.32±0.47 | 7.89±0.42 | 12.87±0.63 | 13.06±0.50 | 12.97±0.39 | 16.67±0.44 | 16.58±0.34 | 16.62±0.26 | 26.39±0.64 | 31.87±2.14 | 27.69±0.73 |

*HW-Height at withers, BL- Body length, CG- Chest girth, PG- Paunch girth, FL- Face length, HL- Horn length, EL- Ear length, TL- Tail length, B.wt- Body weight*

*Average body measurements of adult Long hair goats*

| TRAITS | | Adults | |
|---|---|---|---|
| | Females (34) | Male (21) | Overall (55) |
| Body Height | 45.71±0.61 | 48.43±1.52 | 46.75±0.71 |
| Body Length | 56.35±0.81 | 58.62±1.73 | 57.22±0.83 |
| Chest Girth | 68.71±1.03 | 71.24±2.21 | 69.67±1.06 |
| Paunch Girth | 77.44±1.40 | 75.71±2.20 | 76.78±1.20 |
| Face Length | 15.59±0.28 | 16.19±0.45 | 15.82±0.24 |
| Horn Length | 7.79±0.71 | 13.43±1.74 | 9.98±0.88 |
| Ear Length | 11.77±0.35 | 10.70±0.38 | 11.35±0.27 |
| Tail Length | 9.24± 0.23 | 9.71±0.29 | 9.42±0.18 |
| Body Weight | 25.79±1.05 | 31.48±2.45 | 28.22±1.26 |

### Genetic and Phenotypic Variation associated with Tick Infestation in Indian Cattle

Explorative preliminary survey of Barabanki and Malihabad area near Lucknow was carried out; Data on tick infestation on individual were collected. Animals of breeds like Sahiwal, Gir, Rathi, Jersey & crossbreds are more preferred by farmers in the area. On the basis of morphological studies, the ticks identified are Rhipicephalus (Boophilus) microplus and Hemaphysalis bispinosa (>20 ticks had been reported till date for domestic animals). Rhipicephalus microplus infestation is most common (70%) and considered to be economically important tick species. Females were more suceptible than male (60.82%), animals less than one year of age group were more infected (73.33%), than animals greater of four years age (48.92%). Information in terms of standard physiological parameters (rectal temperature, respiratory rate, body surface temperature and pulse rate) were collected from experimental animals during Sept-Oct and Feb-March periods from two animal farms in Malihabad and one State Govt farm in Barabanki.

Tick infestation

## Conservation of AnGR

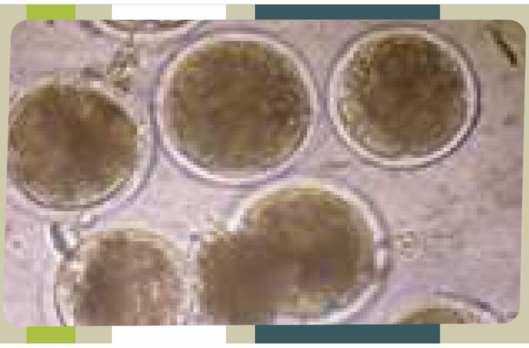
### Conservation of Sahiwal and Hariana cattle at Gaushalas

A total of 105 cows of Hariana & graded and 14 of Sahiwal & graded were identified based on physical characteristics and health soundness in the Shri Krishan Gaushala Jundla, Nising, Gondar and Uplana. Identified cows were ear tagged and kept in separate enclosures at these Gaushals. Among the identified cows, 90 of Hariana and 26 of Sahiwal were inseminated with elite male semen of Hariana and Sahiwal, respectively. Semen doses of Sahiwal (240) and Hariana (640) breed were transferred to these Gaushals for AI of selected cows. All the selected cows were given deworming and mineral mixture. Health camps were organised in all the three Gaushalas with the help of State Animal Husbandry Department. A total of 17 calves were born to the inseminate cows in these Gaushalas. In Sahiwal, daily milk yield ranged from 4.0 to 10.0 kg. In Hariana daily milk yield ranged from 1.0 to 4.0 kg. In Hariana cows birth weight ranged from 12.0 to 14.4 kg.

Sahiwal calf

### Ex Situ Conservation of Indigenous Sheep utilizing Cauda Epididymal Spermatozoa

An extender containing citrate buffer, sugar, egg yolk and antibiotics has been developed for freezing epididymal sperms and frozen semen doses prepared. The storage of testies at low temperature indicated suitability of utilizing them for extraction of epididymal sperms for their conservation even after extended hours post slaughtering of rams. In vitro fertilization revealed that frozen epididymal spermatozoa retains the fertility potential.



In vitro fertilization of sheep ova by epididymal sperm and Zygote formation

### National Gene Bank

Germplasm repository at Gene Bank NBAGR is being strengthened by preserving diversified form of germplasm (semen, embryos, DNA, epididymal sperms and somatic cells). Large number of frozen semen doses were added during the period. New initiatives were taken by preserving the germplasm inform of embryos and somatic cells of different breeds and species. The current status of germplasm repository is given below:

Germplasm stored in Gene Bank

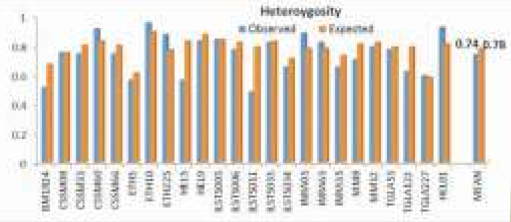
| Germplasm | Units/Species/Breeds |
|---|---|
| Frozen Semen | 138674 doses of 45 breeds from 7 species |
| DNA | 40 breeds of 5 species |
| Embryo | Ongole, Kankrej and Gir |
| Epididymal | 1500 doses of three breeds of goat and sheep |
| Somatic Cells | 404 vials from five animals of double humped camel |

## Genetic Characterization and Genomics

### Genetic Characterization of Laddakhi Cattle

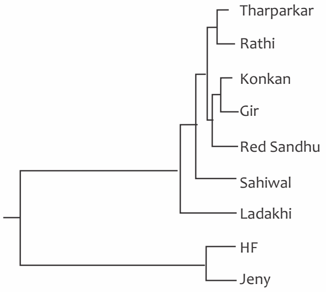
***Micro-satellite based genetic characterization***

The FAO recommended bovine specific microsatellite markers were utilized to genotype 48 animals of Ladakhi cattle.



Allelic Heterozygosity of Ladakhi Cattle

Various within breed diversity indices measured using bovine specific microsatellite markers viz., mean number of alleles (9.79±0.94); mean effective number of alleles (4.73±0.69) mean observed heterozygosity (0.749±0.014), mean expected heterozygosity (0.788±0.068), reflected sufficient genetic diversity in Ladakhi cattle. The phylogenetic analysis revealed genetic distinctness of Ladaakhi population with respect to other analyzed Indigenous breeds of cattle



Phylogenetic relationship of Ladakhi cattle with other cattle

***Mitochondrial DNA based diversity analysis***

To uncover the mtDNA diversity status of Ladakhi cattle, a total of 40 random animals were utilized to amplify 1142 bp region of bovine mtDNA between positions 15601 to 404, that included all the D-loop and flanking sequences at both ends. The number of haplotypes observed in Ladakhi cattle was 15 while haplotypic diversity was 0.942+ 0.00186. Observed nucleotide diversity and pair wise nucleotide differences was 0.00384 and 3.489, respectively. Within breed-wise population demography indices of Ladakhi cattle was comparable to other Indian cattle breeds No significant deviations from neutrality were identified in haplotypes from Ladakhi or other cattle breed (Tajima's D:-1.5332, 0.10>P>0.05). In Ladakhi cattle, out of the 15 haplotypes, five were shared with other breeds, indicating similarity with other Indicine breeds. A high proportion of haplotypes (10, 66.7%) were scored only once, indicating the existence of sufficient mtDNA haplotypic diversity in Ladakhi cattle. To explore the demography history and population expansion of Ladakhi cattle, mismatch distributions was estimated. The data set for Ladakhi cattle showed a predominant unimodal peak at around 2 differences (mismatches), while a much smaller peak at around 29 mismatches. Individuals from major group differed from each other by 1 to 6 mismatches, while the individuals from minor group differed by 32 to 35 mismatches. The presence of a major and minor peak separated by a large time interval suggested complex expansion events in Ladakhi cattle

### *Characterization of genes associated with high altitude adaptation*

Several genes related to high latitude hypoxia viz., arginase 2 (ARG 2), Forkhead box R2 (FoxR2), ADAM metallopeptidase domain 17 (ADAM17), matrix metallopeptidase7 (MMP7) and Hypoxia-inducible factor 1-alpha (HIF1A) were sequence characterized in 24 animals of Ladakhi cattle and compared with other Indian native cattle and two Bos taurus breeds. Several single nucleotide variations (SNPs) were identified in 5'- and 3'-untranslated region (UTRs), and coding region of these genes. In future these SNPs could be utilized as genomic resource for understanding the molecular mechanism of high altitude adaptation in Ladakhi cattle.

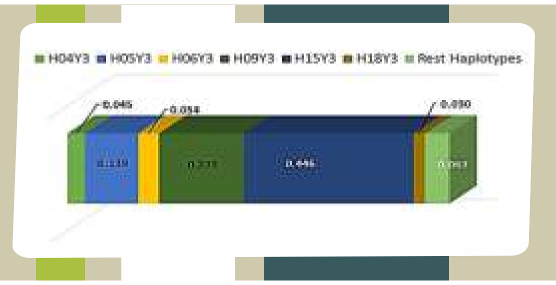
Considering the fact that Ladakhi cattle is the lifeline of local people of Leh-Ladakh region, efforts should be made to recognize and register this important cattle genetic resource. Farmers and stake holders should be educated to maintain the purity of this population and avoid mixing of local cattle with exotic Jersey cattle. Strategies should be designed to improve the management practices and production traits of this important cattle population and breed society should be established to conserve and propagate Ladakhi cattle.

### Y-Chromosome Haplotypic Diversity

Haplotype diversity based on seven Y-chromosomal microsatellites was explored in 202 bulls representing 18 native cattle breeds of India. A total of nineteen *Bos indicus* specific haplotypes were identified. These haplotypes shared the previously described haplogroup/patriline Y3. The six most common haplotypes, H4Y3, H5Y3, H6Y3, H9Y3, H15Y3 and H18Y3, had a total frequency of around 93.56% . They were recorded in 9, 28, 11, 45, 90 and 6 individuals and shared by 5, 7, 1, 6, 11 and 2

*Variations in genes associated with high altitude adaptation showing contrasting frequencies across Ladakhi cattle vis a vis breeds from low altitude*

| Gene | Total Variations | Variations with frequencies | | |
|---|---|---|---|---|
| | | **Variation: Position** | **Low altitude breeds** | **Ladakhi cattle** |
| ADAM1 | 12 | | | |
| | | C/A: 3'UTR (C/EBP;Oct-1) | 0.946 | 0.048 |
| | | A/C:3'UTR (HNF-1) | 0.054 | 0.952 |
| FOXR2 | 4 | None of the variation was observed with contrasting differences | | |
| ADAM17 | 15 | | | |
| | | A391G : Glu/Gly | 0.64 | 0.12 |
| | | C1365T: Pro/Ser | 1.00 | 0.12 |
| MMP7 | 12 | | | |
| | | C548A: Pro/Pro | 0.72 | 0.08 |
| | | G587T: Glu/Pro | 0.86 | 0.12 |
| HIF1α | 16 | | | |
| | | C839T : Tyr/ Tyr | 1.00 | 0.25 |

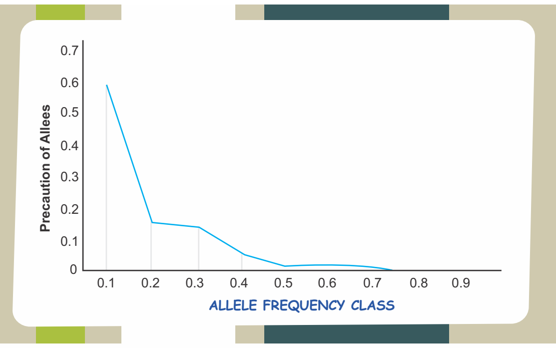


Y chromosome Haplotypes in Indian Cattle Breeds

breeds, respectively. Their segregating frequencies were ranging from 2.97 % to 44.56%. The frequency of other 13 rare haplotypes was 6.40%. Haplotype H15Y3 had the highest frequency (44.56%) and mostly represented in six lineages (Ongole, Sahiwal,Vechur, Gir, Rathi and Punganur). The second most common haplotype (H09Y3, 22.28%) was observed to be most frequent in three breeds (Kankrej, Mewati and Nagori). The 13 rare haplotypes were observed with low frequencies exclusively in one lineage, which was different for each haplotypes, except for the H6Y3. Khillar lineage showed exclusive haplotype H6Y3 with a high frequency (55%). Overall Y-chromosome haplotype diversity of Indian native cattle breeds, without subdivision into lineages, was 0.38. The average FST value (0.42) over all *B. indicus* breeds indicated a considerable amount of the variation is explained by breed differences. All these haplotypes are reported for the first time and not been observed earlier in any National/International cattle breed.

## Genetic Diversity in Bargur Buffalo

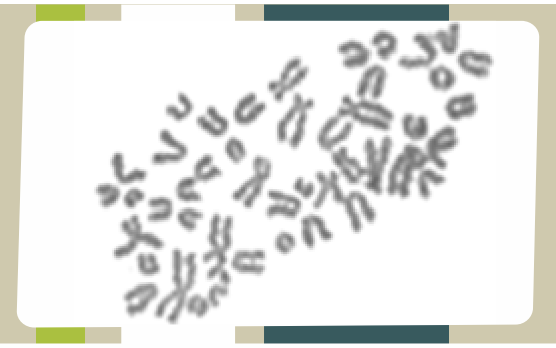
The Bargur buffaloes are riverine type with 50 number (2n) of chromosomes. This is supported by the Mt D-Loop hyper variable segment haplotype analysis. The haplotypes obtained were compared with ASW, Manipuri, Marathwada, Murrah, South Kanara and Toda buffaloes. A total of 40 haplotypes were observed with an 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. A total of 24 loci of neutral microsatellite markers were PCR amplified and genotyped in the population. All the loci studied in the population were polymorphic. Overall average number of alleles was 8.00±0.55 and average effective number of alleles was 3.85±0.25. The average observed (HO) and unbiased expected (uHe) heterozygosity were 0.66±0.04 and 0.71±0.032 for Bargur 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 Bargur buffalo and gives L-shaped curve. The milk analysis revealed 8.59±0.62% fat and 9.10±0.19% SNF in Bargur buffalo milk.



Mode Shift Analysis in Bargur Buffalo

## Diversity in Buffalo Populations of Odisha

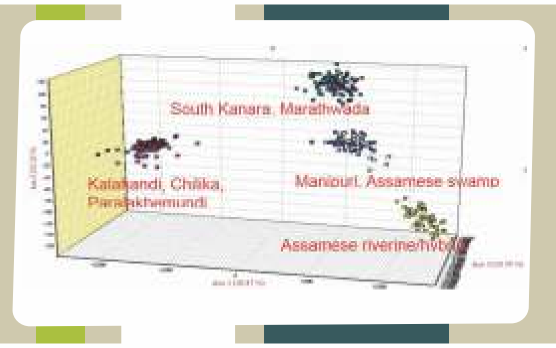
A survey was conducted in the breeding tract of Chilika buffaloes of Odisha. Twenty villages of five different blocks of Puri, Ganjam and Khorda districts, were visited. Total 73 blood samples were collected, majority from Krushnaprasad block of Puri district, where pure Chilika buffaloes are mainly concentrated. Most of the Chilika buffaloes in the area of Rambha in Ganjam and Balugaon in Khorda districts have been crossed with Murrah. In Bhusandpur block of Khorda district, pure Chilika buffaloes were found only in one village, Bidharpur, located at the banks of Chilika Lake. Blood samples from 34 animals were also collected for cytogenetic screening and 21 for sera samples. Histopaque purification of PBMCs carried out from 20 blood samples and RNA purified was utilized for real-time expression of



Swamp-riverine hybrid metaphase spread of Chilika male buffalo

*Serum profiles for kidney function tests and cortisol in Chilika, Paralakhemundi and Murrah buffaloes (10 samples each collected at moderate THI)*

| Breed | Urea | Creatinine | Ur/Crtn | Na | K | Cl | P | Uric Acid | Cortisol |
|---|---|---|---|---|---|---|---|---|---|
| Chilika | 21.2 | 0.9 | 25.421 | 134.35 | 7.801 | 99.16 | 8.76 | 0.54 | 0.844 |
| Paralakhemundi | 13.4 | 0.96 | 15.99 | 132.7 | 7.454 | 97.63 | 6.16 | 0.77 | 0.785 |
| Murrah | 11 | 1.56 | 7.623 | 136.5 | 5.076 | 100.43 | 5.53 | 0.39 | 0.842 |
| *Reference value (bovines) | 6--27 | 1--2 | NA | 132-152 | 3.9-5.8 | 95-110 | 5.6-6.5 | NA | 0.47-0.75 |



Plot of multivariate correspondence analysis showing distribution of animals of eight buffalo breeds/populations

heat adaptation related genes. Real-time PCR analysis of different set of constitutively expressed genes to select most suitable one for normalization of data, showed RPS15 and GAPDH as the most stably expressed genes. Cytogenetic screening of 30 Chilika buffaloes revealed presence of one male swamp-riverine hybrid (49n) animal, rests being riverine (50n). Hybrid animal found was from west cost of Chilika-Bidharpur village of Bhusandpur block in Khorda District.

Biochemical tests run on sera samples collected from 10 animals each of Chilika, Paralakhemundi and Murrah buffaloes showed relatively higher urea/creatinine ratio in Chilika, compared to Paralakhemundi and Murrah, an indication of Chilika being *Bovine reference values better adapted to dehydrated conditions animals are subjected to during grazing in the salty water of Chilika lake. However, serum cortisol levels did not show any significant variation across three buffalo populations.

Microsatellite data generated for 23 markers on Chilika, Kalahandi and Paralakhemundi after comparison with other riverine and swamp buffaloes revealed considerable diversity across populations. Mode shift analysis divulged absence of bottleneck in all the three populations. Phylogenetic analysis has shown grouping of Assamese swamp into separate group from riverine buffaloes, Odisha buffaloes grouping close together.

### Genetic Diversity in Sheep Populations of Karnataka State

Phenotypic and genetic characterization of Mouli and Yalaga sheep populations of Karnataka was accomplished under field conditions. Genetic diversity studies were carried out using FAO recommended microsatellite markers. The values for effective number of alleles, mean observed heterozygosity and gene diversity were 5.23, 0.637 and 0.783 in Mouli and 4.865, 0.596 and 0.757 in Yalaga sheep respectively. Similar tendencies of three variables reflected the Mouli and Yalaga sheep populations to be under mutation drift equilibrium. A normal L-shaped curve under Mode shift test suggested absence of

*Microsatellite markers' diversity based pair-wise $F_{ST}$ (above diagonal) and Nei's genetic distance (below diagonal) among different buffalo populations*

| | ASW | MN | ASW-SL | CH | PMN | SK | MTW | KH |
|---|---|---|---|---|---|---|---|---|
| ASW | ----------- | 0.249 | 0.183 | 0.304 | 0.227 | 0.192 | 0.163 | 0.306 |
| MN | 0.144 | ---------- | 0.030 | 0.307 | 0.243 | 0.175 | 0.152 | 0.365 |
| ASW-SL | 0.117 | 0.029 | ---------- | 0.262 | 0.196 | 0.131 | 0.118 | 0.303 |
| CH | 0.209 | 0.206 | 0.191 | ---------- | 0.062 | 0.228 | 0.231 | 0.095 |
| PMN | 0.172 | 0.178 | 0.163 | 0.056 | ---------- | 0.159 | 0.161 | 0.073 |
| SK | 0.144 | 0.15 | 0.127 | 0.155 | 0.134 | ---------- | 0.076 | 0.219 |
| MTW | 0.129 | 0.137 | 0.118 | 0.156 | 0.136 | 0.046 | ---------- | 0.225 |
| KH | 0.199 | 0.217 | 0.201 | 0.092 | 0.076 | 0.158 | 0.162 | ---------- |

*(ASW-Assamese swamp, MN-Manipur, ASW-SL- Assamese Silcher, CH-Chilika, PMN-Paralakhemundi, SK-South Kanara, MTW-Marathwada, KH-Kalahandi)*

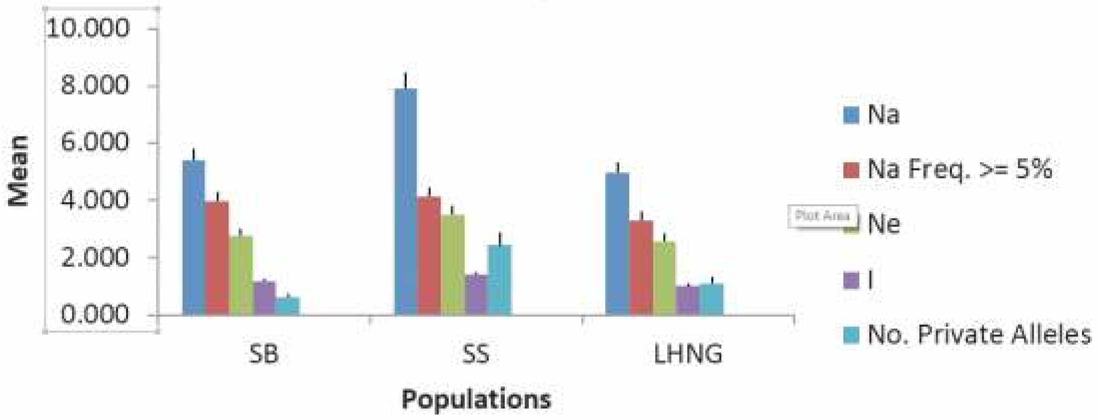
a recent reduction in the effective population size or a genetic bottleneck.

### Molecular and Physio-biochemical Evaluation of Heat Stress in Indian Sheep

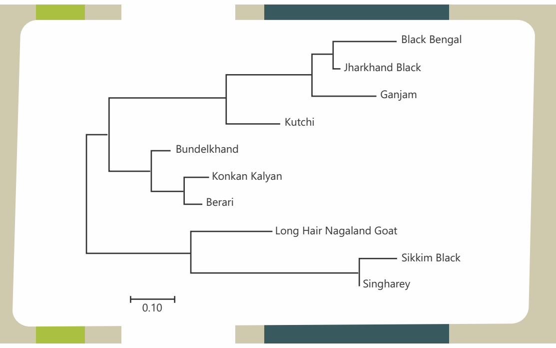
The research was conducted to study how thermo-tolerance is modulated by HSP90 and HSP70 gene polymorphism and its association with hemato-physio-biochemical parameters, supported by their expression profiles in Chokla, Magra, Marwari, and Madras Red sheep breeds. Least square analysis revealed significant effect ($P < 0.05$) of season and breed on all the physiological parameters, i.e., temperature, respiratory rate, and pulse rate (a.m. and p.m.), as well as hematological parameters like Hb, packed cell volume, total erythrocyte count (TEC), neutrophil/lymphocyte (N/L) ratio, and total leukocyte count (TLC). There was a significant influence ($P < 0.05$) of breed on biochemical parameters such as glucose, SGOT, phosphorous, triglyceride, and cholesterol. Eight fragments were amplified and sequenced in HSP90, and 70 genes and 13 single-nucleotide polymorphisms (SNPs) were identified. Tetra-primer amplification refractory mutation system PCR, PCR-RFLP, and allele-specific PCR genotyping protocols were developed for large-scale genotyping of five SNPs. A significant difference ($P < 0.05$) of rectal temperature (a.m.), respiratory rate (p.m.), triglyceride, and total protein was observed at SNP01; albumin at SNP2; pulse rate (p.m.) at SNP3; and rectal temperature (p.m.), pulse rate (p.m.), Hb (g/dL), and N/L ratio at SNP4 and TLC at SNP5. Gene expression analysis revealed higher expression in less adapted animals with Madras Red < Magra < Chokla < Marwari expression pattern. Predominant allele was found to be superior in most of the SNPs (SNP1-4) indicating the selection acting in directional manner (positive selection). Finally, it is concluded that TACCA haplotype combination of SNP1-SNP2-SNP3-SNP4-SNP5 might be of some selection advantage for the identification of animals more adaptable to heat stress. A total of 80 plasma samples (10 animals per breed and per season) of Chokla, Marwari, Magra and Madras Red breed were used for the estimation of cortisol level by ELISA. The mean values for the Chokla was found to be 4.78±1.35 ng/ml, whereas for Marwari it was found to be 6.74±1.35 ng/ml. The level of serum cortisol in Magra sheep breeds was found to be 9.14±1.46 ng/ml. In Madras Red sheep the mean value was found to be 7.19±1.38 ng/ml. The cortisol level was found to be higher in summer (7.85±0.98) than winter season (6.07±0.97). There was no significant effect ($P<0.05$) of cortisol level among breed, season and 5 identified SNPs of HSP90AA1 and HSP70 genes.

### Genetic Diversity in Nagaland Goats

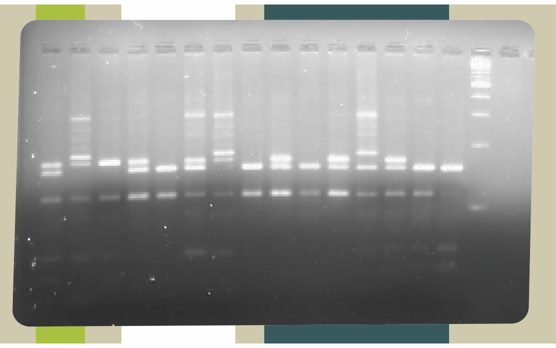
Microsatellite based genetic diversity in terms of allelic number, heterozygosity, inbreeding coefficient, Shannon's information index, polymorphic information contents were estimated using a battery of 25 markers. The observed number of alleles across the loci ranged from 2 (ETH225 & OarJMP29) to 9 (ILSTS058) with 5.00 ± 0.393 mean number of alleles per locus. The observed heterozygosity ranged from 0.043 (ETH225) to 0.786 (OMHC1) with an overall mean of 0.347±0.040 whereas effective hetrozygosity ranged from 0.045 (OarJMP29) to 0.815 (ILSTS058) with an overall mean of 0.499±0.051. The observed heterozygosity across the loci was less than effective hetrozygosity except for ILSTS059, OarJMP29, ILSTS34, ILSTS022 and RM088. The decreased heterozygosity pointed



*Allelic diversity analysis of Nagaland Goat Population*



Neighbour joining consensus tree showing long hair Nagaland goats distinctly



Amplified MHC class II DRB 3.2 locus from Black Bengal goat digested with Hae III

towards the reduction of genetic diversity in the population. The population tested for HW equilibrium indicated departure from Hardy-Weinberg Equilibrium (HWE) as chi-square value for most of the loci were significantly different (from the tabulated value, $P<0.05$). The difference between the observed and expected heterozygosity can also be attributed to the non-random mating among the individuals and possibility of inbreeding. This was also reflected by the positive FIS (0.258 ± 0.063) which varied from -0.467 (ILSTS022) to 0.776 (ETH225). The polymorphic information content value of a marker ranged from 0.045 (OarJMP29) to 0.815 (ILSTS058) with an overall 0.494 ±0.052 revealing its usefulness in determining the genetic diversity. Shannon's information index varying from 0.110 to 1.811 with mean value 1.006±0.105 also supported the usefulness of primers used. A normal 'L' shaped distribution of mode–shift test, suggested the absence of bottleneck i.e. the reduction in the effective population size of Nagaland goats.

On comparing with goats of Sikkim state and other goat breeds from plain region, Nagaland goats form a separate cluster indicating their genetic distinctness. In view of the distinct phenotype, genotype of long hair goat and commercial utility of its hair, this particular population needs propagation and further genetic improvement.

### Caprine MHC Class II antigens

The Class II Major Histocompatibility Complex exon 2 DRB3.2 locus which is involved in antigen presentation has been observed to exhibit a very high level of genetic variability in humans, murines, bovines/ ruminants. MHC Class II DRB3.2 locus was amplified was amplified by polymerase chain reaction from the Black Bengal (n=15), Barbari (n=15), Beetal (n=15), Osmannabadi (n=15) and Sangamneri (n=15) animals of indigenous goat breeds of the Indian subcontinent using the gene specific primers for amplification. The amplified product was put to digestion by restriction enzyme HaeIII and RsaI. The PCR-amplified products were digested with the restriction endonuclease (s) HaeIII and RsaI (New England Biolabs, Ipswich, MA). Digestions were performed in 200 µl PCR tubes, using a thermal cycler. After heat denaturation of the enzymes at 90°C for 30 min, the restriction fragments were resolved on high resolution agarose gel (3.5 to 4.0 percent) in order to resolve the digested fragments. A 10bp/ 50bp/100bp DNA ladder was used as a DNA size marker. The fragments were visualized by ethidium bromide staining of the gels. The analysis of the digestion patterns obtained is in progress.

### Genetic Diversity in Donkeys of Andhra Pradesh

The brown type donkeys of Andhra Pradesh, which are mainly concentrated in Kurnool and Anathapur districts, were evaluated for within breed genetic diversity and bottlenecks using heterologous microsatellite markers. The genomic DNA, isolated from twenty eight blood samples collected from the breeding tract, were amplified by PCR using FAM and HEX labeled primers and resolved for alleles on automatic DNA sequencer. In all twenty loci of the horse origin were tested and only twelve loci gave scorable results. Rest of the loci either did not amplify (HMS3 and HMS7) or did not resolve properly (VHL20) or showed less than four alleles (HMS5, HMS6, HTG4, ASB17 and COR22) in the studied population. At the twelve loci included in the final analysis, the PCR product size range varied from 76-92 bp at locus HTG6 to 257-273 bp at locus COR18. The observed number of alleles varied from 4 (VHL209) to 10 (AHT5 and HTG7) with a mean of 6.92 ±1.83. The effective number of alleles ranged from 1.62 (VHL209) to 7.91 (AHT5) with a mean of 4.21 ± 2.06. The observed heterozygosity ranged from 0.32 (HMS2) to 0.92 (AHT5) with a mean of 0.57 ± 0.2. The expected heterozygosity ranged between 0.39 (VHL209) to 0.89 (AHT5 and HTG7) with a mean of 0.72 ± 0.14. The mean genetic diversity estimate (FIS) was 0.21 indicating a moderately high level of inbreeding. The cumulative exclusion probability (PE) of these loci was 0.999892 indicating their suitability for parentage testing in these donkeys. The sign test, standardized differences test, the Wilcoxon test using the allelic frequency data at the studied loci as well as normal 'L' shaped distribution of the allelic frequency indicated the absence of any recent genetic bottleneck in brown type donkeys of Andhra Pradesh. When these donkeys were compared to Spiti donkeys of Himachal Pradesh on the basis of allelic frequency data at these loci they showed Nei's standard and unbiased genetic distances of 0.32 and 0.29, respectively.

### Milk Metabolomics based Characterization

Milk metabolite profiles were generated in the project, as an essential pre-requisite to identify the biomolecule/s which can explain nutritional or technological edge of milk from indigenous cows. During the reported period, milk from Bos taurus, Bos indicus and cross bred cattle raised in intensive system of management was compared with that of indigenous cattle maintained under extensive system. Animals were free ranging and no form of nutrient supplement was provided in extensive system. Milk samples of Indigenous (Sahiwal), exotic (Holstein Friesian) and crossbred (Sahiwal x Holstein Friesian) cows were collected from Government Livestock Farm, Hisar, taking care to minimize the effect of variables affecting milk composition (Season, parity, lactation stage, feed and fodder and health condition). Mid lactation stage animals were selected as the least changes in the milk composition occurs at this stage. The statistical analysis was done using SPSS-one way ANOVA (followed by Post Hoc Test). Significance was set at P<0.05.

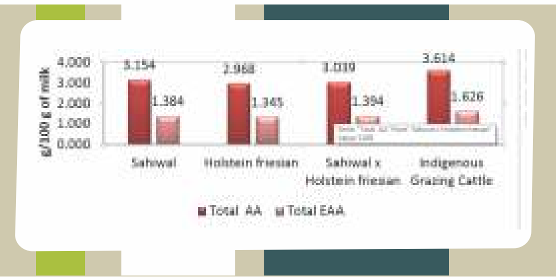
The concentration of nine minerals (Zn, Fe, Na, Ca, Mg, K, Ph, Cu and Cl) was quantified by inductively coupled plasma mass spectrometry (ICP-MS). Significantly higher (P<0.05) concentration of Zinc, Iron, Phosphorous and Copper was present in the milk of indigenous cattle maintained in extensive system. Whereas, Sodium was significantly lower. Calcium, Magnesium and Potassium were not affected by the management conditions. The results indicate that milk of grazing indigenous cows is a rich source of minerals which play important role in metabolism. The total amino acid (AA) content as quantified by HPLC-DAD was highest (g/100 g of milk) for the grazing indigenous cattle (3.61±0.05). Similarly, significantly higher (P<0.05) essential amino acids (EAA) could be deciphered in the milk of grazing indigenous cattle (1.63±0.02) as compared to all the three categories in the intensive system of management.

Fatty acids were quantified by Gas chromatography. Significant differences (P<0.05) were observed among the studied groups with respect to saturated fatty acid (SFA) concentration in the milk. The lowest level was detected in the grazing indigenous group (62.14%). More importantly, significantly lower concentrations of atherogenic (C12, 14 and 16) fatty acids could be recorded in the milk of indigenous cattle under extensive system of management. Considerable differences could be recorded among the extensively and intensively

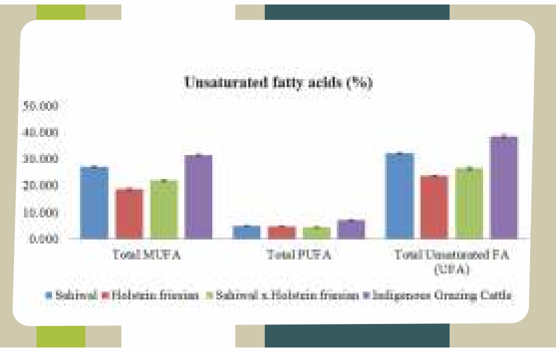
*Mineral profile of milk from cows maintained in intensive and extensive systems of management*

| **Minerals** | | | **Intensive Management** | | **Extensive Management** | | **Significance** | | |
|---|---|---|---|---|---|---|---|---|---|
| | **Sahiwal** | | **Holstein Friesian** | | **Sahiwal x Holstein Friesian** | | **Indigenous Grazing Cattle** | | |
| | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | |
| Zinc | 359.532$^{a}$ | 16.246 | 338.780$^{a}$ | 13.866 | 340.520$^{a}$ | 17.361 | 522.308$^{b}$ | 36.739 | *** |
| Iron | 29.942$^{a}$ | 1.128 | 30.245$^{a}$ | 1.184 | 33.610$^{a}$ | 1.389 | 44.878$^{b}$ | 2.126 | *** |
| Sodium | 41.353$^{a}$ | 0.896 | 47.195$^{b}$ | 1.554 | 48.348$^{b}$ | 2.323 | 25.490$^{c}$ | 1.749 | *** |
| Calcium | 123.177 | 2.000 | 122.250 | 1.955 | 118.533 | 2.609 | 119.098 | 2.521 | ns |
| Magnesium | 13.538 | 0.410 | 12.638 | 0.672 | 13.420 | 0.371 | 13.328 | 0.598 | ns |
| Potassium | 143.387 | 3.921 | 140.080 | 5.979 | 142.895 | 4.363 | 146.078 | 5.463 | ns |
| Phosphorus | 97.168$^{a}$ | 1.876 | 98.020$^{a}$ | 3.296 | 96.345$^{a}$ | 3.573 | 108.988$^{b}$ | 0.997 | * |
| Copper | 9.732$^{a}$ | 0.494 | 9.975$^{a}$ | 0.528 | 10.988$^{ab}$ | 0.751 | 12.235$^{b}$ | 0.645 | * |

*ns – non significant; * P<0.05; ** P<0.01; *** P<0.001*

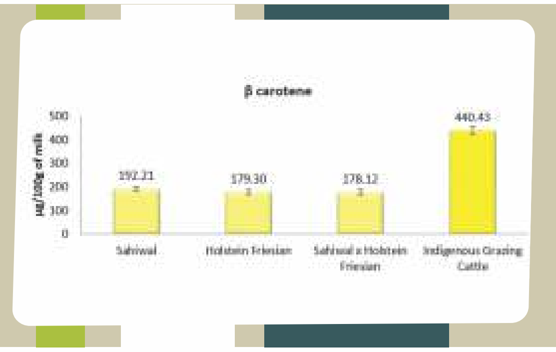


managed groups with respect to the unsaturated fatty acids (UFA). They were highest in milk of grazing cattle (38.58%). This difference was mainly attributed to varying concentration of MUFA which was highest in grazing cattle (31.40%). Similarly, grazing cattle had higher milk PUFA level (7.18%). Similar trend was recorded with respect to total ω6 fatty acids (4.69% in grazing vs 3.87% in Sahiwal). Grazing resulted in higher ω3 fatty acids (1.74%). LA/ALA (2.49) as well as ω6/ω3 (2.72) ratio was significantly lower in the indigenous grazing cattle as compared to intensive management groups, where it varied from 3.07-3.49 and 4.12-4.64, respectively. Milk fat is usually considered as proatherogenic thus atherogenic index (AI) was calculated. Milk of grazing cattle presents the minimum AI index (33.90). These differences in the FA profile can be attributed to the forest grazing that had a negative effect on the SFA and a positive effect on the unsaturated fatty acids.



β carotene concentration was of similar magnitude among the intensively managed cattle groups, where it varied within a narrow range of 178.12 µg/100g (HF x Sahiwal) and 192.21µg/100g of milk (Sahiwal). However, more than two fold concentration was recorded in the milk of indigenous cattle maintained exclusively on grazing. Higher concentration of the β carotene adds value to the milk as carotenoids in cow's milk and consequently in milk products are important for human health and nutrition. Moreover, milk fat carotenoids cause the yellow color of butter and many cheeses, which is positively perceived by many consumers as green image because of its association with grazing animals.

Milk quality traits have become increasingly relevant as consumer awareness of healthy diet is growing. Our results suggest that grazing cattle have favorable milk composition characteristics. Healthfulness of milk obtained from indigenous cattle reared in extensive system of management can be assigned special value, which can become important tool to maintain native genetic resources characterized by low production levels.



### Skeletal Muscle Transcriptome Profiling of Bandur (Mandya) Sheep

Body biometry and weight of rams of Bandur sheep and local sheep of Karnataka were recorded. All the animals were in the two-tooth stage (12-19 months) and their bodyweights ranged from 16-30kg. Carcass measurements like hot carcass weight, back fat thickness, fore saddle, hind saddle, foreleg, hind leg, rib eye area, pH, temperature of carcass, water holding capacity etc were also recorded. The backfat thickness was observed to be slightly greater in Bandur animals as compared to local sheep. Weights of wholesale cuts viz. neck, shoulder, fore shank, brisket, rack, loin, flank etc were measured. Tenderness of different muscles (longissimus dorsi, brachicephalicus, bicep, semimembranosus, psoas major, semitendinosus and tricep) was measured by taking average of shear force for a sample in triplicate. The tenderness values of different muscles of the Bandur sheep had lower values (12.74N-22.65N) as compared to those of local sheep (16.44N-26.19N). The lower shear force values in Bandur sheep indicate greater tenderness which is a desirable trait. Sensory evaluation of the mutton revealed slightly higher juiciness and flavour in Bandur sheep meat but the difference between the two groups was not significant. Further, analysis for concentration of different minerals, fatty acid and amino acid profiling and RNA isolation from the longissimus dorsi muscle is in progress.

### Genome wide Diversity Analysis of Indian Yak Populations

Indian yak populations (Ladakhi and Sikkimi yaks) were considered for the present study. PCR amplification was performed to enrich and add the Illumina specific adapters and flowcell annealing sequences. The pooled samples were sequenced on a single lane of HiSEQ 2000. In Ladakhi and Sikkimi yaks, the number of reads ranged from 1227316 to 1126501. The average GC content of Ladakhi and Sikkimi yaks is 46.52 and 45.80 respectively. The mean read quality Phred score in Ladakhi and Sikkimi yaks ranged from 34.28 to 34.59 respectively.

### Karyotyping and DNA Testing for Screening Genetic Defects in Indian Bovines (Service Project)

Cytogenetic screening of 286 bulls of cattle (125) and buffalo (161) and 8 cows of 22 different government agencies was carried out during 2016-17. Samples were screened for any chromosomal abnormality/aberration. Among the screened samples, two bulls Sahiwal and Red Sindhi were found to carry the chromosomal defect. Total 92 cattle (73) and buffalo (19) bulls of different agencies were screened (DNA testing) for genetic diseases (Bovine leukocyte adhesion deficiency, deficiency of uridine mono phosphate synthase, Citrullinemia and factor XI deficiency). All the animals were found to carry normal genotype.

PCR-RFLP test was developed for Jersey haplotype I ( JH I) and tetra ARMS PCR was developed for Congenital Vertibral Malformation (CVM). Efforts have also been made to develop multiplex tests for FXI deficiency + Citrullinemia and FXI deficiency + BLAD. A revenue of Rs.3,30,800/- was generated through these services.

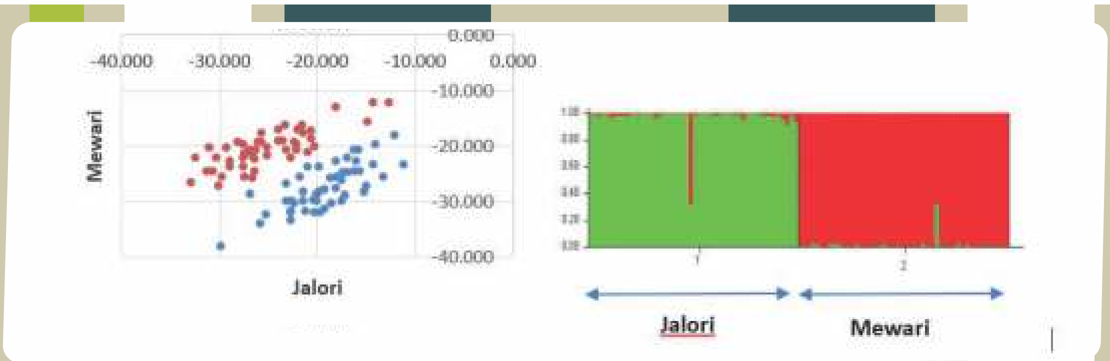
## Network Project on AnGR (Core Lab)

The importance of indigenous livestock breeds and populations lies in their adaptation to local biotic and abiotic stresses and to traditional husbandry systems. However, most of these animal genetic resources do not have boundaries between distinct populations and are overlapping. Microsatellite based genetic characterization was done for the populations being characterized under XII plan under the network project. Measures of diversity which forms the basis for planning their utilization and/or conservation were calculated for ten populations of seven different species. Summary of within breed population estimates are as follows

All the populations except Tibetan sheep exhibited fair genetic variation which is evident from average number of alleles and heterozygosity. Despite high genetic diversity, significant heterozygote deficiency was also observed within seven populations.

The diversity indices pointed towards diminished genetic diversity in the Tibetan, a valuable Himalayan sheep breed classified as endangered. The observed and expected heterozygosity values ranged from 0.150 (BM1314) to 0.9 (OarCP20) with an overall mean of 0.473 0.044 and from 0.329 (BM8125) to 0.885 (BM6526) with an overall mean 0.672 0.030, respectively. Thirteen microsatellite loci exhibited significant ($p<0.05$) departures from the Hardy–Weinberg proportions in the population. Maximum heterozygote deficiency (FIS) was also observed in the Tibetan sheep. The estimate of heterozygote deficiency varied from -0.443 (OarCP20) to 0.668 (OarFCB128) with a mean positive value of 0.302 0.057. A normal 'L' shaped distribution of mode–shift test and non-significant heterozygote excess on the basis of different models suggested absence of recent bottleneck in the existing Tibetan population. In view of the declining population of Tibetan sheep (less than 250) in the breeding tract, need of the hour is immediate scientific management of the population so as to increase the population hand in hand with retaining the founder alleles to the maximum possible extent.

Indications of loss in the variability was also depicted by the higher heterozygote deficiency recorded for the Dharwadi buffalo (FIS = 19%), Hazra chicken (22%) and Arunachali Yak (14%). The consanguinity produced by mating between relatives can be one of the principal causes for loss of heterozygotes in these populations. The strategy of sampling very few animals/ birds from a herd/ flock was followed so as to minimize the artificial substructuring of the samples, the associated Wahlund effect as well as the inclusion of related animals. Therefore, the observed results seem to reveal real inbreeding in population. Ignorance of reproductive strategies is causing undesirable rates of inbreeding. This trend should be properly monitored by governmental and non-governmental organizations involved in promoting



Population assignment & clustering of jalori and mewari camel (STRUCTURE V2.2)

the development of animal husbandry in respective states.

The multi-locus FST values of breed differentiation for Jalori and Mewari camel indicated that only 3.7% of the total genetic variation was due to unique allelic differences between the breeds, with the remaining 96.3% corresponding to differences among individuals within the breed. However, population assignment and Bayesian based analysis established distinctness of two camel populations of Rajasthan. Assignment test correctly assigned 99% animals to their predefined population. All the animals of Jalori were assigned to its population whereas; only one animal of Mewari was assigned to the Jalori group.

Bayesian clustering analysis was used to infer how many clusters or sub-populations (K) were most appropriate for interpreting the camel genotype data without prior information on the number of locations at which the individuals were sampled as implemented in STRUCTURE v2.2. Likely value of K which best captures the variation present in the data following the Bayesian approach was two.

The information generated from the present study is based on the microsatellite markers that have previously been used for indigenous livestock diversity studies. Hence the data can be compared with that of registered breeds to establish their distinction from the catalogued gene pool. Diversity information can also be used in conjunction with the information on physical and phenotypic characteristics and management practices for registration of a population as a breed.

## Externally Funded Projects

### Whole Genome based SNP Mining and Development of Breed Signatures for Dairy and Dual-Purpose Indigenous Cattle (DBT)

72 DNA samples (18 random samples/breed) of Sahiwal, Tharparkar, Gir and Vechur breeds of cattle using 777K SNP chip were genotyped and analyzed using in-house computer scripts and other software's in public domain.1000 markers were identified, which had the higher power to differentiate these cattle populations (Fst>0.28). These 1000 markers account for 39 % of the genetic variation between the breeds. The breeds were clearly classified into small and large sized

*Genetic diversity in livestock populations*

| Species | Breed/population | Ho | He | Na | Ne | FIS |
|---|---|---|---|---|---|---|
| Buffalo | Dharwadi | 0.63±0.03 | 0.78±0.01 | 13.12±0.80 | 5.35±0.45 | 0.19±0.04 |
| Chicken | Hazara | 0.62±0.03 | 0.80±0.02 | 14.96±0.82 | 6.61±0.42 | 0.22±0.03 |
| Sheep | Poonchi | 0.77±0.04 | 0.76±0.02 | 8.56±0.52 | 4.5±0.31 | -0.01±0.04 |
| | Tibetan | 0.47±0.04 | 0.67±0.03 | 5.92±0.39 | 3.7±0.334 | 0.30±0.06 |
| Goat | Bhakarwal | 0.63±0.05 | 0.64±0.04 | 8.26±0.66 | 3.61±0.36 | 0.002±0.03 |
| Donkey | Rajasthani | 0.63±0.07 | 0.62±0.05 | 8.16±0.89 | 3.79±0.53 | 0.07±0.07 |
| Yak | Arunachali | 0.55±0.04 | 0.65±0.04 | 9.32±0.70 | 3.47±0.32 | 0.14±0.04 |
| Cattle | Kosali | 0.69±0.04 | 0.77±0.02 | 11.42±0.88 | 4.99±0.37 | 0.08±0.04 |
| Camel | Jalori | 0.60±0.06 | 0.64±0.05 | 7.84±1.05 | 4.02±0.48 | 0.05±0.05 |
| | Mewari | 0.60±0.05 | 0.66±0.05 | 8.52±0.97 | 4.55±0.98 | 0.09±0.05 |

*Significant (P<0.05); **Significant (P<0.01) differences of mean physiological parameter between the species a,bMean physiological parameter differs significantly (P<0.05) with respect to the resting intervals breeds indicating shared ancestry of large sized milch breeds (Gir, Tharparkar and Sahiwal). The highest linkage disequilibrium (LD) with r2=0.353 was observed in Gir cattle and the lowest LD (r2=0.325) was found in Sahiwal. The total number of haplotype blocks were 8027, 15640 and 14237 in Sahiwal, Tharparkar and Gir cattle, respectively. There were 1138, 1528 and 1762 ROH regions in Sahiwal, Tharparkar and Gir cattle for ROH length >100 Kb. The highest level of heterozygosity (Ho = 0.375, HE = 0.374) were found in the Sahiwal cattle and the lowest Ho (0.359) was observed in Gir cattle in large sized breeds. A total of 48, 30 and 60 genes were found under selective sweeps for Sahiwal-Tharparkar, Sahiwal-Gir and Tharparkar-Gir breed pairs, respectively. The selective sweeps identified in these cattle breeds will help to map the quantitative trait loci (QTL) of economic important traits leading to genome-wide association studies (GWAS) in these cattle breeds.

## Development of Genomic Resources for Indigenous Cattle and Buffalo Breeds ( CaBin)

Over 100 SNPs in cattle across 6 candidate genes related to milk, disease resistance and adaptive traits in indigenous cattle have been catalogued. Lactoferrin gene was sequence characterized in Indian native cattle and identified 19 SNPs. Polymorphic loci have been identified in buffalo TNF-alpha, CXCR2 and NOD-like receptor-1 genes. Cataloguing of SNPs in buffalo TLR2, TLR4, NOD-like receptors-1 & 2, TNF-alpha and CXCR2 genes has been accomplished.

A database has been developed to store the information on genomic variations and sequences in candidate genes related to milk, disease resistance and adaptive traits on cattle and buffalo breeds. It includes gene name, genomic coordinates, sequence data, SNPs, type of SNPs and their frequency in different populations, novelty, related publications, and the information on validation and association. The database has been defined using MySQL. User interface for data entry and data view has been developed using HTML and PHP. It can be searched using key-terms on species, breeds, genes and traits. Compiled data on SNPs and sequences on candidate genes in cattle and buffalo breeds has been entered.

## Transcriptome Analysis and Differential Expression of Genes in Indian Camel – *Camelus dromedarius* and *Camelus bactrianus* ( CaBin)

Tissues of the two camel species along with the data of Illumina 76 base pair paired end reads were 554 Million reads for dromedarian and 309 million reads for bactrian camel. The tissue wise reads available were as follows.

Denovo assembly and annotation of contigs: Next Generation Sequencing data of ten tissues each of Camelus dromedarius and Camelus bactrianus were denovo assembled using five different denovo algorithms which were Trinitiy, Binpacker, Shannon, Soap and Velvet. The contigs obtained were annotated using various database. Primarily the cattle database was used for the purpose but the transcripts which could not be annotated using cattle database but yielded the proteins were annotated with the human transcriptome.

The total number of protein coding genes and non coding genes compared in each of the camel species are given below. The number of protein coding and non coding RNAs upregulated and down regulated are depicted in the table.

| **Tissue** | **No. of Reads (in Millions)** | |
|---|---|---|
| | ***Camelus dromedarius*** | ***Camelus bactrianus*** |
| Kidney | 59.17 | 35.13 |
| Testis | 42.67 | 29.25 |
| Lungs | 62.67 | 31.55 |
| Skin | 61.29 | 35.97 |
| Brain | 62.31 | 33.87 |
| Muscle | 59.04 | 41.02 |
| Liver | 52.69 | 34.49 |
| Heart | 62.63 | 34.15 |
| Hypothalamus | 61.57 | 33.21 |
| Blood | 29.54 | ------- |

In addition to denovo assembly tissue wise the raw reads of the transcriptome of various tissues were separately mapped on the draft genomes available for camel and their relatives viz: Camelus dromedarius, Camelus bactrianus, Camelus ferus and Vicugna pacos. The exercise was carried out for identification of isoforms of various genes in both types of camel.

The isoform analysis of the transcriptome using annotation procedures revealed 3100 genes to have two isoforms, 2000 genes of camel having 3 isoforms, 1200 genes to have four isoforms, 750 genes having 5 isoforms, 500 genes having 6 isoforms and 650 genes having more than 10 isoforms.

Differential expression of genes were carried out using .bed files mapped using the Vicugna pacos using the annotated transcriptome of the species from Ensembl database. The Upregulated genes were subjected to gene ontology to identify the

*Transcriptome analysis of camelus dromedarius and camelus bactrianus*

| Tissue | Protein Co-ding Genes expressed | | Non Coding RNA expressed | | Protein coding Genes Up regulated | Protein coding Genes down regulated | Non Coding RNA's up regulated | Non Coding RNA's down regulated | MicroRNA up regulated | MicroRNA down regulated |
|---|---|---|---|---|---|---|---|---|---|---|
| | Bacterian Camel | Domedari-an camel | Bacterian Camel | Domedari-an camel | Bacterian Camel | Domedari-an camel | Bacterian Camel | Domedari-an camel | Bacterian Camel | Domedari-an camel |
| Hypothalamus | 7108 | 7605 | 56 | 65 | 937 | 2180 | 19 | 4 | 13 | 77 |
| Brain | 7409 | 7579 | 64 | 70 | 349 | 454 | 3 | 8 | 5 | 15 |
| Heart | 6320 | 6937 | 46 | 48 | 635 | 2809 | 12 | 84 | 11 | 14 |
| Kidney | 6534 | 6597 | 48 | 50 | 1766 | 1471 | 11 | 6 | 5 | 12 |
| Muscle | 6502 | 5466 | 42 | 28 | 236 | 2236 | 3 | 13 | 5 | 80 |
| Testis | 7027 | 7168 | 58 | 57 | 2129 | 2026 | 4 | 23 | 47 | 53 |
| Lungs | 7674 | 7794 | 58 | 63 | 286 | 388 | 2 | 0 | 9 | 11 |
| Liver | 4258 | 4143 | 22 | 22 | 1122 | 579 | 2 | 3 | 31 | 9 |
| Skin | 6921 | 7304 | 30 | 37 | 1395 | 1528 | 7 | 18 | 26 | 45 |

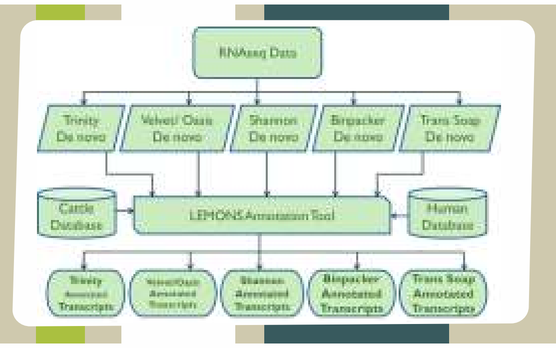
processes. This was carried out for protein coding genes but also for microRNA. The further analysis was carried out using the comparative genomics by converting the Vicugna pacos genes to human genes using suitable conversion software. This exercise was carried out for the ten sets of tissues from bactrian as well as dromedarian camel. The database for Bactrian camel and dromedarian camel have been developed and are at present accessible through the following internet address:

http://14.139.252.118/Dcamel/index.php (for Dromedarian camel)

http://14.139.252.118/Bcamel/index.php (for Bactrian Camel)

The *Camelus dromedarius* transcriptome database (CDTT) has 404527 contig entries submitted to NCBI. The hyperlinked contig IDs of the database provide the sequence available at NCBI. The gene ontology terms of the contigs as annotated with Blast tool (Biological, cellular or molecular functions) are hyperlinked to Amigo2 database. The other annotations are with respect to the enzyme commission numbers and Pf domain. The Pf domain takes the user to the Conserved protein domain family. A search function provides species, tissue as an option has been integrated so that the database can be searched as desired by the visitor. Similarly a SNP search function has been added. The microsatellite search of dinucleotide, trinucleotide etc have been provided. The output provides the contig identifier of the genome, motif type, start and end position of the repeat motif, the score as well as the unit type is depicted. The Left (L) and the Right (R) flanking regions provide 100 base pairs on each side of the repeat motif for utilization of the primer designing. We have integrated blast search tool which can be used for Blast for local Blast in the camel database or the NCBI database. The CDTD 62238 dinucleotide microsatellites, 7275 tri-nucleotides microsatellites and so on. 97437 microsatellites were found in dromedarian camel. The total number of SNP identified and can be visualized are 392179.

Similarly for Bactrian camel (CBTD) there are 307343 contigs in all. The total number of SNPs are 277435 which can be visualized against the genome and six frame translation. Other functions of the database are same as that of dromedarian camel.



Work flow for *De novo* Assembly and annotation of transcripts

## CRP on Biodiversity

Somatic cell bank is extremely important for the recovery of endangered species. Thus double-humped camel (Camelus bactrianus) ear marginal tissue fibroblast cell line from five samples, stocking 60 cryogenically-preserved vials (1×10¬6 cells/ml) per animal, was successfully established by using primary explant technique and cell cryopreservation. The cells showed typical fusiform morphology with centrally located oval nuclei with radiating, flame like or whirlpool like migrating patterns.

Four different commercially available media, known to support fibroblast cultures were tested with respect to growth potential for camel fibroblasts. Maximum total cell count with same seeding (80,000 cells) and under similar culture conditions was 6,75,000, 3,05,000, 13,90,000 and 10,05,000cells/ml for MEM, DMEM+High glucose, DMEM+Ham's F12 (1:1) and fibroblast specific media (HiFibroXLTM), respectively. Hence, DMEM+Ham's F12 (1:1) with 10% FBS was used in subsequent passages. Cells followed a typical sigmoid growth curve with population doubling time of 30.6 hrs. Epithelial and fibroblast cells initially grew together. However, fibroblast cells outgrew their epithelial counterparts in subsequent passages.

Selection of media for secondary culture of camel fibroblast

| Characteristics | MEM | DMEM + High Glucose | DMEM + Ham's F12 | Fibroblast Specific Media (HiFibroXL™) |
|---|---|---|---|---|
| Total cells, 80% confluency | 6,75,000 | 3,05,000 | 13,90,000 | 10,05,000 |
| % Viability | 99.25 | 99.25 | 99.2 | 97.5 |
| Morphology at Day 5 | | | | |

RT-PCR was performed at different passages of individual samples using primers specific to Cytokeratin19 (CK19) and Osteopontin (OPN) in order to confirm the origin of cells and to identify cross-contamination with non-fibroblast cells. Osteocytes were absent from the beginning whereas, epithelial cells were eliminated after 1st passage.

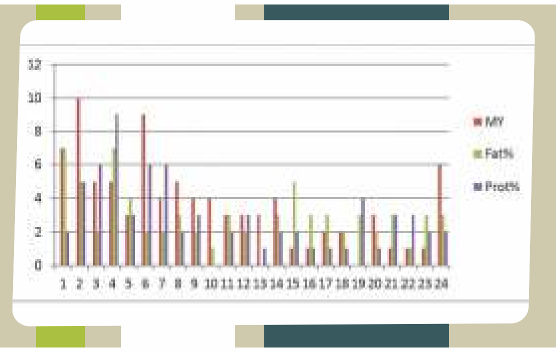
Thus the cells were cryopreserved at 4th to 6th passages. Chromosome karyotyping showed normal diploid (2n = 74) number. Cells were free from microbial contaminations. Cells had more than 90% viability in culture after 1 month of cryopreservation. These cells were morphologically indistinguishable from the cell stocks prior to freezing. This research, not only preserves important genetic resource of Bactrian camel at the cell level, but also serves as a valuable resource for genome, post genome and somatic cell cloning research.

## Identification of Markers for Economic Traits and Transcriptomics Study in Buffalo and Goats (CRP on Genomics)

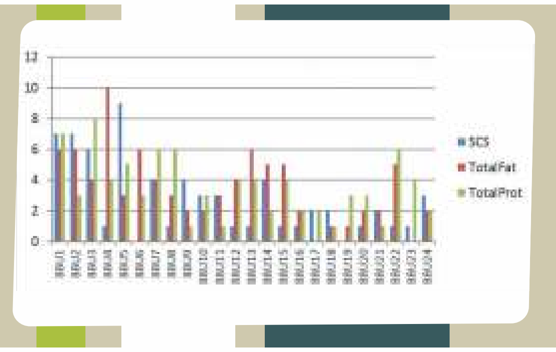
### *SNP discovery and Genotyping of animals with phenotypic records*

Genotyping by Sequencing (GBS) technique was used for creating a reduced representation library from genomic DNA for the purpose of discovering and scoring SNP variants. All the 12 Sires and their daughters were genotyped for these 6215 SNPs which cover all the autosome of buffaloes.

The data was analysed family wise for different chromosomes (12 half sib families). The significance of the QTLs was tested using the permutation test. The analysis was later combined for the detection of QTLs on the basis of results of 12 half sib families and each of the 24 autosomes of buffaloes. The combined analysis of the QTLs obtained family wise was done using Biomercator. The graphs of QTLs on each of the 24 autosomes (5 metacentric and 19 acrocentric chromosomes) for milk fat and milk protein percentage and total fat yield and total protein yield, Age at first calving and Age at first heat and somatic cell score were prepared. The traits i.e. Milk yield, Fat percentage, Protein percentage, Somatic cell count, Total Fat Yield, Total Protein yield, Age at first calving, Age at first heat, were analysed for the detection of QTLs. A total of 65 QTLs have been identified for the somatic cell score in buffaloes. The QTLs were present on all autosome except the p arm of BBU4 and autosome BBU6 and BBU19. This invention shall help in selection of sires for low somatic cell count for mastitis resistance in buffaloes. A total of 68 QTLs have been identified for age at first heat in buffaloes. The QTLs were present on all the 24 autosomes except p arm of BBU1 and autosomes BBU6 and BBU19. A total of 86 QTLs have been identified for age at first calving in buffaloes. The QTLs were present on all the 24 autosomes except autosomes BBU10, BBU22 and BBU24. A total of 87 QTLs have been identified for the milk yield in buffaloes. The QTLs were present on all the autosomes except the q arm of BBU3 and p arm of BBU4. No QTL for milk yield was



Chromosome wise number of QTLs identified for Milk yield and milk composition (Fat and Protein Percentage %)



Chromosome wise QTLs identified for Somatic Cell Score (SCS), Total Fat and Total Protein in buffaloes

identified on BBU19. A total of 310 QTLs have been identified for the fat percent, protein percent, total fat yield and total protein yield during first lactation in buffaloes. The number of QTLs were 71 for milk fat percentage, 70 for milk protein percentage, 84 for total milk fat yield and 85 for total milk protein yield. The QTLs were present on all the autosomes BBU1 to BBU24 except q arm of BBU3 and autosome BBU13 for milk fat percentage and except q arm of BBU3 and autosome BBU10 for milk protein percentage and except p arm of BBU2 and BBU5 and autosome BBU17 & BBU23 in total milk fat yield and except p arm of BBU4 in total milk protein yield.

***Development of a Medium Density SNP chip***

We utilised the genotyping by sequencing technology with 15 populations of buffalo distributed throughout the country (Murrah, NiliRavi, Mehsana, Pandharpuri, Jaffarabadi, Banni, Chilika, UP buffaloes, Swamp buffaloes of North East, Nagpuri, Bhadawari, Tarai, Marathwada, Kalahasthi, Kerala and Toda) populations were utilised for preparation of a genome wide chip for buffaloes. A total of 98346 SNPs have been identified which are genome wide and have passed the quality control parameters for development into an SNP Array. This medium density SNP array can be used for genomic selection in buffaloes and shall cater to both riverine and swamp buffaloes. The mean distance among the SNPs is 27.9 Kb.

***Buffalo QTL database***

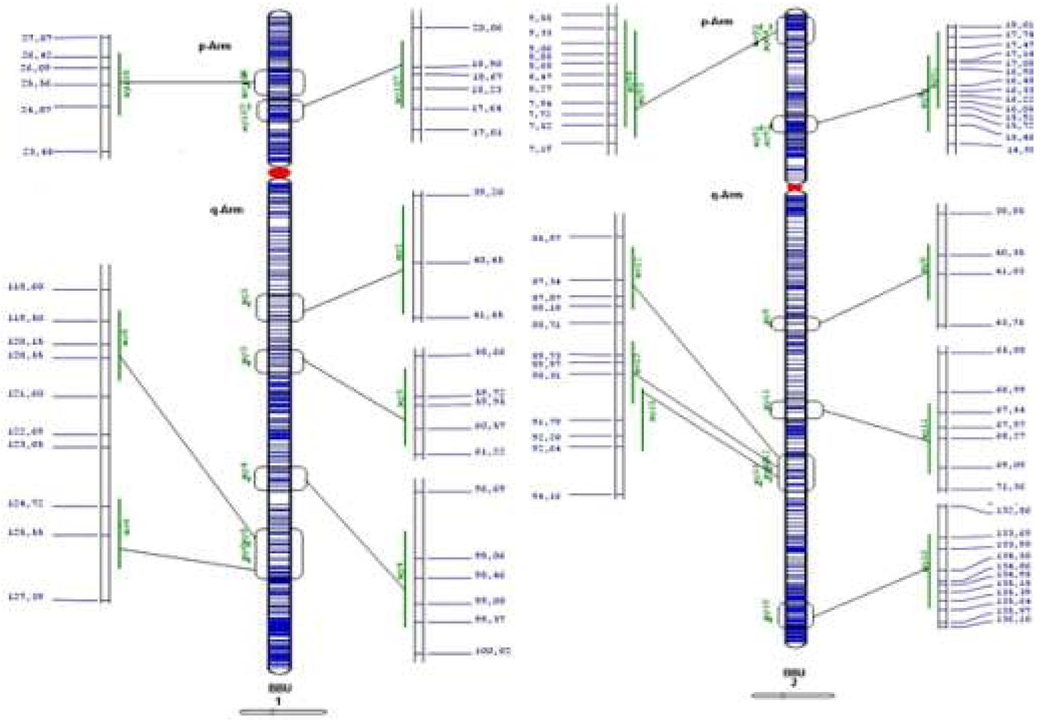
All the identified quantitative trait loci in buffaloes have been compiled in the form of a buffalo QTL database. It provides all the information about the QTL of buffaloes for various economic traits. The buffalo QTL database is accessible through the following site:

http://14.139.252.118:8084/BuffaloQTL/

The QTLs have been identified for various economic traits based on the meta analysis of QTLs based on 12 sire half sib families. One can select the trait from the menu and then click the desired trait. It leads to 24 autosomes. The viewer can choose the chromosome of choice and this displays the various QTLs that have been identified. The QTLs are hyperlinked to the detailed information about the QTL. At the bottom is the information about the genes underlying the QTL region for the trait. The click leads to a set of genes that underlie the chromosomal region. Information is also provided about the name, ensemble ID (for both the human genes and or cattle genes). The names are hyperlinked to take a visitor to the Ensembl database. The genes that are colored pink are the genes which have already been associated with the trait of interest in human or cattle or both the

*Number of genes identified for different milk traits*

| Trait | Genes Identified | Genes Reported |
|---|---|---|
| Milk yield | 3819 | 1697 |
| Fat % | 2412 | 1438 |
| Protein % | 2638 | 1130 |
| Total Fat | 3095 | 1274 |
| Total Protein | 3505 | 1570 |
| Somatic Cell Score | 3342 | 1479 |



Location of QTLs for milk yield in bufalloes

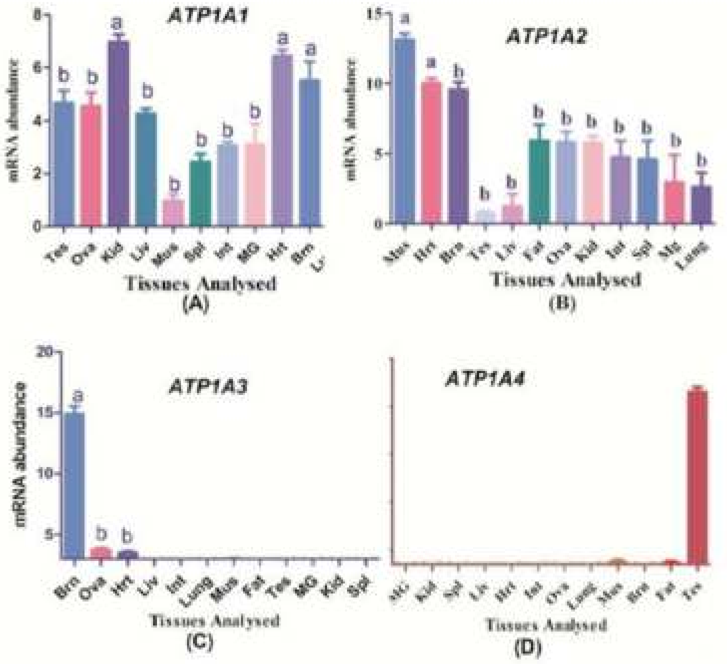
species. The genes underlying the QTL were identified using comparative genomics.

Comparative genomics was utilised for the identification of the gene underlying the QTLs regions of interest. We utilised the Buffalo- Cattle and Cattle - Human Synteny to identify the genes. The QTL positions on the chromosomes for milk yield (as representative of a trait) has been shown in above figure.

### Genome Data Mining to Unravel Molecular basis of Thermotolerance and Adaptation to Diverse Environments in Native Cattle and Buffaloes (National Fellow project)

#### *Identification of differentially expressed genes, biological processes and pathways*

The transcriptome analysis of PBMCs from local native cattle of Ladakh from high altitude and Sahiwal cattle from low altitude resulted in identification of several hundred differentially expressed genes, biological processes, molecular functions and pathways. Additionally, transcriptional pattern of hypoxia inducing factor-1 (HIF-1) and several of its regulated genes in PBMCs samples of different cattle types adapted to high altitude hypoxia and low altitude normoxia conditions was also attempted. The data revealed distinct transcriptome signature of PBMCs in Sahiwal and Ladakhi cows as revealed by hierarchical, k-means clustering and distinct heat maps (Fig 1). Some of the most up-regulated genes in Ladakhi cows viz; INHBC, ITPRI, HECA, ABI3, GPR171, HIF-1α, VEGFA, NOS2, MYH2, PRKAA1 were involved in hypoxia response, stress response and biological regulation. In Sahiwal cows, the top most up-regulated genes included eEF1A1, GRO1, CXCL2, DEFB3, TGFB3, BOLA-DQA3 were involved in immune function, and inflammatory response indicating their immune potential and active host defence mechanism to combat the pathogens prevalent in the tropical conditions. The metabolic and signalling pathways most impacted in the study were, MAPK signalling, electron transport chain, apoptosis, IL2 signalling, TGF-β receptor signalling, Toll-like receptors signalling, TNF-alpha and NF- kB signalling and GPCRs indicating signatures of adaptive evolution of these two cattle types in response to the diverse environments. Validation of transcriptome data using qPCR revealed significant increase in expression of hypoxia associated genes like HIF-1 and its regulated genes viz., glucose transporter 1 (GLUT1), vascular endothelial growth factor (VEGF) and hexokinase (HIK) in high altitude cattle in Ladakhi cows suggesting their pivotal role in high altitude adaptation. Tissue specific expression abundance of isoforms of Na/K ATPase gene in riverine buffaloes: RNA analysis showed tissue specific expression of ATP1A1, ATP1A2, ATP1A3 and ATP1A4 isoforms. The expression level of ATP1A1 was high



mRNA level of ATP1A1, ATP1A2, ATP1A3 and ATP1A4 genes across various tissues of buffaloes.

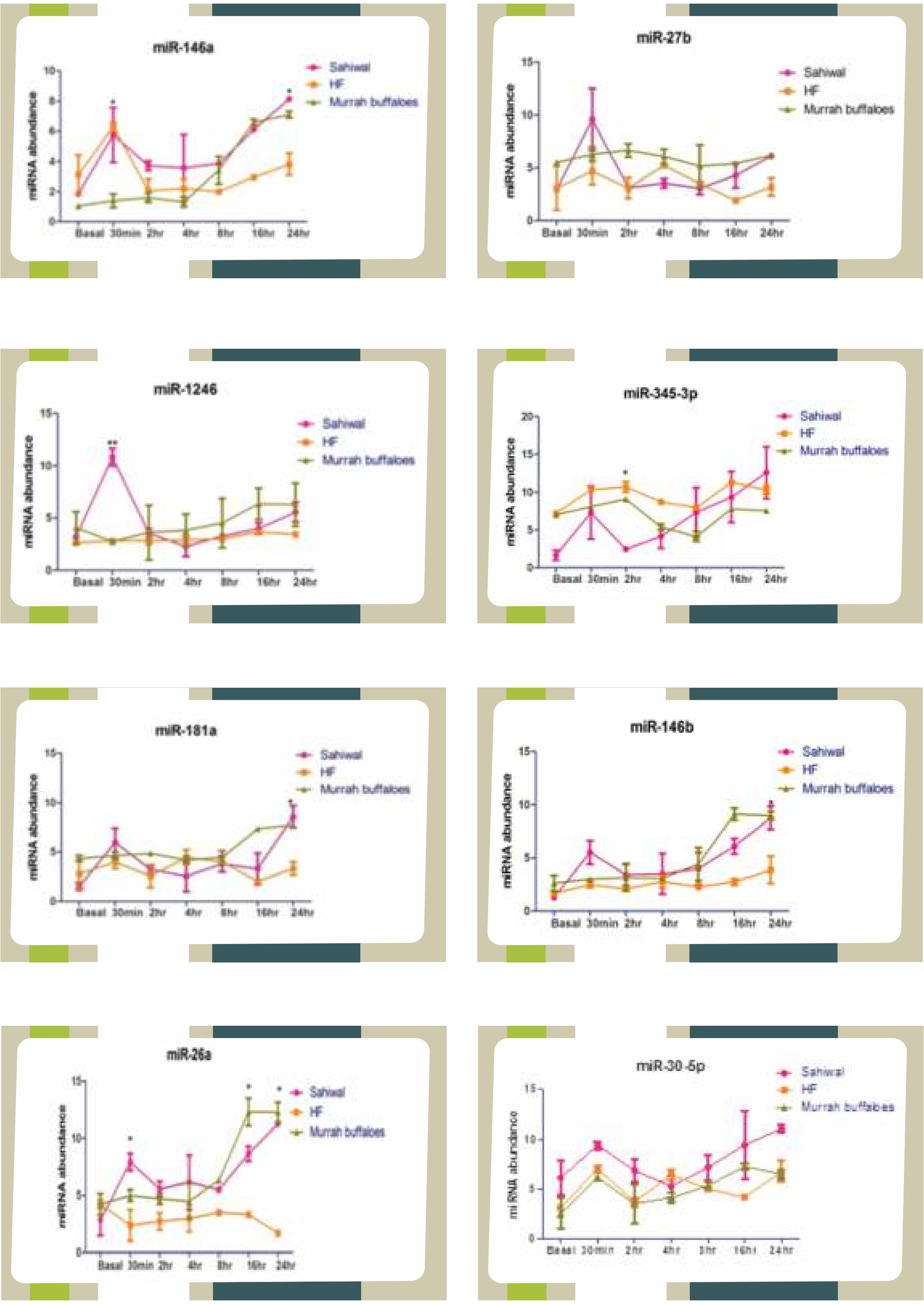
in kidney (6.96), heart (6.43), brain (5.51) and lung (5.42); while intermediate level in testis (4.7), ovary (4.56), liver (4.24), fat (4.03) and low in the mammary gland (3.09), intestine (3.06), spleen (2.43) and muscle (0.96). ATP1A2 abundance was highest in muscles (13.11) followed by heart (10.01), brain (9.56), fat (5.95), ovary (5.83), kidney (5.78), intestine (4.77), spleen (4.62), mammary gland (2.97), lung (2.63), liver (1.25) and testis (0.80). In contrast to the ubiquitous expression of ATP1A1 and ATP1A2; ATP1A3 and ATP1A4 showed tissue specific expression. ATP1A3 was most abundant in brain (14.55) with lower expression in ovary (3.7) and heart (3.5). ATP1A4 also showed tissue specific expression pattern in buffaloes; primarily restricted to testis (21.13). The ubiquitous expression of ATP1A1 and ATP1A2 and tissue-specific manner expression of ATP1A3 and ATP1A4 observed in this study pointed towards the critical role that these isoforms of Na+/K+-ATPase gene might be playing in maintaining the ionic concentration in the cells and tissues in which they are expressed.

### *Effect of heat stress on cellular parameters in Sahiwal, HF Cattle and Murrah buffaloes*

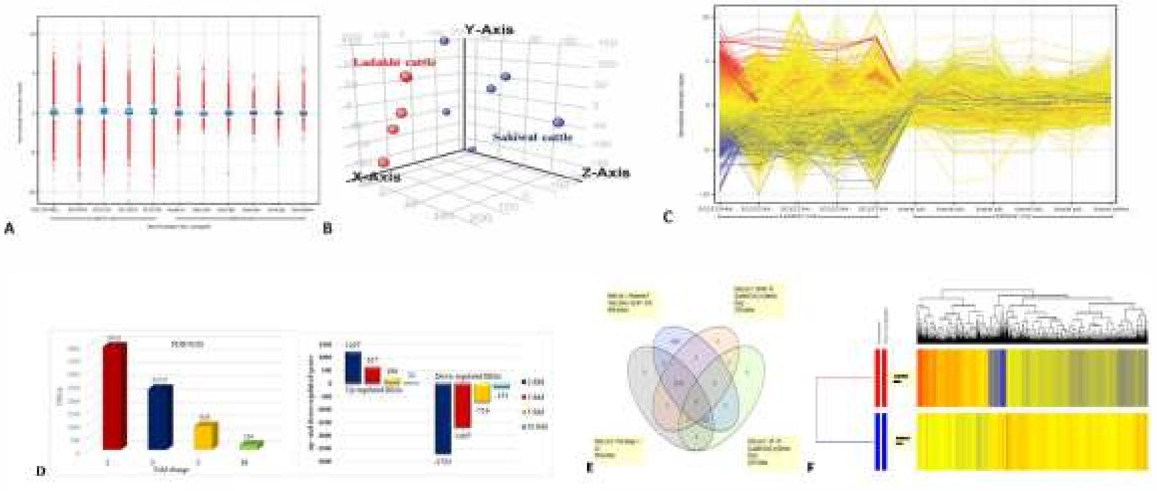
In order to assess the effect of heat stress on PBMCs, cell viability & cytotoxicity and apoptosis parameters were recorded in unstressed (CTR), and heat stressed (TRT) PBMCs recovered at different time points in Sahiwal cows, Holstein Friesian (HF) cows and Murrah buffaloes. The cell viability count for TRT samples was lower than CTR. Reduction in viability was highest for HF cows, followed by Murrah buffaloes and Sahiwal cows. The percent reduction in viability was significantly higher in HF at time points 4hr, 16 hr and 24hr post heat stress. The percent increase in cytotoxicity was significantly ($p<0.05$) higher in HF cows than others. The increase in loss of plasma membrane integrity might have occurred due to either apoptosis or necrosis of PBMCs in response to heat stress as indicated by release of dead-cell proteases. The percent increase in cytotoxicity of PBMCs was significant at 30 min, 2hr and 4hr time points post heat stress in HF in comparison to Sahiwal and Murrah buffaloes. Cytotoxic levels, apoptosis was highest in PBMCs of HF cows and reached to the maximum level at 16hr and 24hr post heat stress showing higher rate of cell death. The study indicated superior cellular tolerance of Sahiwal cows than HF and Murrah buffaloes

### *MicroRNA profiling*

The 12 microRNAs (miR-26a, miR-27b, miR-181a, miR-181b, mir-1246, miR-19a, miR-19b, miR-345-3p, miR-30-5p, miR-146a, miR-146b and miR-199a-3p) selected for the present study were associated with stress and immune response. The expression pattern of each of these microRNAs indicate their responsiveness to heat stress. Immediately post heat stress (30 min) almost all the miRNAs



Relative miRNA level in PBMCs of Murrah buffaloes, Sahiwal and HF cows in response to heat stress. Statistical difference in expression was determined by the ANOVA1 test followed by Tukey's multiple comparison tests. * indicate significant differences between time points ($p<0.05$)



Distinct transcriptome signature between tropically adapted Sahiwal cows and high altitude Ladakhi cows

showed significant ($p<0.05$) induction in their expression, especially in Sahiwal PBMCs.

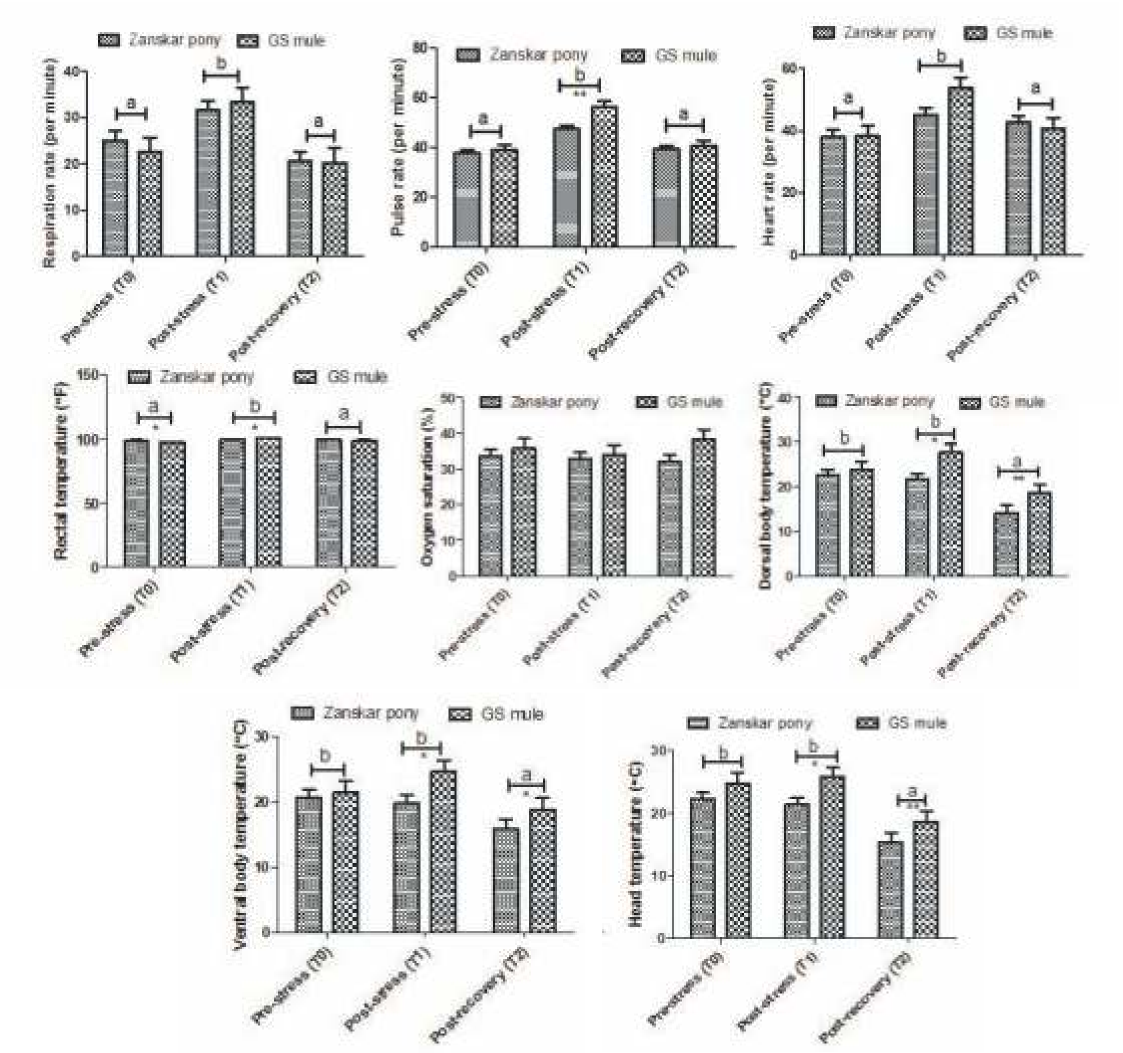
***In-silico analysis of SNPs impact on protein structure of bovine HSP70.1 gene***

In-silico analysis of 15 nsSNPs (12 from dbSNPs and 3 from native Indian cattle breeds) identified four highly deleterious nsSNPs {(rs443101756 (T145P), rs444047738 (G201), rs444047738 (G201R) and rs439440803 (A259D)}. The analysis with PROVEAN, I-Mutant, PANTHER, PhD-SNP and SNPs & GO tools revealed pathogenic nature of these 4 nsSNPs. The results suggest that application of computational pipeline as followed in the present study could provide an alternate approach to select potential target SNPs for assessing their impact on protein structure and function.

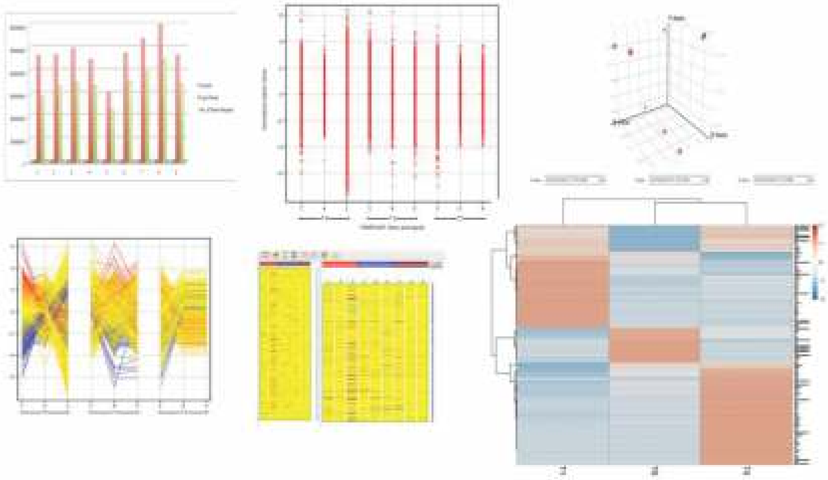
### Identification of Genes and Molecular Pathways associated with endurance trait in Zanskar ponies adapted to high altitude of Ladakh region (DIHAR-DRDO project)

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. Data recording for each animal was carried out on three time points i.e. pre-stress (T0), post- stress (T1) and post recovery period (T2). Physiological parameters viz. respiration rate (RR), pulse rate (PR), heart rate (HR), rectal temperature (RT), dorsal body temperature (DBT), ventral body temperature (VBT) and head temperature (HT) in both the species; Zanskar ponies and GS mules were recorded. The results revealed that, GS ponies had significantly higher PR, SaO2, DBT, VBT and HT than Zanskar ponies. The RR, PR, HR and RT increased significantly during the T1 period and come down to almost normal level during T2 period in both the animals. 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. Hence, the 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.

An effort was also made to generate RNA seq based transciptome data of 9 PBMCs samples 3 each from pre-exercise (T0), post- exercise (T1) and post recovery period (T2) groups. This 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.



Physiological parameters (Means and standard errors) in Zanskar ponies and GS mules with respect to different resting intervals

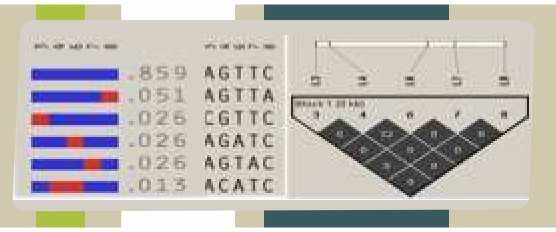


RNA seq based transcriptome analysis of Zanskar PBMCs (Pre and Post stress)

## Delineating Beta Casein Variants in Indian Cows and Potential Health Implications of A1A2 Milk (NASF project)

### *Sequence characterization of beta casein gene in Indian native and exotic cattle to find out allelic variations*

Sequence characterization of beta casein gene was carried out to determine the variants/haplotypes across Indian native (Gir, Tharparkar, Rathi, Red Sindhi, Sahiwal, Amritmahal, Kangyam, Red Kandhari, MalnadGidda, Umblacherry, Ladakhi, Hariana, Ongole, Kankrej, Deoni, Nagori, Ponwar), crossbred (Karan fries) and exotic (Holstein Frisian) cattle. Sequencing of 2,021 bp amplicon; contig of 1,854 bp (-1,653 to +201) was generated for β-CN 5'-flanking region. Search for potential TFBSs from TRANSFAC database revealed a total of 13 different putative sites. Apart from consensus sequences of TATA box, CAAT box and C/EBP, other predicted transcriptional factors included Oct-1, HNF, C/EBP, AP, TBP, NF-Y, YY1, Pit1, POU1F1a, PR, GR and MAF. The distribution of SNP with an average of every 236 bp (7 SNP/1653bp) revealed the promoter region of β-CN to be highly conserved among the casein cluster genes. Amongst the 7 variations (-1582, C>T; -1385, T>C; -1373, G>A; -1340, C>G; -1270, T>G; -1219, T>C and -109, C>G) detected within the -1653bp promoter region across Indian cattle breeds; variations at three sites -1582 (C>T), -1373(G>A) and -1340 (C>G) were found to be located within the potential binding sites for Oct-1, POU1F1a and Oct-1 TFs, respectively, which might possibly be involved in gain or loss of potential TFBSs.



Number of haplotypes and LD across variations in the UTRs and coding region

On comparative analysis with Bos taurus, 4 INDELS were found at positions -1430 (-/T), -893 (-/C), -848 (-/T) and -833 (-/T) and were not located within any potential TFBSs. In all the Indian cattle sequence, a T insertion appeared at –848 with reference to B. taurus sequence (M55158), which differs from the original database sequence. Amongst the known seven variations (C-109G T-264C, C-352T, T-474C, T-520(-), T-851A and A-928G) in the β-CN promoter region, only C-109G variation was observed in Indian native cattle breeds. The location of most of the TFs was conserved across Bos taurus and B. indicus. Throughout the region screened, variation at -1340 (C/G) in the promoter region exhibited maximum frequency (0.67) while, variations at 198 (A/-) and 199 (A/-) showed least frequency (0.08). Among the Indian cattle, Rathi was most variant (1.00) whereas, Kangayam has least (0.31) mutation frequency.

characterization revealed the observed length of 5' and 3' UTR in Indian native cattle breeds to be 56 and 358 bp respectively. A search for putative transcription factor binding sites revealed two potential TFBS (EBPalp,c/EBP) within the 5'UTR while 23 TFBS were observed in 3'UTR. Comparative sequence across Indian native, crossbred and exotic cattle revealed monomorphic nature of 5' UTR, as all the TFBS and other regions were conserved. Conversely, 3'UTR was polymorphic with four variations.

Comparative sequence analysis of coding region of β-CN across indicine, crossbred and exotic cattle revealed a total of 4 variations. All the four variations (C301A, C467G, A493G and G530T)

*Variations in exonic regions of β-CN across different cattle types*

| Position | Change | Allele | | Frequency | |
|---|---|---|---|---|---|
| | | | INC (460) | KF (105) | HF (57) |
| 301 (dN)) | C/A | C | 0.97 | 0.76 | 0.74 |
| 467 (dN) | C/G | C | 0.96 | 0.80 | 0.88 |
| 493 (dN) | A/G | A | 0.99 | 1.00 | 1.00 |
| 530 (dN) | G/T | G | 1.00 | 0.98 | 1.00 |
| 778 | A/G | A | 0.96 | 0.87 | 0.82 |
| 803 | T/A | T | 1.00 | 0.94 | 1.00 |
| 879 | T/A | T | 0.99 | 1.00 | 1.00 |
| 1017 | C/A | C | 0.99 | 1.00 | 1.00 |

*INC: Indian native cattle; KF: Karan Fries; HF: Holstein Friesian; Number in the parenthesis indicate number of animals sequenced.*

detected in the exon VII (coding region) across Indian, exotic and crossbred cattle were nonsynonymous causing a change at codons 101 Pro/His, 156 Pro/Ala, 165 and 151 Glu/Asp, respectively.

***Haplotypes linkage disequilibrium across identified variants of beta casein gene***

In Indian cattle, frequency of all known variations was low, e.g the frequency of A1 (allele A at position 301) and B (G at position 467) was only 3 and 4 percent respectively as compared to 24 & 20% in KF and 26 & 12 in HF animals. A total of 6 haplotypes were observed and amongst these A2 type occurred with maximum frequency of 0.86.

The values obtained after pairwise calculation of linkage disequilibrium (LD) among 8 variations indicated low level of LD. The important variation C301A was not under LD with any of other variation. The analysis based on LD running from one marker to another indicated moderated LD for variation G530T and C1017A with the other variations (G530T, A778G and T803A) but G530T, A778G and T803A were not in LD with each other.

# RESEARCH PROJECTS AND PUBLICATIONS

- Research Projects
- Publications
- Patents and Technologies
- Awards

## Research Projects

### Completed IRC Projects

1. Characterization and evaluation of indigenous cattle of Sikkim, Meghalaya and Nagaland states. - RK Pundir, PK Singh and PS Dangi.
2. Characterization and evaluation of Ladakhi cattle. - Monika Sodhi, M Mukesh, RK Pundir and Vijay K Bharti (Leh).
3. Characterization and evaluation of non-descript cattle population of Konkan region of Maharashtra. - PK Singh, RK Pundir, PS Dangi, Monika Sodhi (w.e.f. Oct. 2016), BG Desai and DJ Bhagat (Dr. BS Konkan Krishi Vidyapeeth, Dapoli)
4. Identification, characterization and evaluation of buffalo population(s) of Chhattisgarh State. - Vikas Vohra, RS Kataria and Mohan Singh (CoVAS-C K V).
5. Phenotypic and genetic characterization of burgur buffalo. - KN Raja, Vikas Vohra, AK Mishra, P Ganapathy
6. Identification, characterization and evaluation of lesser known sheep populations of Karnataka state. - Anand Jain, VS Kulkarni, Reena Arora and Dinesh Kumar Yadav
7. Characterization of Nagaland long hair goat. - NK Verma, RAK Aggarwal and N Savino (SASRD, Nagaland Uni. Medziphema).
8. Phenotypic and genetic characterization of donkeys of Andhra Pradesh. - Rahul Behl, SK Niranjan, RK Vijh, (DK Sadana up to 31.12.14) and M.V. Dharma Rao (Lam, LRS, Gantoor, AP) and P Panduranga Reddy (LRS, Mahanandi, w.e.f.May, 2016).
9. Ex-situ conservation of indigenous ovine genetic biodiversity utilizing cauda epididymal spermatozoa. - RAK Aggarwal and D Malakar (NDRI).
10. Milk metabolomics based characterization of indigenous, exotic and crossbred cows. (8.14) - Rekha Sharma, MS Tantia, RAK Aggarwal, Sonika Ahlawat and Ajit Dua, PBTI (from Dec., 14)

### Completed External Funded Projects

11. Research Program during 12th Plan (2012-2017) Scheme Center for Agricultural Bioinformatics (CaBin) IASRI New Delhi.

(i) Development of genomic resources for indigenous cattle and buffalo breeds. - Ramesh Kumar Vijh (CPI- w.e.f. 5.07.2015). Avnish Kumar (CPI- up to 04.07.2015), Manishi Mukesh, RS Kataria, Monika Sodhi and SK Niranjan.

(ii) Transcriptome analysis and differential expression of genes in two species of Indian Camel: *Camelus dromedarius* and *Camelus bactrianus*. - Ramesh Kumar Vijh, Sonika Ahlawat and A R Rao (IASRI, New Delhi)

### Ongoing IRC Projects

1. Phenotypic and genetic characterization of buffalo populations of Odisha - RS Kataria, SK Niranjan, Vikas Vohra (NBAGR), Sanat Mishra and SK Das (OUAT, Odisha). April, 2014 to March, 2018 (Four Years)
2. Deciphering the molecular basis of male sub-fertility or sterility in bovines - Sonika Ahlawat, Rekha Sharma and Sachinandan De (NDRI) and Reena Arora (from Nov.2014). April, 2014 to March, 2018. (Four Years)
3. Identification of genetic and phenotypic variation associated with tick infestation in Indian cattle - Karan Veer Singh, S Jayakumar, Vikas Vohra and Kamal Jaiswal, (BBAU Lucknow). April, 2016 to March, 2019 (Three years)
4. Haplotypic diversity of Indian cattle breeds based on Y-Chromosome specific markers - Indrajit Ganguly and Sanjeev Singh. April, 2014 to March, 2018 (Four years).
5. Skeltal muscle transcriptome profiling of Bandur (Mandya) sheep - Reena Arora, Sonika Ahlawat and RK Vijh. April, 2016 to March, 2019(Three years)
6. Molecular and physio-biochemical evaluation of heat stress protein genes in Indian sheep breeds - Sanjeev Singh, Indrajit Ganguly, KN Raja, HK Narula (CSWRI) R Venkataramanan (TANVASU) and Anita Ganguly, LUVAS. April, 2014 to March, 2018 (Four Years).
7. Study of the genetic variability present across the goat major histocompatibility complex class II antigens - Jyotsna and NK Verma. April, 2015 to March, 2018 (Three Years).
8. Genome wide diversity analysis of Indian Yak populations - Jayakumar S, SP Dixit and Karan

Veer Singh. April, 2015 to March, 2018 (Three Years).

9. Karyotyping and DNA testing for screening genetic defects in Indian bovines.(Service project) - SK Niranjan and Jayakumar S. April, 2016 to March, 2021(Five years)

10. Conservation of Sahiwal and Hariana cattle at Gaushalas - RK Pundir, Arjava Sharma, PK Singh, AK Mishra and KN Raja. April, 2015 to March, 2020. (Five Years).

11. Phenotypic Characterization of Chitarangi and Dumba sheep in their native tract - AK Mishra, S Singh and Anand Jain. April, 2015 to March 2018 (Three Years).

12. Classification of indigenous sheep breeds of India based on morphometric traits using classical and heuristic methods - Dinesh Kumar Yadav and Avnish Kumar. April, 2016 to March, 2018 (Two Years)

13. Network project on animal genetic resources - Arjava Sharma (w.e.f.01.10.2013) Director NBAGR, Project coordinator and MS Tantia (I/c, Network Project) . 1992- Contd.

14. Characterization of Bidri and Nandidurga goats of Karnataka - MS Tantia, PK Vij, VS Kulkarni (UAS, Dharwar) and VB Shettar& HM Yatish (KVAFSU, Bidar). April, 2016 to March, 2018 (Two years)

### External Funded Projects

1. Whole genome based SNP mining and development of breed signatures for dairy and dual-purpose indigenous cattle - SP Dixit, Jayakumar S, AK Dang (NDRI), MA Iquebal (IARI), Dinesh Kumar (IASRI) and Avtar Singh (NDRI). 9th July, 2014 to 8th July, 2017.

2. Delineating Beta Casein Variants in Indian Cows and Potential Health Implications of A1A2 Milk (NASF) - Monika Sodhi, M Mukesh, RS Kataria and SK Niranjan. July, 2015 to June, 2018

3. Identification of genes and molecular pathways associated with endurance traits in Zanskar ponies adapted to high altitude region (DRDO) - Manishi Mukesh, Monika Sodhi, SK Niranjan and RS Kataria, & Ashok Mohanty (NDRI) and Vijay Bharti (Defence Institute of High Altitude Research, Leh). July, 2015 to November, 2017.

4. CRP on Agro-biodiversity - MS Tantia, PK Vij, RAK Aggarwal and Rekha Sharma . April, 2015 to March, 2017.

5. ICAR-AGRI Consortia Research Plate form project on Genomics - RK Vijh, Reena Arora, Sonika Ahlawat, Jayakumar S and SP Dixit. June, 2015 to March, 2017.

6. Genome data mining to unravel molecular basis of thermo tolerance and adaptation to diverse environment in native cattle and buffaloes (National Fellow) - Manishi Mukesh. May, 2011 to May, 2016 extended up to May, 2021

## Publications

### Research Articles

1. Ahlawat S, De S, Sharma P, Sharma R, Arora R, Kataria RS, Datta TK, Singh RK (2017) Evolutionary dynamics of meiotic recombination hotspots regulator PRDM9 in bovids. Molecular Genetics and Genomics, 292 (1): 117-131.

2. Ahlawat S, Sharma R, Arora R, Jaiswal L, Chopra M, Brahma B, Datta TK, De S (2016). Conserved architecture of RAD51 recombinase in ruminants revealed through molecular cloning and characterization. Indian Journal of Animal Sciences 86 (12) 1420-1426.

3. Ahlawat S, Sharma P, Sharma R, Arora R and De S (2016). Zinc finger domain of the PRDM9 gene on chromosome 1 exhibits high diversity in ruminants but its paralog PRDM7 contains multiple disruptive mutations. PLoS ONE, 11(5): e0156159.

4. Ahlawat S, Sharma P, Sharma R, Arora R, Verma NK, Brahma B, Mishra P and De S (2016). Evidence of positive selection and concerted evolution in the rapidly evolving PRDM9 zinc finger domain in goats and sheep. Animal Genetics, 47:740-751.

5. Ahlawat S, Sharma R, Roy M, Mandakmale S, Prakash V and Tantia MS (2016). Genotyping of novel SNPs in BMPR1B, BMP15 and GDF9 genes for association with prolificacy in seven Indian goat breeds. Animal Biotechnology, 27 (3): 199-207.

6. Arora R, Kulkarni VS, Jain A and Yadav DK (2016). Yalaga Sheep - A microsatellite based genetic profile. Indian Journal of Animal Science, 86 (10): 1155-1158.

7. Dhiman A, Mishra SK, Dubey PK, Goyal S, Sehgal M, Niranjan SK, Sodhi M, Mishra BP, Kataria RS (2017). Identification of genetic variation in NOD-like receptor 2 gene and influence of polymorphism on gene structure and function in buffalo (Bubalus bubalis). Research in Veterinary Science, 115: 43-50.

8. Dixit S, Kumar S, Vyas MK, Singh MK, Pathodiya OP, Sharma A and Jayakumar S (2016). Characterization of sequence variation in caprine growth hormone gene and its association with milk production traits in two Indian goat breeds. Journal of Livestock Biodiversity, 6: 25-32.

9. Dixit S, Vyas MK, Kumar S, Singh MK, Pathodiya OP, Sharma A and Jayakumar S (2016). Association of the polymorphisms detected in β –lactoglobulin (β-LG) gene with milk production traits in Sirohi and Jamunapari breed of Indian goats. Journal of Livestock Biodiversity, 4: 24-29.

10. Dubey PK, Goyal S, Mishra SK, Arora R, Mukesh M, Niranjan SK, Kathiravan P, Kataria RS (2016). Identification of polymorphism in fatty acid binding protein 3 (FABP3) gene and its association with milk fat traits in riverine buffalo (Bubalus bubalis); Trop Anim Health Prod.48(4):849-53.

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12. Gaur U, Tantia MS, Mishra B, Bharani STK, Vijh RK and Chaudhury A (2017). Mitochondrial D-loop analysis for uncovering the population structure and genetic diversity among the indigenous duck (Anasplatyrhynchos) populations of India. http://dx.doi.org/10.1080/24701394.2016.1267158

13. Gaur U, Tantia MS, Mishra B, Bharani STK, Vijh RK and Chaudhury A (2016). Population structuring of land and coastal ducks (Anasplatyrhynchos) using microsatellite markers. Current Science, 110:1977-1983.

14. Gokhale, SB, Aggarwal, RAK, Bhagat, RL, Shirsath, T, Chavda, M (2016). A note on conception rate and sex ratio in A.I. bred Jaffarabadi buffalo. International Journal of Food, Agriculture and Veterinary Sciences 6 (3): 21-25.

15. Goyal S, Aggarwal J, Dubey PK, Mishra BP, Ghalsasi P, Nimbkar C, Joshi BK and Kataria RS (2017). Expression Analysis of Genes Associated with Prolificacy in FecB Carrier and Non-carrier Indian Sheep. Animal Biotechnology, DOI: 10.1080/10495398.2016.1262869.

16. Jyotsna Dhingra Behl, Priyanka Mishra, NK Verma, SK Niranjan, PS Dangi, Rekha Sharma, Rahul Behl (2016). Nucleotide polymorphisms in the bovine lymphotoxin A gene and their distribution among Bos indicus zebu cattle breeds. Gene 579: 82-94.

17. Kapila N, Sharma A, Kishore A, Sodhi M, Tripathi PK, Mohanty AK and Mukesh M (2016). Impact of heat stress on cellular and transcriptional adaptation of mammary epithelial cells in riverine buffalo (Bubalus bubalis). PLOS ONE 11(9): e0157237.

18. Kaur R, Ankita S, Sodhi M, Sharma VL, Kumari P and Mukesh M (2016). Understanding Na+/K+-ATPase alpha isoforms expression characteristics in heat stressed mammary epithelial cells of riverine buffaloes (Bubalus Bubalis), International Journal of Animal Biotechnology, 6: 10-15.

19. Kumar B, Avasthe R K, Islam R, Bhuttia P, Mishra A K and Tantia M S. 2016. Characterization and evaluation of Tibetan sheep: a key source of livelihood in alpine ecosystem of Sikkim Himalaya, Journal of Livestock Biodiversity, 6(2): 51-55.

20. Kumar M, Vohra V,Ratwan P and Chakravarty AK. (2016). SNP identification in thioesterase domain of fatty acid synthase gene in Murrah buffaloes. The Journal of Animal and Plant Science. 26(6): 1828-1832.

21. Kumar S, Ganguly I, Singh S, Sodhi M and Bhakat M (2017). Y-chromosome variation in Indian native cattle breeds and crossbred population. Indian Journal of Animal Research, 51: (1)1-7.

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24. Mishra AK, Raja KN, Vohra V, Singh S and Singh Y (2016). Phenotypic traits and performance of Kajali Sheep: a lesser known ovine genetic resource of Punjab, India. Indian Journal of Animal Sciences, 86(11): 1279-1282
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### Technical / Popular Articles

1. सिक्किम राज्य की सीरी गाय : निरंतर घटती संख्या एक बड़ी चिंता, राकेश कुमार पुंडीर, प्रमोद कुमार सिंह एवं प्रदीप सिंह डांगी। पशुधन प्रकाश, सप्तम अंक : 1–4।
2. चिलिका – उड़ीसा राज्य की एक विशिष्ट भैंस, रविन्द्र सिंह, सुशांत कुमार दास, शैलेन्द्र कुमार मिश्र, एस.के. निरंजन वोहरा एवं रणजीत सिंह कटारिया। पशुधन प्रकाश, सप्तम अंक : 5–7।
3. आंध्र प्रदेश के भूरी किस्म के गधे, राहुल बहल, एस.के. निरंजन, आर.के. विज एवं एम वी धर्मा राव। पशुधन प्रकाश, सप्तम अंक : 14–16।
4. भारत की विशाल एवं बहुमूल्य गो–सम्पदा : एक सिंहावलोकन, प्रमोद कुमार सिंह एवं लवी शर्मा। पशुधन प्रकाश, सप्तम अंक : 17–24।
5. शुष्क एवं अर्ध–शुष्क क्षेत्रों में पाई जाने वाली भेड़ों की अनुकूलनशीलता का अध्ययन, संजीव सिंह, इन्द्रजीत गांगुली, के महेश सिंह, के एन राजा एवं अनिल कुमार मिश्र। पशुधन प्रकाश, सप्तम अंक : 28–33।
6. जैविक पशुधन उत्पादन : भारतीय परिपेक्ष में एक उभरता व्ययवसाय, अविनाश सिंह, हिमानी शर्मा, रेखा शर्मा, सोनिका अहलावत, रीना अरोड़ा एवं मधु सूदन टाँटिया। पशुधन प्रकाश, सप्तम अंक : 73–77।
7. माइटोकॉड्रियल डी.एन.ए – पशुधन प्रजातियों के विकास एवं वशावली रूप रेखा के लिये एक चिन्हक, रीना अरोड़ा, राकेश कुमार, अंजू शर्मा, याशिला गिरधर, सोनिका अहलावत एवं रेखा शर्मा। पशुधन प्रकाश, सप्तम अंक : 80–87।
8. उच्च तुंगता के वातावरण में पशुधन का शारीरिक एवं आनुवांशिक स्तर पर अनुकूलन, प्रीती वर्मा, मोनिका सोढ़ी, अंकिता शर्मा, प्रवेश कुमारी एवं मनीषी मुकेश। पशुधन प्रकाश, सप्तम अंक : 114–118।
9. उ.प्र. और मध्य प्रदेश के संदर्भ में पशुधन और दुग्ध उत्पादन के विकास में प्रमुख समस्याएं और उनका निदान – सत्येन्द्र पाल सिंह, रेशम सिंह एवं संजीव सिंह। पशुधन प्रकाश, सप्तम अंक : 56–61।
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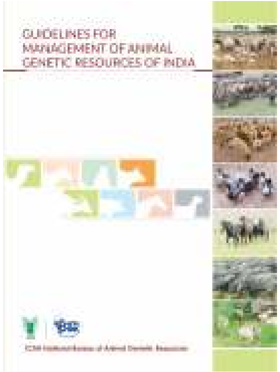
## Books

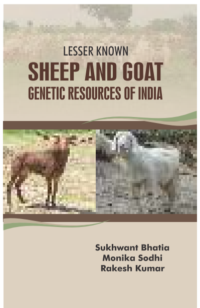
- Guidelines for Management of Animal Genetic Resources of India. P.K. Vij, M.S. Tantia, P.K. Singh, R.A.K. Aggarwal, R.S. Kataria, Monika Sodhi, K.N. Raja, B.K. Joshi, Arjava Sharma and S.K. Niranjan (Ed.). National Bureau of Animal Genetic Resources, Karnal.



- Lesser known sheep and goat resources of India. S Bhatia, M Sodhi and R Kumar (Ed.). Narendra Publication house, Delhi.
- IP Protection and technology transfer in Indian Perspective. Jayakumar S, Karanveer Singh, P.K. Singh and Arjava Sharma (Ed.). ICAR-NBAGR, Karnal.
- Conservation of Indigenous Domestic Animal Diversity. Pundir, R.K., Raja, K. N., Vohra V., and Sharma A (Ed.). ICAR-NBAGR, Karnal.
- Strategies for characterization and conservation of animal and poultry genetic resources. Sonika Ahlawat, KN Raja, Rekha Sharma and Arjava Sharma (Ed.). iCAR, NBAGR, Karnal.

## Monograph/Bulletin/ Compendium

- Kajali - A mutton type sheep by Mishra A K, Raja K.N., Vohra Vikas, Singh S and Singh Y. A monograph # 95/2016, ICAR-NBAGR, Karnal, India Pp:34.
- Intellectual Property Rights and related aspects in the area of agriculture and livestock sector. Arora R, Jayakumar S, Singh K.V. (Ed). ICAR-NBAGR, Karnal.
- Skill upgradation in laboratory methods. Arora R, Singh K.V, Jayakumar S. (Ed.). ICAR-NBAGR, Karnal.
- Dry Dairy Units – Management and Utilization of unproductive cattle of India. Arjava Sharma, Ashutosh Joshi, Shivanand Kanshi, Vineet Bhasin, Bhushan Tyagi and PK Singh (Ed.). Animal Science Division, Indian Council of Agricultural Research, New Delhi.



## Patents and Technologies

- Patent entitled "Genome wide QTLs for age at first calving in buffalos" by Dr. R.K. Vijh and Dr. Upasna Sharma filed to Indian Patent Office, New Delhi on 23rd June 2016. (Patent Application No. 201611021505).
- Patent entitled "Genome wide QTLs for milk fat percentage, milk protein percentage and total milk fat" by Dr. R.K. Vijh and Dr. Upasna Sharma filed to Indian Patent Office, New Delhi on 23rd June 2016. (Patent Application No. 201611021506).
- Patent entitled "Genome wide QTLs for milk yield in buffaloes." by Dr. R.K. Vijh and Dr. Upasna Sharma filed to Indian Patent Office, New Delhi on 23rd June 2016. (Patent Application No. 201611021507).
- Patent entitled "Genome wide QTLs for somatic cell counts in buffaloes." by Dr. R.K. Vijh and Dr. Upasna Sharma filed to Indian Patent Office, New Delhi on 23rd June 2016. (Patent Application No. 201611021508).

## Awards

- Dr. NK Verma, Pr. Scientist, received Dr. PG Nair Award – 2016 for his outstanding

contribution in the area of characterization and Conservation of AnGR.

- Dr. P.K. Singh, Pr. Scientist received Reviewer Excellence Award. 2016. From ARCC, Karnal for contribution in reviewing the research articles for the Indian Journal of Animal Research & Asian Journal of Dairy and Food Research.
- Dr. RK Pundir, Pr. Scientist received Second best paper award for his presentation on 'सिक्किम राज्य की सीरी गाय – निरंतर घटती संख्या, एक बड़ी चिंता during Hindi Saptah, September 19, 2016, NBAGR, Karnal.
- Dr. RK Pundir, Pr. Scientist received fellowship of National Academy of Dairy Sciences.
- Dr. AK Mishra, Pr. Scientist and his editorial committee received Ganesh Shankar Vidyarthi Hindi Krishi patrika puraskar; 2016, 2nd prize for 5th edition of Pashudhan Prakash.
- Dr. A K Mishra, Pr. Scientist received Editorial Excellence Award -2016; for Indian Journal of Animal Research, published by Agricultural Research Communication Centre, Karnal.
- Dr. AK Mishra, Pr. Scientist and his team received 2nd Best Poster presentation award for the poster entitled 'Lesser known sheep population of northern and western India' during National seminar on "Improvement of small ruminant production system for livelihood security" held at ICAR-Central Sheep and Wool research Institute, Avikanagar via Jaipur (Rajasthan), from 9.3.17 to 10.3.17.
- Dr. Monika Sodhi, Pr. Scientist received Best oral presentation award for the paper entitled 'Unravelling New Variants of Beta Casein Gene in Different Cattle Types and Genotype Specific Expression Pattern across Lactation Stages' during International symposium on "Biodynamic Animal Farming for Management of Livestock Diversity under the Changing Global Scenario" & XIV Annual Convention of SOCDAB-2017 held on Feb 8-10 2017 at the College of Veterinary & Animal Sciences (KVASU), Mannuthy, Thrissur, Kerala.
- Dr Manishi Mukesh, Pr. Scientist and National Fellow, received National Fellow Position for IInd term of 5 years
- Dr Manishi Mukesh, National Fellow received an Eminent Scientist Award during an International Seminar on "Agriculture and Food for Inclusive Growth and Development' organized by Smagra Vikas Society at CSIR-NBRI, Lucknow on 14-15 Jan. 2017
- Dr. Manishi Mukesh Pr. Scientist, National Fellow and his team received Best Poster Award for the poster entitled 'Molecular, Cellular and Transcriptomic Evidences of Superior Heat Tolerance Potential of Indian Native Cattle' during Ist International Agro-biodiversity Congress held at New Delhi from 6-9 Nov 2016.
- Dr.Sanjeev Singh, Sr. Scientist received Award in Research Excellence during "International Seminar on Agriculture and Food for Inclusive Growth and Development" organized by Samagra Vikas Welfare Society, held at NBRI, Lucknow during 14-15 January, 2017.
- भारतीय कृषि अनुसन्धान समिति तथा कृषि अनुसन्धान संचार केंद्र, करनाल भारतीय कृषि अनुसंधान पत्रिका में प्रकाशित मौलिक शोध पत्र में उलेखनिये योगदान तथा राष्ट्र एवं राजभाषा हिंदी की सेवा करने के लिए वर्ष 2016 में डॉ. इन्द्रजीत गांगुली को "कृषि विज्ञान गौरव" की मानद उपाधि से अलंकृत किया है.
- Dr. Jayakumr S, Scientist received Life membership of National Academy of Biological Sciences (NABS)
- Dr. Jayakumr S, Scientist received Fellowship from the "Association for the advancement of Biodiversity science"
- Dr. Jayakumr S, Scientist and his team received second best paper award for his paper entitled "Changes occurring in the receptors of blood neutrophils during implantation in Sahiwal cows" published in the "Dairy Production Area" in the Indian Journal of Dairy Science for the calender year 2015.
- NBAGR Exhibition Stall received, Frist prize at International Agro biodiversity Congress (IAC), 2016 held at NASC, New Delhi from 6th to 9th November, 2016.
- NBAGR Exhibition Stall received, Second prize at Krishi Kumbh 2016 (Regional Agriculture Fair) held at Muzzaffarnagar, Uttar Pradesh from 28th to 30th Nov. 2016.

# TRAINING AND CAPACITY BUILDING

- Trainings
- Exhibitions
- Visit of Farmers and Students
- Mera Gaon Mera Gaurav

# TRAINING AND CAPACITY BUILDING

## Trainings

### Trainings Organized

- An Awareness and skill up gradation program on "Intellectual Property Rights and related aspects in the area of agriculture and livestock sector" from July 13-15, 2016 for Scientists at NBAGR, Karnal.
- योग्यता वृद्धि एवं व्यक्तिगत विकास from 1-3 September 2016, for Skilled Supporting Staff.
- Training Program on "Skill upgradation in laboratory methods" from 3 -5 October 2016, for Technical staff at NBAGR, Karnal.
- A Short Course on Advanced tools for Conservation of domestic Livestock Diversity was organized during October 17-26, 2016 sponsored by Education Division, ICAR, New Delhi at NBAGR, Karnal.
- A model training course on "Stratergies for characterization and conservation of animals and poultry genetic resources" at ICAR-NBAGR from Nov. 15-22, 2016. Sponsored by Directorate of agriculture extension, ICAR.
- A brain storming session on animal genetic resources of Nagaland state was organized in collaboration with NLDB on 18th Nov., 2016 at Kohima.
- Training cum awareness Programme on "IP Protection and Technology Transfer in Indian Perspective" was organized during 30-31st January 2017 at ICAR-NBAGR, Karnal.

- XIV National symposium on "Biodynamic Animal Farming for the Management of Livestock Diversity under changing Global Scenario" was organized by Kerala Veterinary and Animal Sciences University, SOCDAB & NBAGR, Karnal at College of Veterinary Sciences and Animal Husbandry, Mannuthy (Thrissur) during 8-10th Feb 2017.
- A brain storming session on phenotype and genetic characterization of animal genetics resources. March 16-17, 2017.

### Trainings Attended

1. Dr. P.K. Vij, Principal Scientist attended Management Development Programme on "Leadership Development (a pre-RMP Programme)' organized during 7-18 June, 2016 at ICAR, NAARM, Hyderabad.
2. Dr. P.K. Vij, Principal Scientist attended Training and Awareness Programme on 'IP Protection and Technology Transfer in Indian perspective' organized during January 30-31 2017 at ICAR-NBAGR, Karnal
3. Dr. M.S. Tantia, Pr. Scientist participated in training programme on Emotional Intelligence at work place centre for Organization development at ICAR-NAARM, Hyderabad from 30 January - 3 February, 2017.
4. Dr Jayakumar and Dr. Sonika Ahlawat, Scientists attended 6 days training programme on "Computational approaches for NGS data analysis and genomic selection" at ICAR-IIWBR, Karnal during October 13-18, 2016.
5. Dr. Reena Arora, Pr. Scientist participated in

competency enhancement programme for effective implementation of training function by HRD Nodal Officers of ICAR at NAARM Hyderabad, from 16-18 February, 2017.

6. Dr. KN Raja, Scientist participated in skill development for sustainable livestock productivity in the Genomic Era at CAS, ICAR-NDRI, Karnal, from 6-26 March, 2017.
7. Dr. P.S. Dangi, ACTO participated in short course on Advanced tools for conservation of Domestic Animal Diversity at ICAR-NBAGR, Karnal from 17-26 October 2016.
8. Sh. Ramesh Kumar and Smt. Parvesh Kumari, Technical Officers participated in Basic training on routine chemical analysis at ICAR-NDRI from 18-23 July, 2016.
9. Sh. Naresh Kumar, Sh. Rakesh Kumar, Sh. Subhash Chander and Smt. Parvesh Kumari, Technical Officers participated in training programme on Handling and care of lab animals at ICAR-NDRI, from 19-24 September 2016.
9. Smt. Parvesh Kumari, Sh. Naresh Kumar, Sh. Ramesh Kumar, Sh. Rakesh Kumar and Sh. Subhash Chander, Technical Officers participated in training programme on Skill upgradation in laboratory methods, at ICAR-NBAGR from 3-5 October 2016.
10. Sh. Jitaram, Assistant and Sh. Satish Kumar, UDC participated in training programme on HRMS and Payroll in MIS/FMS system at ICAR-IASRI from 18-19 April 2016.
11. Sh. Satish Kumar, UDC participated in training programme on Implementation of NIC'S eProcurement solution through CPP Portal, at ICAR- IARI, New Delhi from 16-17 June 2016.
12. Sh. Kishan Lal, Sh. Seva Ram, Sh. Ram Sagar, Sh. Deepak and Sh. Satbir, Skill supporting Staffs participated in training programme on योग्यता वृद्धि एवं व्यक्तिगत विकास at ICAR-NBAGR, from 1-3 September 2016
13. Sh. Harvinder Singh, Sr. Technical Officer attended training cum awareness Programme on "IP Protection and Technology Transfer in Indian Perspective" was organized during 30-31st January 2017.

## Exhibitions

Organized AnGR exhibitions to sensitize farmers about the benefits of indigenous animals during following events :

- Farmers-Scientist interactive workshop and Seed Day at Indian Institute of Wheat and Barley Research, Karnal on 17th October, 2016.
- 9thNational Livestock championship and livestock Expo at Mukatsar, Punjab, from 2nd to 4th December, 2016.
- Pashu Mela-2016 held at Guru AngadDevVeterinary and Animal Science University, Ludhiana (Punjab) from 22nd to 23rd September, 2016.
- First International Agro biodiversity Congress (IAC), 2016 held at NASC, New Delhi from 6th to 9th November, 2016.

- KrishiKumbh 2016 (Regional Agriculture Fair) held at Muzzaffarnagar, Uttar Pradesh from 28th to 30th Nov. 2016.
- Buffalo Mela and exhibition on 4th Feb., 2017 on occasion of 33rd foundation day of Central Institute of Research on Buffalo, Hisar.
- 2ndAgri Leadership Summit 2017 held at SurajkundMela ground, Faridabad from 18th to 20th March, 2017.

## Visit of Farmers and Students

Farmers & students from different places & colleges visited NBAGR during the reported period and were exposed to the various activities of the bureau. Lectures were delivered by the bureau staff briefing about the importance of registered breeds and non descript populations of different species.

## Mera Gaon Mera Gaurav

ICAR-NBAGR in collaboration with ICAR-IARI regional center carried out various extension activities in the adopted villages of district Karnal under Mera Gaon Mera Gaurav programme. Livestock keepers and farmers were made aware of good agriculture and animal husbandry practices. All queries of farmers related with agriculture and livestock keeping were addressed.

*Summary of activities organized under MGMG by Institute/SAU*

| S. No. | Name of activity | No. of activities conducted | No. of farmers participated/ benefitted |
|---|---|---|---|
| 1. | Visit to village by teams | 26 | 1684 |
| 2. | Interface meeting/ Goshthies | 24 | 958 |
| 3. | Mobile based advisories | 14 | 1485 |
| 4. | Literature support provided | 15 | 324 |
| 6. | Awareness created | 17 | 2062 |
| 7. | Linkages developed with other agencies | 06 | 1293 |

n Mohapatra
ARE & DG, ICAR

# OTHER ACTIVITIES

- Library
- Important Meetings
- Celebrations
- Sports
- Staff Welfare Activities
- Vigilance Week
- Distinguished Visitors
- Rashtriya Swachhta Abhiyan

## Library

The NBAGR library has been playing an important role in serving the scientists and technical staff of the bureau. Library Advisory Committee (LAC) is guiding force in the management of the library issues pertaining to purchase of scientific books/journals etc. The Bureau LAC was reconstituted on 19.5.2016. Books and journals worth Rs. 9, 96,842/- were procured in the library during the period. Thirty Indian/foreign journals have been subscribed for the benefit of scientific readers. Presently NBAGR Library is enriched with the following literature :

| | |
|---|---|
| Total collection | 4174 |
| No. of books added | 20 |
| No. of Indian/Foreign Journals subscribed | 30 |
| No. of News papers subscribed | 7 |

## Important meetings

### IRC Meeting

Annual Institute Research Committee meeting was held on April 27-28, 2016 in which the final reports of completed research projects presented by the scientists were discussed. A new service project and 4 new research projects were also discussed and approved.

Mid-Term Institute Research Committee (IRC) meeting was held on October 6-7, 2016. Progress of twenty four institute projects and seven externally funded projects was reviewed and approved.

### RAC Meeting

Meeting of Research Advisory Committee (RAC) was held on 3rd April, 2017 at 11:00 AM under the Chairmanship of Dr. S.L. Goswami, Vice Chancellor, Banda University of Agri. & Tech., Banda (UP). Dr. Arjava sharma presented an overview of the institute. The heads of division also presented the activities of their respective division.

### IBSC Meeting

Meeting of Institutional Biosafety Committee (IBSE) constituted for monitoring the research projects engaged in cloning, recombinant DNA, transgenic and applying biosafety guidelines was held on 27 Dec, 2016. The research projects falling under the purview of IBSC were reviewed and necessary permissions granted.

### ITMC Meeting

Institute Technology Management Committee Meeting (ITMC) Meeting was held on 4th April 2016 to discuss four applications for filing of patent at Indian Patent Office, New Delhi. ITMC approved all the four application for patent filing with certain modifications.

## Celebrations

### Independence Day

On India's 70th Independence Day, Dr. Arjava Sharma unfurled the tricolor and addressed the members of the Bureau family. In his address, Director appreciated the scientific progress made by the Bureau. He also highlighted the responsibilities of each member towards the nation as a whole and farming community in particular. A cultural program and quiz competition was also organized wherein the staff and their wards participated actively.

### Foundation day

ICAR-NBAGR celebrated its 33rd Foundation Day on September 21, 2016. Dr. Gaya Prasad, Vice

Chancellor, Sardar Vallabh Bhai Patel University of Animal science and Technology, Meerut was the chief guest on this occasion. Dr. GP Singh, Director, ICAR-IIWBR, Karnal and Shri Gopal Swami Ji were the guests of honour. Best worker awards were given to the staff in different categories. Sh. Rakesh Kumar, Technical Officer, Sh. Satish Kumar, UDC and Sh. Ram Sagar, SSS were honored with best worker awards. Dr. PG Nair Award -2016 was conferred on Dr. NK Verma, Principal Scientist, for his outstanding contribution during last three years. The authors of First, Second and Third best popular article published in the Pashudhan vol. 6 of the year 2015 were awarded for their contribution. The winners of various competitions held during the 'Hindi Chetna Pakhwara' were also given prizes on this occasion.

### Republic Day

ICAR-NBAGR joined the entire nation in celebrating India's 68th Republic Day. Dr. Arjava Sharma hoisted the national flag Staff children presented a cultural programme which was followed by a quiz competition.

### Agricultural Education Day

On December 3, 2016, 70 students from OPS Vidya Mandir and Dyal Singh Public School, Karnal were invited to participate in the Agricultural education day celebration. Talks on 'Livestock biodiversity and its impact on national economy' and 'Career opportunities in biotechnology' were organized on this occasion.

### National Science Day

On February, 28, 2017, National Science Day was celebrated. Students from Adarsh Public School, Karnal were invited to participate in the celebration. They were exposed to various activities of the bureau. Talks on opportunities in livestock sector were deliberated upon by the scientists of bureau.

### National Productivity Week

The Productivity week was celebrated from 12 – 18, 2017. The theme of the week was "From Waste to Profits through Reduce, Recycle and Reuse." The lectures on "Emotional Intelegence" and "Productivity Enhancement" were held on this occassion.

## Sports

Annual Sports Meet of ICAR-NBAGR was organized from January 21-25, 2017. Various sports events like Volley Ball (Smashing), Basket Ball, Table tennis, Carom Board, Chess, Long Jump, 100 & 200 meter race, Short-Put, Javelin Throw, Discus Throw and Cycle Race (fast and slow) were organized on their occasion. Thirty five staff members including 30 males, 5 females and 18 staff children participated in this meet. Dr. Arjava Sharma, Director of the Bureau honored the winners with medals and certificates on January 26, 2017.

## Staff Welfare Activities

Following major activities were undertaken by NBAGR Staff Welfare Fund Scheme during 2016-17.

- From the SWFS funds, ex-gratia payment of Rs. 15000/- was made to the grieved family of Late Sh. Sopal, UDC who expired on 13-04-2016 .
- A free eye and diabetes check-up camp sponsored by Shri Hari Hospital, Karnal, was organized by SWFS for the staff and their family members on 05-07-2016.
- On behalf of SWFC, New Year Day was celebrated at NBAGR on 02-01-2017.
- Retirement function was organized for Sh. Sewa Ram, Skilled Supporting Staff of NBAGR on 31-03-2017.

## Vigilance Week

During Vigilance week observance from 31 October to 5 November, 2016, the staff of NBAGR was administered the Vigilance Awareness Pledge on 31st October, 2016 by the Director, NBAGR. A program was held for the staff of institute on 29-10-2015, on the topic "Satyanishtha badhane evam bhrashtachaar unmoolan mein janta ki bhagidaari"/सत्यनिष्ठा बढ़ाने एवम् भ्रष्टाचार उन्मूलन में जनता की भागीदारी" in which participants from scientific and administrative staff placed their views. Two lectures were organized during week for the staff of NBAGR. One lecture was delivered by Mr. D.D. Verma, Comptroller, ICAR-NDRI on General Finance Rules and procurement procedures. Another lecture delivered was by Mr. K.P.S. Gautam, Chief Administrative Officer, ICAR-NDRI on Central Civil Services (conduct) rules.

## Distinguished Visitors

- Dr.H.Rahman, Deputy Director General (AS), ICAR, New Delhi visited on 06.02.2016.
- A team from Doordarshan Channel visited on 31.05.2016.
- The Secretary (ADF), Min. of Agri. & Farmers Welfare, Govt. of India, visited on 25.06.2016.

- Dr. T.Mohapatra, Secretary, DARE & DG, ICAR, New Delhi visited on 03.11.2016.
- Dr.James M. Reecy from ISU visited on 04-05.11.2016.
- Sh Chhabilendra Roul, Additional Secretary (DARE) & Secretary (ICAR), New Delhi visited on 30.11.2016.
- A team from Livestock and Crop Registry India Ltd. (LCRI), Pune visited on 14.02.2017.

### Other Visitors

- The newly recruited scientists of BAIF visited on 22-23.07.2016.
- The participants of Training Programme on “Breeding Soundness Examination (BSE) of Bull and Andrological Examination for VO and QCO of Semen Station” of NDRI visited on 19.08.2016.
- The newly recruited faculty members of Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar visited on 19.01.2017.
- The Trainees of the Training Programme from Telengana on “Recent Advances in Animal

Husbandry and Dairying” at NDRI visited on 15.02.2017.

- The Trainees of the Training Programme on “Skill development for sustainable livestock productivity in the genomic era” at NDRI visited on 08.03.2017.

### Rashtriya Swachhta Abhiyan

During various cleanliness drives the office and residential campus was maintained neat and clean under Rashtriya Swachhta Abhiyan. A cycle rally was also organized to spread the message of cleanliness.

स्वच्छता पखवाडा: संस्थान में १६ से ३१ अक्तूबर २०१६ के दौरान स्वच्छता पखवाडा मनाया गया जिसके अन्तर्गत “स्वच्छ भारत की परिकल्पना” विषय पर ब्यूरो परिवार के सदस्यों ने अपने विचार रखे।

# PERSONNEL

- Personalia
- Promotions
- Superannuation

## Personalia

### Scientific

| Sl. No. | Name | Designation |
|---|---|---|
| 1. | Dr. Arjava Sharma | Director |
| 2. | Dr. R.K. Vijh | Principal Scientist |
| 3. | Dr. Anand Jain | Principal Scientist |
| 4. | Dr. M.S. Tantia | Principal Scientist |
| 5. | Dr. P.K. Vij | Principal Scientist |
| 6. | Dr. N. K. Verma | Principal Scientist |
| 7. | Dr. R.A.K. Aggarwal | Principal Scientist |
| 8. | Dr. P.K. Singh | Principal Scientist |
| 9. | Dr. R.K. Pundir | Principal Scientist |
| 10. | Dr. R.S. Kataria | Principal Scientist |
| 11. | Dr. Anil Kumar Mishra | Principal Scientist |
| 12. | Dr. Monika Sodhi | Principal Scientist |
| 13. | Dr. Satpal Dixit | Principal Scientist |
| 14. | Dr. Jyostna Behl | Principal Scientist |
| 15. | Dr. Dinesh Kumar Yadav | Principal Scientist |
| 16. | Dr. Reena Arora | Principal Scientist |
| 17. | Dr. Manishi Mukesh | Principal Scientist |
| 18. | Dr. Avnish Kumar | Principal Scientist |
| 19. | Dr. Rahul Behl | Principal Scientist |
| 20. | Dr. Rekha Sharma | Principal Scientist |
| 21. | Dr. Vikas Vohra | Senior Scientist |
| 22. | Dr. Saket Kumar Niranjan | Senior Scientist |
| 23. | Dr. Indrajit Ganguly | Senior Scientist |
| 24. | Dr. Sanjeev Singh | Senior Scientist |
| 25. | Dr. P. Kathiravan | Senior Scientist |
| 26. | Dr. Karan Veer Singh | Senior Scientist |
| 27. | Dr. K.N. Raja | Scientist (S.S.) |
| 28. | Dr. Jayakumar S. | Scientist ( S.S) |
| 29. | Dr. Sonika Ahlawat | Scientist ( S.S) |

# PERSONNEL

## Technical Staff

| Sl. No. | Name | Designation |
|---|---|---|
| 1. | Dr. P. S. Dangi | Chief Technical Officer |
| 2. | Sh. S. K. Jain | Asstt. Chief Technical Officer |
| 3. | Dr. P.S. Panwar | Senior Technical Officer |
| 4. | Sh. Sanjeev Mathur | Senior Technical Officer |
| 5. | Sh. Harvinder Singh | Senior Technical Officer |
| 6. | Sh. Sat Pal | Technical Officer |
| 7. | Sh. Jamer Singh | Technical Officer |
| 8. | Smt. Pravesh Kumari | Technical Officer |
| 9. | Sh. Naresh Kumar | Technical Officer |
| 10. | Sh. Ramesh Kumar | Technical Officer |
| 11. | Sh. Rakesh Kumar | Technical Officer |
| 12. | Sh. Subhash Chander | Technical Officer |
| 13. | Sh. Ashok Kumar | Senior Technical Assistant |
| 14. | Sh. Om Prakash | Senior Technical Assistant |
| 15. | Sh. Ramesh Chand | Senior Technical Assistant |
| 16. | Sh. Balvinder Singh | Sr. Technician (Driver) |

## Administrative Staff

| Sl. No. | Name | Designation |
|---|---|---|
| 1. | Sh. Sunil Kumar | F&AO |
| 2. | Sh. Karambir | PS to Director |
| 3. | Sh. Balkar Singh | Asstt. Admn. Officer |
| 4. | Sh. Pawan Kr. Gupta | Asstt. Fin. & Account Officer |
| 5. | Sh. Ramesh Behl | Assistant |
| 6. | Smt. Anita Chanda | Personal Assistant |
| 7. | Smt. Amita Kumari | Personal Assistant |
| 8. | Smt. Indu Bala, Steno | Steno Gr.III |
| 9. | Smt. Shashi Bala | Assistant |
| 10. | Sh. Jita Ram | Assistant |
| 11. | Sh. Yoginder | Assistant |
| 12. | Sh. Satish Kumar | Upper Division Clerk |
| 13. | Sh. Shiv Chander | Lower Division Clerk |
| 14. | Smt. Neerja Kaul | Lower Division Clerk |
| 15. | Sh. Naresh Kumar | Lower Division Clerk |
| 16. | Sh. Babu Ram | Lower Division Clerk |

### Skilled Supporting

| Sl. No. | Name | Designation |
|---|---|---|
| 1. | Sh. Krishan Lal | Skilled Supporting Staff |
| 2. | Sh. Sewa Ram | Skilled Supporting Staff |
| 3. | Sh. Ram Sagar | Skilled Supporting Staff |
| 4. | Sh. Deepak | Skilled Supporting Staff |
| 5. | Sh. Satbir | Skilled Supporting Staff |

## Promotions

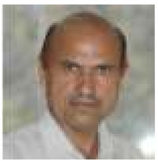
1. Dr. JayaKumar S, Scientist, has been promoted to the next post of Scientist Senior Scale w.e.f 07.01.2013.
2. Dr. Sonika Ahlawat , Scientist, has been promoted to the next post of Scientist Senior Scale w.e.f 15.12.2014.
3. Dr. P.S. Dangi, has been promoted to the next higher post of Chief Technical Officer w.e.f. 01.07.2015.

## Superannuation

1. Sh. Sewa Ram, skilled supporting staff superannuated on 31.03.2017.

## Obituary

Bureau family is grieved by the untimely demise of Sh. Sopal who left for heavenly abode on 13.04.2016



*Sh Sopal (1961-2016)*


तिमाही हिंदी व्याख्यान/कार्यशाला
भाकृअनुप - राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो,
करनाल हरियाणा

# हिन्दी खण्ड

- निदेशक की कलम से
- कार्यकारी सारांश
- राजभाषा संबंधी गतिविधियाँ

# निदेशक की कलम से .....

मैं, भा.कृ.अनु.प.–राष्ट्रीय पशु आनुंवाशिकी संसाधन ब्यूरो के वार्षिक प्रतिवेदन 2016–17 दवारा संस्थान की प्रमुख गतिविधियों और उप्लब्धियों को प्रस्तुत करते हुए अत्यधिक हर्ष का अनुभव कर रहा हूँ। ब्यूरो की स्थापना के बाद से ही संस्थान लगातार देश के घरेलू पशु आनुवांशिक की पहचान, लक्षण वर्णन, मूल्यांकन और संरक्षण की अनिवार्य गतिविधियों के तहत उद्देश्यों को पूरा करने के लिए ईमानदारी से प्रयास कर रहा है। मुझे यह बताने मे प्रसन्नता है कि पिछले एक वर्ष के दौरान ब्यूरो के वैज्ञानिकों ने लद्धाख क्षेत्र के नए गोवंश, जो वहां की कठिन जलवायु के अनूकुल है तथा व्यापक प्रबंधन प्रणाली के तहत ए–2 दूध भी पैदा करती है, का वर्णन किया। इसके अलावा पूर्वोत्तर और कोंकण क्षेत्र की गोवंश, तामिल नाडू की बरगूर और उड़ीसा राज्य की भैंसों का भी लक्षणीकरण किया, और साथ ही नई नस्ल के रूप में पंजीरण के लिए उपयुक्त पाया गया। लघु रोमन्थियों और अन्य प्रजाति के पशुधनों में हमारे वैज्ञानिको ने कर्नाटक के मौली और येलगा भेड़, राजस्थान और पंजाब की चितरंगी और दुम्बा भेड़ , नागालैडं के लम्बे बाल वाली बकरी और आंध्र प्रदेश के स्थानीय गधों का भी अध्ययन किया। हरियाणा और साहिवाल गायो के संरक्षण के लिए गोशालाओं के माध्यम से कृत्रिम गर्भाधान दवारा 17 बछड़ो का उत्पादन किया गया। जीन बैंक की जर्मप्लाज्म रिपोजिटरी को अधिक वीर्य भ्रूण, एपिडिडिमल शुक्राणु, डीएनए के अधिकाधिक नमूने तथा खुराकें और दैहिक कोशिकाओ को एक्स सीटू गतिविधि के रूप मे संरक्षित करके, मजबूत किया गया। बैक्ट्रियन ऊँट की फाइब्रोब्लास्ट सेल लाइन के विकास और सरंक्षण के लिए नई पहल की गई। वाई–क्रोमोसोमल माइक्रोसैटेलाईट आधारित विविधता भी 18 पशु नस्लों में पूरी की गई। हमने पाया कि चराई वाली गायों में एम यू एफ और आवश्यक अमीनो एसिड सामग्री स्टाल पर खिलाये जानवरों की तुलना में अधिक है। बांडूर भेड़ के मांस मे उच्च कोमलता के संकेत मिले। नोडल एजेंसी होने के नाते ,ब्यूरो ने नौ नई नस्लों को पंजीकृत कर कुल पंजीकृत नस्लों की संख्या को 160 तक पहुंचाया। ब्यूरो वैज्ञानिकों के प्रयासों के कारण ही बाहय वित्त पोषित परियोजनाओं के अतंर्गत भी आश्चर्यजनक परिणाम मिले। नेटवर्क प्रोजेक्ट के तहत पशुधन और मुर्गी की दस विभिन्न नस्ल एवं आबादी आनुवाशिंक रूप से वर्णित की गया। ड्रोमेडेयरियन और बैक्ट्रियन ऊँट के दस विभिन्न उत्तकों का प्रतिनिधित्व करने वाला डी–नोवो ट्रांसक्रिप्टोन असेंबली का निर्माण किया गया। साथ ही इन दोनों प्रजातियों के एसएनपी तथा अन्य पशु प्रजातियों के उत्पादन रोग प्रतिरोध के अनुकूल लक्षणों से संबधित उम्मीदवार जीनों के लिए डेटाबेस तैयार किया गया। भैस में जिनोटाइपिंग के माध्यम से दूध, वसा और दूध प्रोटीन प्रतिशत के लिए क्यूटीएल की पहचान की गई। 15 भैंस आबादी वाले एसएनपी डेटा का उपयोग करके एक मध्यम घनत्व एसएनपी चिप

भी विकसित की जा रही है। नेशनल फेलो स्कीम के अंतर्गत , ट्रासक्रिप्टोम डेटा उत्पन्न किया गया , जिससे गायों और भैंसो मे उष्म सहिष्णुता के लिए जिम्मेदार कई जीन और उनकी क्रियाशैली की पहचान करने में मदद मिली । डीआरडीओ द्वारा वित्त पोषित परियोजना के तहत जनसकारी घोडों की हाइपोकसिक सहनशीलता के लिए जिम्मेदार जीन की पहचान पर काम किया गया। ए 1/ए 2 बीटा केसिन संस्करणों के स्वास्थय के प्रभाव पर आधारित परियोजना में बीटा केसिन जीन के अनुक्रम लक्षण वर्णन दवारा देसी गोवंश में कई न्यूक्लियोटाइड विविधताओं की पहचान की गई। संस्थान में वर्तमान में पांच वित्त पोषित और एक राष्ट्रीय सहयोगी सहित 20 अनुसंधान परियोजनाएं कार्यरत्त हैं।

पिछले एक साल के दौरान हमारे वैज्ञानिको ने 48 अनुसंधान और कई तकनीकी व लोकप्रिय लेख प्रकाशित किए मानव संसाधन विकास कार्यक्रम के तहत क्षमता निर्माण पर छह प्रशिक्षण कार्यक्रम आयोजित किए गए। विभिन्न शोध परियोजनाओ के तहत प्रगति की समीक्षा के लिए, आईआरसी और आरएसी की बैठकों को समय पर आयोजित किया गया। पशु संसाधन की उपयोगिता पर पशुपालकों के बीच प्रदर्शनी, वैज्ञानिक सत्र और व्याख्यान आयोजित करके जागरूकता उत्पन्न की गई। वैज्ञानिकों दवारा प्राप्त व्यक्तिगत पुरस्कारों के अलावा, 'पशुधन प्रकाश' पत्रिका के प्रकाशन के लिए संस्थान ने आईसीएआर के गणेश शंकर विद्यार्थी पत्रिका पुरस्कार (द्वितीय) प्राप्त किया । गत वर्ष ब्यूरो ने कई प्रतिष्ठित व्यक्तियों को आकर्षित किया जिसमें डॉ त्रिलोचन महापात्रा , सचिव (डेयर) किसान कल्याण मत्रांलय , भारत सरकार व महा निदेशक , भारतीय कृषि अनुसन्धान परिषद , डॉ एच रहमान भूतपूर्व उप महा निदेशक (मत्स्स एवं पशु विज्ञान), डॉ जे.के. जेना, वर्तमान उप महा निदेशक ( पशु विज्ञान) तथा आयोवा स्टेट यूनिवर्सिटी अमरीका के डा. जेम्स एम रीसी शामिल थे।

मैं डॉ त्रिलोचन महापात्रा,सचिव (डेयर) किसान कल्याण मंत्रालय, भारत सरकार व महा निदेशक, भारतीय कृषि अनुसधांन परिषद डॉ. एच रहमान, भूतपूर्व उप महा निदेशक (पशु विज्ञान) , डॉ जे.के. जेना,वर्तमान उप महा निदेशक (मत्स्य एवं पशु विज्ञान) और डॉ. आर एस गाँधी,सहायक महा निदेशक (एपी और बी ) और डॉ. विनीत भसीन, प्रधान वैज्ञानिक को उनके लगातार समर्थन और मार्गदर्शन के लिए हृद्य से धन्यवाद करता हूँ। संस्थान की प्रगति में योगदान के लिए सभी वैज्ञानिक,तकनीकी, प्रशासनिक अधिकारी और अन्य कर्मचारियों का शुक्रिया अदा करता हूँ। मैं, इस दस्तावेज के आकार में ब्यूरो की उपलब्धियों को संकलित करने के लिए तथा समय पर इस वर्षिक प्रतिवेदन 2016-17 के प्रकाशन के लिए संपादकीय टीम की सराहना करते हुए बधाई देता हूँ।

**(अर्जव शर्मा)**
**निदेशक**

# कार्यकारी सारांश

राष्ट्रीय पशु आनुंवशिक संसाधन ब्यूरो करनाल भारत की एक अग्रणी संस्था है जो देश के पशुधन और कुक्कुट संसाधनो की पहचान, मूल्यांकन, लक्षण वर्णन, संरक्षण और उनके सतत् उपयोग एवं पशु आनुवंशिक संसाधन प्रबंधन, नीतिगत मुद्दों और उनके क्षमता निर्माण पर कार्य करती है। सन 2013 में संस्थान के अधिदेश को पूरा करने के लिए पशु आनुवंशिक संसाधन, पशु आनुवांशिकी एवं पशु जैव प्रौद्योगिकी विभाग बनाए गए। इनके अलावा पशुधन सूचना और नेटर्वक प्रोजेक्ट इकाई भी काम कर रहीं हैं।

वित्तीयवर्ष 2016–17, के दौरान संस्थान की गैर–योजना के अंतर्गत संयुक्त रूप से आबंटित 1014.00 लाख रू. के मुकाबले कुल 990.49 लाख रूपए खर्च हुए। इस अवधि के दौरान नेटर्वक परयोजना के अंतर्गत कुल प्राप्त 101.00 लाख रूपये में से 100.93 लाख रूपए व्यय हुए। वर्ष के दौरान 24.81 लाख रूपये राजस्व प्राप्ति का लक्ष्य के मुकाबले रूपये 34.70 लाख प्राप्त हुए.

राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो नस्ल पंजीकरण हेतु देश की एक अग्रणी संस्था है। वर्ष के दौरान नस्ल पंजीकरण समिति द्वारा पशुधन और कुक्कुट की नौ नई नस्लों के पंजीकरण को मंजूरी दी गई। इसमें गाय की बद्री, बकरी की टेरेसा और कोड़ी अडू, भेड़ की चेवादु और केन्द्रपाड़ा, सुअर की तेनी वो, निकोबारी व डूम और चिकन की कौनायन शामिल है। इनको शामिल करने के पश्चात् अब देश में कुलपंजीकृत 160 स्वेदेशी नस्लें हैं, जिसमें गाय की 40, भैंस की 13, बकरी की 26, भेड़ की 42, घोड़े व् टट्टू की 6, ऊंट की 9, सुअर की 6, गधे की 1 और मुर्गियों की 17 नस्लें हैं।

जम्मू कश्मीर के लद्दाख की देशी गाय का लक्षणीकरण सर्वेक्षण के माध्यम से किया गया। लद्दाखी गाय छोटे आकार की शांत गाय है, इसका रंग काला भुरा, बाल लम्बे गुच्छे दार व चमकदार होते हैं। कूबड़ पूर्ण विकसित नही होता, सींग मध्यम और आगे से घुमावदार होते हैं। यह प्रतिदिन 2 से 5 लीटर तक दूध देती है जिसमें वसा की मात्रा 5.24 प्रतिशत होती है। लद्दाखी गाय में ए 2 एलील की बारंबारता 0.90 पाई गई है।

भारत के उत्तर–पूर्वी राज्यों की देशी नस्ल की गायों के गुणों का अध्ययन किया गया। इन राज्यों के गोवंशी पशु दूध, मांस, खाद व खेती के लिए पाले जाते हैं। इनका शारीरिक आकार छोटा व मध्यम होता हैं। सिक्किम की सीरी गायों को छोड़कर बाकी सभी भूरे रंग की होती हैं। ये प्रतिदिन 1 से 5 किलो दूध देती हैं। नागालैंड और सिक्किम की देशी गाय का शरीर आकार मेघालय की तुलना में बड़ा होता है।

महाराष्ट्र के कोंकण क्षेत्र के गोवंशी पशुओं का लक्षणीकरण सर्वेक्षण के माध्यम से किया गया। कोंकण क्षेत्र की गाय शरीर में छोटे आकार का होता है और कूबड़ छोटे से मध्यम आकार का होता है। जबकि बैल मध्यम आकार के होंते है। ये औसतन 2.23 किग्रा प्रतिदिन दूध देती है परन्तु कुछ उत्तम गायें 5 से 6 लीटर प्रतिदिन दूध देती हैं। कोंकण पशुओं की संख्या अपने प्रजनन क्षेत्र में पर्याप्त है एवं यह एक नस्ल के रूप में पंजीकृत होने योग्य है।

तमिलनाडु की बरगुर भैंस का सर्वेक्षण किया गया। इनको मुख्य रूप से दूध, मांस और खाद के लिए पाला जाता है। ये भैंस औसतन 1.5 से 2 लीटर दूध प्रतिदिन देती है। इनकी ऊँचाई कम (102.10) से.मी. होती है जिसके कारण ये पहाड़ी इलाको में आसानी से चराई कर सकती हैं। इन भैंसो को शून्य निवेश प्रणाली के तहत पाला जाता हैं।

कर्नाटक राज्य की मोली और यलगा भेड़ का सर्वेक्षण किया गया। मौली भेड़ गहरे लम्बे शरीर व लम्बी टांग वाली होती है, शरीर का रंग सफेद या भूरे रंग के धब्बे या बिना धब्बे का होता है। आंखो के आस–पास भूरे रंग का घेरा पाया जाता है। नाक रोमन होती है। यलगा भेड़ मध्यम आकार की होती है इनका रंग सफेद, बाल छोटे, चेहरा सफेद रंग का होता है। जिसके ऊपर विभिन्न आकार के काले या भूरे रंग के धब्बे पाए जाते हैं।

चितरंगी भेड़ का सर्वेक्षण पंजाब के फजिलका, मुक्तसर और राजस्थान के श्री गंगा नगर क्षेत्र में किया गया। इसका रंग सफेद होता है एवं इनके आंखो, थूथन और कान पर लाल/भुरे रंग के धब्बे होते हैं। भेड़ो के कान लम्बे होते हैं। जिनके अंतिम सिरे पर विभिन्न आकार एवं प्रकार के कटाव पाए जाते हैं। व्यस्क नर का वजन 40 से 95 किलोग्राम और मादा का वजन 26 से 74 किलोग्राम होता है। इससे उत्तम प्रकार की गलीचा किस्म की ऊन प्राप्त होती है जो कालीन बनाने के लिए प्रयोग की जाती है। इसके ऊन के रेशे की औसत लम्बाई 5.90 सेमी होती है।

शुष्क क्षेत्रों में पाली जाने वाली मोटी पूंछ वाली दुम्बा भेड़ के लक्षणीकरण के लिए राजस्थान में सर्वेक्षण किया गया। इनके कान बड़े आकार के होते है, इनकी पूँछ में वसा का जमाव या

पूँछ का मोटा होना ही इनकी मुख्य विशेषता है। इनको मुख्यत: ईद पर कुर्बानी के लिए पाला जाता है एवं इनका धार्मिक महत्व भी है व व्यस्क नर का औसतन वजन 90.92 किग्रा. और मादा का औसतन वजन 66.33 किग्रा. किग्रा होता है।

भेड़ के आठ समूहों (कोल्हापुरी, लोनांद, मारवाड़ी, मुजफ्फरनगरी, मडग्याल, संगमनेरी और सोलापुरी) को सात शरीरिक लक्षणों के आधार पर क्लासिकल डिस्क्रिमिनैट फक्शन एनालिसिस और कृत्रिम न्यूरल नेटवर्क (एएन एन) मार्डेल का उपयोग करके वर्गीकृत किया गया। विभिन्न विश्लेषणों के परिणाम ($P<0.001$) इनहें अभेदकर (डिस्क्रिमिनेंटिंग) बताते हैं। ए एनएन मॉडल ने विभिन्न संयोजनों में 99 प्रतिशत से अधिक सटीकता प्रदान की हैं।

नागालैंड की स्थानीय लम्बे बाल वाली बकरी का उसकी विशेषता के आधार पर मूल्यांकन किया गया। ये मध्यम आकार की होती हैं एवं विभिन्न रंग के प्रारूपों में पाई जाती है। मुख्य रूप से काली और सफेद रंग की होती है लेकिन भूरे रंग और काले रंग की मिश्रित रंग की बकरियां भी पाई जाती हैं। इनकी नाक सीधी और कान सीधे और क्षैतिज होते हैं। वयस्क नर का औसत भार 31.79 किग्रा होता हैं। नागालैंड के आदिवासी लोग इनके बालों का प्रयोग व्यापार में भी करते हैं।

भारतीय गोवंश मवेशियों में चिचड़ी(टिक)संक्रमण के फिनोटिपिक एवं आनुवंशिक विभिन्नताओं का अध्ययन किया गया। मादायें, नर की तुलना में अधिक संवेदनशील पाई गई एवं वर्ष से कम उम्र वाले पशुओं में संक्रमण अधिक पाया गया।

साहिवाल और हरियाना गाय के संरक्षण के लिए एक परियोजना के तहत करनाल (हरियाणा) जिले की चार गौशलाओं का चयन किया गया। वर्ष के दौरान हरियाणा नस्ल की कुल 90 गाय और साहिवाल नस्ल की 26 गायों को कृत्रिम गर्भाधान द्वारा गर्भित कराया गया। पिछले वर्ष कुल 17 बच्चे पैदा हुए।

एक्स- सीटू द्वारा देशी भेड़ के नस्लों के सरंक्षण की परियोजना के तहत कौड़ा एपीडिडेमल शुक्राणु प्रजनन करने में सक्षम पाया गया। वर्ष के दौरान संस्थान के राष्ट्रीय जीन बैंक को विभिन्न नस्लों के वीर्य, भ्रूण, डी एन ए, एपीडिडेमल शुक्राणु एवं दैहिक कोशिका के द्वारा और अधिक सुदृढ़ किया गया।

माइक्रोसैटेलाइट आधारित विविधता विश्लेषण द्वारा लद्दाखी मवेशियों में पर्याप्त विविधता का पता लगाया गया, इस अध्ययन में औसत अलील्स के संख्या 9.79 पाई गयी. फाईलोजेनेटिक विश्लेषित लद्दाखी मवेशियों को अध्ययन की गयी अन्य नस्लों से अलग दर्शाता है। माइटो-कोंड्रिअल -डीएनए आधारित हैप्लोटिक विविधता 942 थी।

अठारह देशी गो नस्लो के 202 सांडो में, सात वाई-गुणसूत्रीय माइक्रो-सैटेलाइट आधारित हैप्लोटाइप्स विविधता की जांच की गयी। कुल 19 बॉस इंडिकस सम्बंधित हैप्लोटाइप्स की पहचान की गयी। 6 सर्वाधिक सर्वनिष्ठ हैप्लोटाइप की बारंबारता 94 प्रतिशत थी।

माईटोकोंड्रियल डी लूप विश्लेषण के दौरान बरगुर भैंस में कुल 40 हैप्लोटाइप्स प्राप्त हुए जिनकी औसत हैप्लोटाइप्स विविधता 0.9524 एवं न्यूक्लेओटाइप विविधता 03894 थी। माइक्रोसैटलाइट स्तर पर कुल औसत अलील्स की संख्या 8 एवं पर्यवेक्षित हेट्रोजायगोसिटी 0.066 पाई गयी। एफ.आई. एस. 0.056±0-0037 पायी गयी.

चिलिका, परलखमुंडी एवं मुर्राह भैंसो के रक्त (सीरा)नमूनों का जैव रासायनिक परीक्षण यह दर्शाता है कि चिलिका में परलखमुंडी एवं मुर्राह भैंसों की तुलना में यूरिया/क्रीटेंनिन अनुपात, अपेक्षाकृत अधिक पाया गया जो कि चिलिका भैंस की निर्जलीकरण स्थिति में बेहतर अनुकूलनशीलता को दर्शाता है 23 माइक्रो सैटेलाइट आधारित विविधता विश्लेषण चिलिका, परलखमुंडी, मुर्राह, नदीय एवं दलदलीय भैंसों में पर्याप्त विविधता दर्शाता है।

राष्ट्रीय पशु आनुवांशिक संसाधन ब्यूरो, भारत सरकार की नीती के अनुसार, देशभर के प्रजनक नरों की सायटोजेनेटिक स्क्रीनिंग और डी.एन.ए. स्तर पर विभिन्न रोग परीक्षण हेतु परामर्श सेवा प्रदान कर रहा है जिसक उद्देश्य आनुवंशिक दोषों का पता लगाना है। वर्ष के दौरान कुल 286 प्रजनक नरों एवं 8 गायों की सायटोजेनेटिक स्क्रीनिंग की गयी। 2 सांडों में गुण सूत्र असमान्यता पाई गई।

नेटवर्क परियोजना के तहत बराहन्वी योजना के दौरान लक्षणीकृत किये गए पशु नस्लों का आनुवंशिक गुण निर्धारण किया गया। इसके अंतर्गत 7 विभिन्न पशु प्रजातियों के पशु समूहों (नस्लों) का अध्ययन विभिन्नता ज्ञात करने के लिए किया गया। अध्ययन से पता चलता है कि तिब्बतन भेंड़ को छोड़ कर अन्य सभी समूहों / नस्लों में पर्याप्त आनुवंशिक विभिन्नता विद्यमान है। एफ.आई.एस. मान (आनुवंशिक विभिन्नता) धारवाड़ी भैस में 19 प्रतिशत, हाजरा मुर्गी में 22

प्रतिशत तथा अरुनाचली याक में 14 प्रतिशत पायी गयी.

साहीवाल, थारपारकर, गिर और वेचूर गौवंश के डीएनए नमूने 777 के एसएनपी चिप का इस्तेमाल करके आनुवंशिक विरूपित किये गए। कुल 1000 मार्करों की पहचान की गई जो नस्लों के बीच 39 प्रतिशत आनुवंशिक भिन्नता दर्शाते थे तथा इनमें मवेशी आबादी को अलग करने के लिए उच्च शक्ति (एफएसटी 0.28) थी। नस्लों को स्पष्ट रूप से छोटे और बड़े आकार के नस्लों में वर्गीकृत किया गया जो बड़े आकर की दूध वाली नस्लों के साझा वंश का संकेत देते हैं। गिर में संबंध असंतुलन उच्चतम और साहीवाल में सबसे कम पाया गया। विभिन्न नस्लों के जोड़ें में कई जीन चयनात्मक पाए गए, जो आर्थिक रूप से महत्त्वपूर्ण गुणों के क्यू टी एल के मानचित्र बनाने में मददगार होगा।

दूध, रोग प्रतिरोध और पशु और भैंस की नस्लों पर अनुकूली लक्षणों से संबेधित उम्मीदवार जीनों में जीनोमिक विविधताएं और अनुक्रमों की जानकारी संग्रहीत करने के लिए एक डेटाबेस विकसित किया गया। पशु और भैंस की नस्लों में उम्मीदवार जीनों पर एसएनपी और अनुक्रमों पर संकलित डेटा दर्ज किया गया।

ड्रोमेडियन और बैक्ट्रियन ऊंट के दस उत्तकों के एनजीएस डेटा पांच अलग अलग डी नॉओ एल्गोरिदम का इस्तेमाल करते हुए इकट्ठे किये गए। विभिन्न ऊतकों के अलग अलग ट्रान्सस्क्रिप्टम ऊंट और उनके रिश्तेदारों उपलब्ध जीनोम पर मैप किया गया। एनोटेशन प्रक्रियाओं के जरिए ट्रांसस्क्रिप्टो का आईफॉर्म विश्लेषण में पता चला कि ऊंट में कई जीन दो या अधिक आइसोफर्म वाले हैं।

बैक्ट्रियन ऊंट और ड्रमडेडरीयन ऊंट के लिए डेटाबेस विकसित किया गया, वर्तमान में http:// 14.139. 252.118/Dcamel.index.php (ड्रोमेडियरियन ऊंट) http:// 14.139. 252. 118 /Bcamel. index. php के लिए (बैक्ट्रियन ऊँट) के लिए उपलब्ध है। प्रजातियों, ऊतक एक विकल्प को एकीकृत किया गया है ताकि आगंतुक द्वारा वांछित डाटाबेस खोजा जा सके। कुल 392179 और 277435 ने एसएनपी की पहचान की जो क्रमशः ड्रोमेडिन और बैक्ट्रियन ऊंटों मे देखी जा सकती है।

सोमैमैटिक सेल बैंकिंग के लिए प्राथमिक खोजकर्ता तकनीक का उपयोग करके दोहरे कुबड़ वाले ऊंट (कैमलस बैक्ट्रियनस) फाइब्रोब्लास्ट सेल लाइन को सफलतापूर्वक स्थापित किया गया। फाइब्रोब्लास्ट्स के विकास के संबंध में विभिन्न मीडिया का परीक्षण किया गया, सामान्य बढ़ती कोशिकाओं को 4 से 6 पैसेज पैराग्राफ पर शीत-संरक्षित किया गया। यह सेल स्तर पर बैक्ट्रियन ऊंट के महत्त्वपूर्ण आनुवंशिक संसाधन को संरक्षित करने के लिए सहायक होगा।

भैंस में आर्थिक गुणों के लिए मार्करों की पहचान के लिए, अलग-अलग क्रोमोसोम के लिए जीबीएस डेटा का पारिवारिक विश्लेषण किया गया। दुग्ध वसा और दूध प्रोटीन प्रतिशत और कुल वसा उपज और कुल प्रोटीन उपज, पहली गर्मी में उम्र और दैहिक कोशिका स्कोर लिए 24 ऑटोसॉम्स में से प्रत्येक पर क्यू टी एल तैयार किए गए। सभी क्यू टी एल भैंस गुणसूत्रों में वितरित पाए गए। सभी पहचाने गए मात्रात्मक गुण स्थानीय भैंसों का एक भैंस क्यू टी एल डाटाबेस के रूप में http:// 14.139.252. 118:8084/ Buffalo Q T L/ पर संकलित किया गया है।

पूरे देश में भैंस की 15 आबादी को मिलाकर एक मध्यम घनत्व एसएनपी चिप का विकास किया गया। कुल 98346 एस एन पी की पहचान व्यापक जीनोम में की गई जो एस एन पी ऐरे में विकास के लिए गुणवत्ता नियंत्रण मानकों को पारित कर चुके हैं। एसएनपी के बीच का औसत दूरी 27.9 के.बी. पाई गई। यह मध्यम घनत्व एस एन पी ऐरे का प्रयोग भैंसों में जिनोमिक चयन के लिए किया जा सकता है।

देशी मवेशियों और भैंसों में थर्मोटोलायरेंस के आणविक आधार को जानें और विभिन्न वातावरणों के अनुकूलन के लिए जीनोम डेटा खनन किया गया। लद्धाख के स्थानीय देशी मवेशियों और कम ऊंचाई से साहिवाल मवेशियों से कई सौ विभेदित व्यत्त्क जीन, जैविक प्रक्रियाओं, आणविक कार्य और प्रक्रिया की पहचान हुई। क्रमि क्लस्टरिंग और हीट मेप डेटा से पता चलता है कि साहिवाल और लद्धाख गायों में अलग-अलग ट्रांस्क्रिप्टोम हसताक्षर के रूप में पाए गए, क्यूपीसीआर ने हाइपोक्सिया से जुड़े जीनों जैसे एचआईएफ़-1 और उसके विनियमित जीन की अभिव्यक्ति में उल्लेखनीय वृद्धि का उल्लेख किया है, जो सुझाव देते हैं कि लद्धाखी गायों में उच्च ऊंचाई अनुकूल में उनकी महत्त्वपूर्ण भूमिका होती है।

नदी के भैंसों में Na/K ATPase जीनों के आइसोफोर्म की ऊतक विशिष्ट अभिव्यक्ति का अध्ययन किया गया।, एटीपी 1 ए की ऊतक-विशिष्ट पद्धति अभिव्यक्ति, कोशिकाओं और ऊतकों में आयनिक एकाग्रता को बनाए रखने में आईसाफार्म की महत्त्वपूर्ण भूमिका की ओर इंगित करता है।

साहीवाल,एचएफ और मुर्रा भैंसो मे सेलुलर मापदंडो पर गर्मी तनाव का असर मूल्याकंन किया गया। गर्मी तनाव के 4

घंटे,16 घटें और 24 घंटे के बाद एचएफ की पीबीएमसी की व्यवहार्यता प्रभावीरूप से कम थी। साइटोटोक्सीसिटी मे एचएफ गायों में दूसरों की तुलना काफी अधिक ( पी 0.05) थी। साइटोटोक्सीसिटी स्तर एपोपोटोसिस एच एफ गायों के पीबी एम सी मे उच्चतम था और उच्च दर सेल मृत्यु 16 घंटे और 24 घंटे बाद गर्मी तनाव पर अधिकतम स्तर तक पहुंच गयी। अध्ययन ने एचएफ और मुर्रा भैंसो की तुलना में साहीवाल गायों के बेहतर सेलुलर का संकेत दिया। गर्मी तनाव (30 मिनट) के बाद, तनाव और प्रतिरक्षा प्रतिक्रिया से जुड़ी माइक्रोआरएनए ने अपने अभिव्यकित तीनों में से विशेष रूप साहिवाल मे महत्वपूर्ण दिखायी दी।

जंस्कारी घोडों में धीरज (एण्डयुरेंस) गुण के साथ जुडे जीन और आणविक मार्गो की पहचान के लिए लद्धाख क्षेत्र की उच्च ऊँचाई पर 12 जंस्कारी घोड़ों और 6 जी एस खच्चरों पर अध्ययन किया गया। परिणाम बताते हैं कि जी एस खच्चरों में धीरज परीक्षण के बाद जंस्कारी टटटू की तुलना मे विभिन्न शारीरिक मापदंड अधिक पायी गयी। उच्च ऊँचाई पर धीरज अभ्यास से पहले और बाद परिणाम स्वरूप जंस्कारी घोड़ों के ट्रांक्रिप्टोमिक विशलेषण जीन को उपर या नीचे विनियमित पाये गये। तनाव,अजैविक व जैविक उत्तेजना,कीमोकीन,आश्रित प्रोटीन कीनेज, सेल-सेल आसंजन अणुओं से संबंधित कई जीन के व्यायाम के पूर्व और बाद और आराम करने की अवधि के दौरान व्यक्त किए गए।

गोवंश के ए1/ए2 दूध के स्वास्थय के प्रभाव पर परियोजना के अतंर्गत पूरे भारतीय देशी नस्लों,संकर और विदेशी गोवंश में बीटा केसीन जीन के वेरिएंट / हैप्लोप्टाइप्स को निर्धारित करने के लिए अनुक्रम लक्षण वर्णन किया गया। बॉस इंडिकस और बॉस टारॅस मवेशियो के बीच पहचान किए गए कई न्यूक्लियोटिड विविधताएँ की आवृति कम थी। कुल 6 हप्लोटाइप देखे गए और इन ए2 प्रकारों में 0.86 की अधिकतम आवृति पायी गयी।

विविधता विश्लेषण में मौली भेंड़ में प्रभावी आलील्स की संख्या, औसत प्रेक्षित हेट्रोजायगोसिटी एवं जीने विविधता क्रमशः 5.23, 0.637 एवं 0.783 और यलगा भेंड़ में ये मान क्रमशः 4.865, 0.596 एवं 0.757 पाया गया।

चोकला, मगरा, मारवाड़ी एवं मद्रास रेड भेंड नस्लों में एच एस पी जीन बहुरूपता एवं अभिव्यक्ति प्रोफाइल्स और हीमैटो-फिजियों -जैव रासयानिक मानदंडो के साथ सम्बधों का अध्ययन किया गया. जीन अभिव्यक्ति विश्लेषण, अल्प -अनुकूलित पशुओं में अधिक अभिव्यक्ति का होना दर्शाता है।

नागालैंड बकरी के आनुवंशिक अध्ययन प्रेक्षित हेट्रोजायगोसिटी 0.347 पाई गयी। समग्र बहुरूपता (पी आई सी) मान 0.494 पाया गया।

आन्ध्र प्रदेश के स्थानीय खच्चरों में 12 स्कोरेबल लोसाई का पता चला। प्रभावी आलील्स की सख्या 6.92 पाई गयी। आनुवांशिक विविधता मान 0.21 पाया गया जो कि मध्यम स्तर के अन्तः प्रजनन को दर्शाता है।

चराई में पाली गयी देशी (साहिवाल)गाय, विदेशी (होल्सटीन फ्रीजियन) एवं सघन पद्धति में पाले गयी संकर गायों (साहिवाल होल्सटीन फ्रीजियन) के दुग्ध - मेटाबोलाइट्स का तुलनात्मक अध्ययन किया गया। चराई में पाली गयी गायों में प्रोटीन, वसा एवं आवश्यक अमीनो अम्ल की मात्रा अधिक पाई गयी।

बन्दूर भेंड़ के मॉस से सम्बंधित विशेषताओं की तुलना स्थानीय भेंड़ से किया गया। इस अध्ययन के संवेदी (सेंसरी)मूल्यांकन में मांस में थोडा अधिक जुसीनेस एवं विशिष्ठ गंध पाई गयी, हालाँकि यह अन्तर अध्ययन की दोनों भेंड़ो में सार्थक स्तर पर भिन्न नही था। बन्दूर भेंड में शियर फोर्स का मान कम पाया गया जो कि वांछित लक्षण है एवं यह कोमलता (टेंडरनेस) को दर्शाता है।

संस्थान में पिछले वर्ष के दौरान कुल 11 अनुसंधान परियोजनांए पूरी हुई जिसमें 1 बाह्य वित्त पोषित परियोजना सम्मिलित है वर्तमान में 20 अनुसंधान परियोजनाओं पर कार्य जारी है, जिसमें 5 बाह्य वित्त पोषित एवं एक राष्ट्रीय फेलो परियोजना है।

वर्ष के दौरान कुल 48 शोध पत्र संस्थान के वैज्ञानिकों द्वारा राष्ट्रीय और अंतराष्ट्रीय शोध पत्र-पत्रिकाओं में प्रकाशित किए गए। इसके अतिरिक्त 10 तकनीकी/लोकप्रिय लेख 5 किताबें, 4 मोनोग्राफ एवं प्रशिक्षण मैन्युअल भी प्रकाशित हुए , संस्थान द्वारा 4 पेटेंट आवेदन भारतीय पेटेंट कार्यालय में आवेदित किये गए ।

संस्थान द्वारा वर्ष के दौरान 6 प्रशिक्षण एवं एक मस्तिष्क मंथन सत्र भी आयोजित किये गये। “एडवांस्ड टूल्स फॉर कंजर्वेशन ऑफ डोमेस्टिक लाइवसटॉक डाइवर्सिटी” पर एक लघु अवधि प्रशिक्षण कार्यक्रम एवं “ स्ट्रेटेजीज फॉर कैरेक्टराइजेसन एंड कंजर्वेशन ऑफ एनिमल एंड

पोल्ट्री जेनेटिक रिसौर्सस'' पर एक मॉडल प्रशिक्षण कार्यक्रम' भी आयोजित किया गया। इसके अलावा जागरूकता एवं कुशलता उच्चीकरण हेतु भी '' बौद्धिक सम्पदा अधिकार एवं सम्बंधित क्षेत्र' पर प्रशिक्षण कार्यक्रम आयोजित किये गए। तकनीकी अधिकारियों हेतु ''प्रयोगशाला विधियों में कुशलता उन्नयन प्रशिक्षण कार्यक्रम भी आयोजित किया गया।

ब्यूरो के वैज्ञानिको ने ''मेरा गाँव मेरा गौरव'' कार्यक्रम में भाग लिया और विभिन्न गांवों में जा-जाकर किसानों में जागरूकता कार्यक्रम चलाया। संस्थान द्वारा पांच प्रदर्शनियों का आयोजन किसानों में जागरूकता फैलाने के लिए देश के विभिन्न हिस्सों में देशी पशुओं की विशेषताओं के बारे में किया गया।

संस्थान द्वारा पिछले वर्ष के दौरान गणतन्त्र दिवस, स्वतंत्रता दिवस, संस्थान स्थापना दिवस, जैव विविधता दिवस, सतर्कता सप्ताह एवं हिन्दी पखवाड़ा मनाया गया साथ ही वर्ष भर राष्ट्रीय स्वच्छता अभियान भी चलाया गया.

संस्थान के पुस्तकालय में इस दौरान 30 अनुसन्धान जर्नल सब्सक्राइब किये गए एवं 20 किताबें खरीदी गई।

अनुसंधान सलाहकार समिति एवं संस्थान अनुसंधान समिति एवं की बैठकों का समय पर आयोजन किया गया एवं संस्थान में चल रही परियोजनाओं की प्रगति की समीक्षा इन बैठकों के दौरान की गयी।

वर्ष के दौरान वार्षिक खेल-कूद प्रतियोगिता भी आयोजित की गयी जिसमें संस्थान के अधिकारियों एवं कर्मचारियों ने बढ़-चढ़ कर हिस्सा लिया। गत वर्ष के दौरान संस्थान की बास्केट बाल टीम, आई सी ए आर नार्थ जोन स्पोर्ट्स, जो की एन डी आर आई करनाल में आयोजित हुआ था, में रजत पदक के साथ उप विजेता रही।

वर्ष के दौरान कई विशिष्ट व्यक्तियों ने संस्थान का दौरा किया, जिसमें महा निदेशक एवं उप - महा निदेशक (पशु विज्ञान) भारतीय कृषि अनुसंधान परिषद् नई दिल्ली प्रमुख रहे।

संस्थान के वैज्ञानिकों ने देश के विभिन्न भागों में आयोजित विभिन्न प्रशिक्षण कार्यक्रमों, कार्यशालाओं, संगोष्ठियों और सम्मेलनों में भाग लिया।

संस्थान के वैज्ञानिक, राष्ट्रीय डेरी अनुसंधान संस्थान (एन डी आर आई) करनाल एवं भारतीय पशु चिकित्सा अनुसंधान संस्थान (आई वी आर आई) बरेली के संकाय सदस्य के रूप में शामिल हैं एवं एन डी आर आई, करनाल में स्नातकोत्तर विषयों को पढ़ा रहे हैं और साथ ही स्नातकोत्तर एवं पी एच डी (विद्या वाचस्पति) के छात्रों के शोध कार्यों में मार्गदर्शक का कार्य भी कर रहे हैं।

वर्तमान मं संस्थान में कुल 28 वैज्ञानिक, 16 तकनीकी अधिकारी, 16 प्रशासनिक अधिकारी एवं 5 कुशल स्टाफ कार्य कर रहें हैं। वर्ष के दौरान 2 वैज्ञानिकों एवं तकनीकी अधिकारी को पदोन्नति मिली। इस दौरान एक कर्मचारी को सेवानिवृत्ति भी मिली। श्री सोपाल, यू.डी.सी. का वर्ष के दौरान निधन हो गया।

वर्ष के दौरान संस्थान को भारतीय कृषि अनुसंधान परिषद् नई दिल्ली द्वारा गणेश शंकर विद्यार्थी कृषि पत्रिका पुरस्कार के तहत, संस्थान द्वारा प्रकाशित वार्षिक हिंदी पत्रिका '' पशुधन प्रकाश (पंचम अंक)'' को द्वितीय पुरस्कार प्राप्त हुआ।

# राजभाषा संबंधी गतिविधियाँ

### संस्थान राजभाषा कार्यान्वयन समिति की बैठकें

राजभाषा हिंदी के प्रयोग की प्रगति की समीक्षा करनें एवं राजकीय कार्यों में इसके अधिकाधिक प्रयोग को बल देने हेतु विभिन्न बिन्दूओं पर चर्चा करने हेतु संस्थान में राजभाषा कार्यान्वयन समिति की तिमाही बैठकों का निरंतर आयोजन किया जाता है. इस अवधि के दौरान भी नियमानुसार चार संस्थान राजभाषा कार्यान्वयन समिति तथा एक राजभाषा सलाहकार समिति की बैठक का आयोजन किया गया।

### हिंदी व्याख्यान/कार्यशालाओं का आयोजन

संस्थान में राजभाषा हिंदी के प्रचार-प्रसार और संस्थान कार्मिकों को राजकीय कार्यों में हिंदी के अधिकाधिक प्रयोग हेतु जागरूक करने के उदेश्य से संस्थान में तिमाही हिंदी व्याख्यानों/कार्यशालाओं का आयोजन किया जाता है। इसी प्रक्रिया में दिनाँक 15-04-2016 को महिला सशक्तिकरण: भारतीय समाज के सन्दर्भ में विषय पर एक हिंदी व्याख्यान का आयोजन किया गया। विषय पर व्याख्यान हेतु करनाल स्थित महिला थाना की एसएचओ श्रीमती लक्ष्मी देवी को आमंत्रित किया गया था। दिनाँक 18-07-2016 को आयकर विवरणिका भरतें समय ध्यान देने योग्य बिंदु विषय पर हिंदी भाषा में व्याख्यान/कार्यशाला का आयोजन किया गया, जिसमें आयकर कार्यालय करनाल के उप-आयुक्त श्री जी.के. कोहली को आमंत्रित किया गया था। दिनाँक 27-01-2017 को वर्तमान समय के ज्वलंत विषय धन हस्तांतरण का अंकीकरण पर एक हिंदी व्याख्यान का आयोजन किया गया जिसके लिए श्री विशाल अवस्थी, मुख्य विपणन अधिकारी, युबीआई बैंक को आमंत्रित किया गया। ज्ञानार्जन के साथ-साथ कर्मचारियों में राजभाषा प्रयोग के प्रति रूझान बढ़ाने का प्रयास किया गया।

### हिंदी चेतना पखवाड़ा

प्रत्येक वर्ष की भांति इस वर्ष भी संस्थान में दिनाँक 14-09-2016 से 21-09-2016 तक हिंदी पखवाडे का आयोजन किया गया. इस अवधि में विभिन्न प्रतियोगिताएं जिनमें निबन्ध, पत्र, शब्दार्थ/अनुवाद, टिप्पणी/मसौदा, पोस्टर प्रदर्शनी,भाषण, आशु-भाषण, हिंदी शब्द खोज, वैज्ञानिकों हेतु हिंदी शौध पत्र प्रस्तुतीकरण इत्यादि का आयोजन किया गया। इसके साथ-साथ स्टाफ सदस्यों के द्वारा पिछलें वर्ष के दौरान हिंदी भाषा में किये गए कार्यों का मूल्यांकन नकद पुरस्कारों हेतु किया गया।

निबंध लेखन प्रतियोगिता में प्रथम, द्वितीय व तृतीय पुरस्कार क्रमशः श्री राकेश कुमार, श्री कर्मबीर मालिक व श्री रमेश कुमार राणा ने प्राप्त किया।

पत्र लेखन प्रतियोगिता में प्रथम, द्वितीय व तृतीय पुरस्कार क्रमशः श्रीमती अनीता चंदा, श्री कर्मबीर मालिक व श्री राकेश कुमार ने प्राप्त किया।

टिप्पणी मसौदा लेखन प्रतियोगिता में प्रथम, द्वितीय व तृतीय पुरस्कार क्रमशः श्री कर्मबीर मालिक, डॉ. रणजीत कटारिया व श्री राकेश कुमार ने प्राप्त किया।

### पशुधन प्रकाश (वर्ष 2015) के श्रेष्ठ लेख पुरस्कार विजेताओं की सूची

| | | |
|---|---|---|
| प्रथम पुरस्कार | : | रेखा शर्मा, सोनिका अहलावत, प्रियंका शर्मा, प्रदीप विज एवं मधु सूदन टांटिया, एनबीएजीआर,करनाल<br>स्वदेशी कुक्कुट जर्मप्लाज्म : कुक्कुट उत्पादन में सुधार के लिए एक परिसंपति |
| द्वितीय पुरस्कार | : | अरूण कुमार, सिद्धार्थ मिश्रा, इन्द्रोन चौहान एवं एस.एम.के. नकवी, सी.एस.डब्लू.आर.आई, अविकानगर<br>राजस्थान का गौरव सिरोही बकरी व उसका पालन |
| तृतीय पुरस्कार | : | चेतना गंगवार, एस.पी. सिह, महेश डिगे एवं अनुज कुमार सिंह, सिकरवार, सीआईआरजी, मखदूम<br>भारतीय अर्थव्यवस्था में बकरी का योगदान : उत्पाद व उपोत्पाद |

शब्दार्थ/अनुवाद प्रतियोगिता में प्रथम, द्वितीय व तृतीय पुरस्कार क्रमश: डॉ. एन.के.वर्मा, श्री राकेश कुमार व डॉ. रणजीत कटारिया ने प्राप्त किया।

हिंदी शब्द खोज प्रतियोगिता में प्रथम, द्वितीय व तृतीय पुरस्कार क्रमश:श्री कर्मबीर मालिक, व श्रीमती अनीता चंदा , श्री बलकार सिंह व श्री रमेश कुमार राणा तथा डॉ. सोनिका अहलावत व श्रीमती अमिता कुमारी ने प्राप्त किया।

पोस्टर प्रतियोगिता में प्रथम मनोज कुमार, अंकिता शर्मा, प्रीती वर्मा, प्रवेश मुंजाल, निकिता, शैलेश स्वामी, मनीषी मुकेश एवं डॉ. मोनिका सोढ़ी  ने प्राप्त किया।

शौध-लेख प्रस्तुतीकरण प्रतियोगिता में ब्यूरों के वैज्ञानिकों के द्वारा पूर्व के दो वर्षों के दौरान किये गए शौध-कार्य में प्रथम डॉ. रणजीत सिंह कटारिया, द्वितीय डॉ. राकेश कुमार पुंडीर एवं तृतीय पुरस्कार डॉ. मोनिका सोढ़ी ने जीता. प्रोत्साहन पुरस्कार डॉ. एन.के.वर्मा तथा डॉ. के.एन. राजा को दिया गया।

हिंदी भाषण प्रतियोगिता विषय स्वरोजगार और पशुपालन में प्रथम पुरस्कार  सुश्री अंकिता को द्वितीय पुरस्कार (संयुक्त) रूप से श्री प्रदीप गुप्ता मिला।

हिंदी आशु भाषण प्रतियोगिता में प्रथम पुरस्कार डॉ. मोनिका सोढ़ी, द्वितीय पुरस्कार कुमारी हिमानी शर्मा तथा तृतीय पुरस्कार सुश्री अंकिता ने जीता. वर्ष 2015-16 के दौरान हिंदी भाषा में किये गए उत्कृष्ट कार्य हेतू प्रथम पुरस्कार श्री बाबू राम ने जीता।

### पशुधन प्रकाश के सप्तम अंक का विमोचन

ब्यूरों के स्थापना दिवस के सुअवसर पर पशुधन प्रकाश प्रकाश के सप्तम अंक का विमोचन डॉ. गया प्रसाद, उपकुलपति, सरदार वल्लभभाई पटेल कृषि एवं प्रोध्योगिक विश्वविद्यालय, मेरठ, द्वारा किया गया।

### पशुधन प्रकाश को गणेश शंकर विद्यार्थी पुरस्कार

विशिष्ट उपलब्धि के अंतर्गत इस अवधि के दौरान भारतीय कृषि अनुसन्धान परिषद् द्वारा पशुधन प्रकाश के पांचवे अंक (वर्ष-2014) को गणेश शंकर विद्यार्थी कृषि पत्रिका पुरस्कारों के अंतर्गत द्वितीय पुरस्कार से सम्मानित किया गया।

भाकृअनुप
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