# वार्षिक प्रतिवेदन
# ANNUAL REPORT
## 2013-14






राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो
(भा.कृ.अ.प.)
करनाल – 132001 (हरियाणा) भारत
National Bureau of Animal Genetic Resources
(I.C.A.R.)
Karnal - 132 001 (Haryana) India

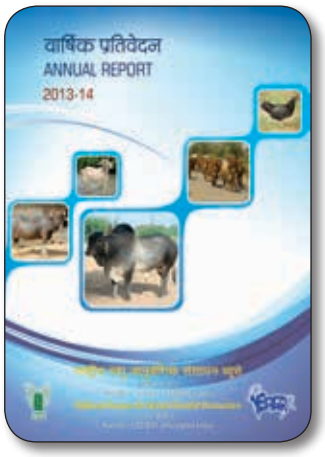
United Nations Decade on Biodiversity

# वार्षिक प्रतिवेदन
# ANNUAL REPORT

**2013-2014**


राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो
(भा.कृ.अ.प.) करनाल – 132001 (हरियाणा) भारत

**National Bureau of Animal Genetic Resources**
(ICAR) Karnal - 132001 (Haryana) India




## Credit Line...

***Published by***

Dr. Arjava Sharma, Director
National Bureau of Animal Genetic Resources
Karnal - 132001 (Haryana) India

***Compiled by***

Dr. NK Verma, Principal Scientist
& I/C, P M E Cell

***Editors***

Dr. NK Verma, Principal Scientist
Dr. PK Singh, Principal Scientist
Dr. RS Kataria, Principal Scientist
Dr. Rekha Sharma, Senior Scientist
Dr. Saket Kumar Niranjan, Senior Scientist
Dr. Sonika Ahlawat, Scientist

***Photographs***

Sh. Moti Ram, T-5

***Assistance***

Dr. PS Dangi (A.C.T.O)
Ms. Indu Bala, Steno Gr.III

***Printing***

Intech Printers & Publishers
343, 1st Floor, Mughal Canal Market,
Karnal - 132001, Haryana
Tel: 0184-4043541, 3292951
E-mail: jobs.ipp@gmail.com

## Contents



2013-14

# FOREWORD

I feel privileged to present Annual Report of National Bureau of Animal Genetic Resources for the period 2013-14. This document presents salient features of the work done by scientists along with the glimpses of other peripheral activities of the Bureau. Working for the mandate during the year 2013-14, we completed the characterization of some lesser known populations of indigenous livestock, which included Sanchori, Manipuri and Belahi cattle; Gojri buffalo and Harringhata Black chicken. The characterization of Sigharey goat, Deccani sheep ecotypes, Kajali sheep and Rajapalayam dog is under way. As part of *ex-situ* conservation program, gene bank activity has been strengthened by adding 15821 semen doses from Tharparkar cattle, Mehsana buffalo, Osmanabadi & Assam Hill goat, Zanskari & Marwari horse, French donkey and Arunachali yak.

In the area of gene characterization and functional genomics, characterization of important caprine candidate genes like BMPR1B, GDF9, BMP15 controlling the fecundity and INBB, JY-1 and AA-NAT genes for reproductive traits was undertaken by identifying novel SNPs and their associations with traits. Adaptation to varied climatic conditions is important for survivability and maintenance of performance potentials of all livestock species. Projects were carried out to understand the thermo-tolerance at varying temperature humidity index across the indigenous cattle and buffalo. The temporal profile of heat shock proteins was determined in response to varying heat shocks in native, exotic cattle and buffaloes. We have also completed two National Agricultural Innovation Projects successfully. The research carried out under these projects resulted in to filing of fourteen patents and commercialization of four technologies. The Bureau continued to provide consultancy services for cytogentic screening of breeding bulls and 372 bulls were screened for cytogenetic parameters during last year.

IRC meetings were held in time to evaluate the progress of ongoing research projects. Awareness on AnGR was generated among masses by holding exhibitions, brain storming session and lectures. A Brain storming workshop on conservation and productivities was organized at NASC complex, Delhi in collaboration with Trust for Advancement of Agricultural Services (TAAS). Another brain storming session on AnGR of Manipur was also organized at Imphal in collaboration with state A.H Deptt. of Manipur, where in the breeding policy and conservation strategies of AnGR of Manipur was discussed. Scientists published their research findings in scientific journals of national and international repute. They were also awarded at different fora for their

outstanding contributions. A new edition of NBAGR Profile with updated information of Bureau's achievements was published this year. The Bureau has obtained ISO 9001:2008 certificate for its quality services. Apart from the routine activities, the staff of bureau participated and excelled in ICAR sports also. Bureau hosted one National Symposium on 'Harmonizing Phenomics and Genomics for Sustainable Management of Livestock for Upliftment of Rural Masses' in collaboration with Society for Conservation of Domestic Animal Biodiversity (SOCDAB) in the month of February, 2014 in which 166 delegates from different parts of the country participated and presented their scientific work. Apart from this, various dignitaries from the country and abroad visited the institute and interacted with the scientists. The Infrastructure of Bureau has been strengthened by adding one more wing of laboratories The livestock information management unit has been enriched with the installation of a high Performance Computing (HPC) system at the Institute. Sh. Arvind Kaushal, Secretary, ICAR also visited and addressed the bureau staff.

I wish to extend my sincere thanks to Dr. S Ayyappan, Secretary DARE & DG, ICAR and Dr. KML Pathak, DDG (AS) for their support and guidance. I am also thankful to my entire staff who is continuously striving to bring name and fame to this institute. Suggestions for improvement are always welcome on the Director's address.

**(Arjava Sharma)**
Director

# EXECUTIVE SUMMARY



National Bureau of Animal Genetic Resources and National Institute of Animal Genetics 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 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 'Identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country'. The objectives of the Bureau are:

- To conduct systematic surveys to characterize, evaluate and catalogue farm livestock and poultry genetic resources and to establish their National Database.
- 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.

Total expenditure under Non-plan and Plan was Rs. 1062.77 Lakhs against the total receipt of Rs. 1064.69 Lakhs during the financial year 2013-2014. Under Network project, total expenditure was 38.82 Lakhs against Receipt of Rs. 39 Lakhs during the period. Revenue generated during the year 2013-2014 was Rs. 33.15 Lakhs against the target Rs. 27.70 Lakhs during the financial year 2013-2014.

High Performance Computing (HPC) system has been installed in the Computer Center at NBAGR. It is Linux cluster with one master node, one login node, 16 compute nodes, 20 terabytes of Network Attached Storage and 20 terabytes of File System Storage. Bioinformatics software like CLC-bio Genomic Server for genomic and proteomic data analysis, and Discovery Studio for proteomics studies has been installed.

SNP density on cow genomic DNA encompassing 12 genes related with milk traits has been evaluated. The homology based study could help in placing of SNPs on genomic sequence, which will be useful in marking the SNPs rich areas of genomic DNA of livestock species.

Three popular phylogeny estimation methods -RAxML, PhyML and MetaPiga were compared. The study shows that phylogenies of size 100 taxa can be estimated using PhyML with little degradation in tree accuracy as compared to RAxML. Performance of MetaPiga with veryhigh K-score and symmetric difference was poor.

Tissue-specific *in-silico* SNP mining from EST retrieved from NCBI has been performed for different tissues of pig and cow. ESTs were primarily processed using the online tool EGassembler and assembled into contigs using the CAP3tool. SNPs were searched for their presence in the dbSNPdatabase. The number of SNPs was 27247 across 4 tissues of pig, whereas, 14032 across 3 tissues of cow. Database on tissue-wise SNPs was developed using MySQL. Perl scripts were written to parse and fill the tissue-wise SNPs data in the database. Web interface was developed using PHP language.

Sanchori cattle of Rajasthan was phenotypically characterized. Sanchori cattle are mainly distributed in Sanchore, Bhinmal and Raniwada tehsils of Jalore district of Rajasthan. Sanchori cattle has good milk production potential. Peak milk yield was reported to be 6-18 kg per day in a lactation period ranging from 8-15 months. The overall daily milk yield was 9.08±0.16 litres per day based on records of 276 cows in different months and order of lactation.

Local cattle population of Manipur state was characterized in 13 villages of Imphal-East, Imphal-west and Churachandpur districts. Animals are small size, having well built, stout and cylindrical body. Coat colour was dark brown in majority animals. Daily milk production ranged from 2.0 to 4.50 kg. Average per day milk yield was 2.65±0.18 kg. A pair of bullock may plough about 1.0 acre of land in 6 to 8 hours.

In Belahi cattle, overall average daily milk yield and 305 day milk yield were estimated as 3.25 ± 0.15 kg and 1014.43 ± 45.46 kg respectively, in 79 cows belonging to 5 herds.

A new indigenous buffalo 'Gojri', generally under migration in Himachal Pradesh and Punjab state was identified and characterised. Gojri buffalo possess black coat colour with brown thick hair; white patches may be present on face. Horns are medium to large sized with curved orientation which moves backwards and then towards front to complete the loop. Gojri buffaloes are reared for milk, draft power and manure /dung. Adult males are used for agricultural work and transport purpose. Gojri buffalo is lighter, smaller and shorter than Murrah and Nilli Ravi.

Local goat of Sikkim 'Singharey' was characterized in East and West districts of Sikkim. Singharey goats are small to medium sized having coat colour varying from tan or light brown to brown with a mixing of grey/white hair. Most of the goats possessed stripes on face extending from base of horn to the muzzle. In breeding males, black ring is present around the neck but not in castrated males. Milk production is approximately 300 – 500 ml per day. Twinning is very common.

Three ecotypes-Solapuri, Madgyal and Kolhapuri of Deccani sheep were surveyed and characterized in respective Solapur, Sangli and Kolhapur districts of Maharashtra. Coat colour varied from white with brown patches/spots in Madgyal to black with white patches in Solapuri. Kolhapuri sheep were mottled, black mingled with varying shades of brown and offwhite. All the ecotypes had a straight backline and a medium length thin tail. Madgyal and Solapuri sheep had a typical roman nose. Substantial sexual dimorphism was observed in Madgyal, Solapuri and Kolhapuri ecotypes.

Kajali, a lesser known sheep population distributed in Sangrur, Barnala, Ludhiana and adjoining districts of Punjab was characterized. Kajali is primarily reared for mutton. It is large in size with well built body. The coat colour of Kajali is primarily white but dark brown and black animals were also found. 'Kajali' name is derived from black circles around the eyes; a distinguishing characteristics of this breed. It has Roman nose, long and pendulous ears and long tail reaching upto the ground. Both sexes are polled however in some males horn were also noticed. The preliminary results indicate that the Kajali sheep is phenotypically different from other sheep breeds of the region.

Harringhata Black chicken of West Bengal was surveyed to record flock structure and size, management practices across Nadia and North 24 Pargana districts. Estimated population

of Harringhata Black in the breeding tract is 63600. Average flock size was 7.9, including 3.25 Harringhata Black birds. Plumage colour is black. Some cocks have brown feathers on neck and wings. Comb is red and mainly single. Earlobe is red or white. Beak is black. Body weight at 10 months of age was 1.1 kg in hens and 1.3 kg in cocks. Average age at first egg was 5.63 months. Average number of eggs per cycle was 12.32 and annual egg production was 45 with brooding and 98 without brooding.

Survey on Rajapalayam dog breed was conducted in Rajapalayam taluk of Virudhunagar district of Tamil Nadu. Rajapalayam dogs are medium in size with compact body, tucked-up abdomen with white coat color and pink skin, nostrils and eyelids, semi-dropping ears, semi-curved tail and straight top-line. The eyes are golden in color and the nasal bridge is straight. Rajapalayam dogs are mainly used for guarding of farm and farm houses.

Frozen semen doses (15,821) of 5 species and their 8 breeds have been added to repository in GeneBank. The National GeneBank at NBAGR now stores about 1,28,074 frozen semen doses belonging to forty one breeds of seven species (Cattle, Buffalo, Goat, Sheep, Camel, Equine and Yak).

Genetic characterization of Belahi cattle was carried out using microsatellite based genotyping. The mean observed and effective number of alleles found to be 9.31 and 4.38, respectively. The candidate genes affecting the milk production were PCR amplified and RFLP based characterization was done in 50 samples of Belahi cattle.

Fifty one loci out of 75 were considered differentiating the 3 cattle breeds-Gir, Sahiwal, Tharparkar. The mean observed heterozygosity was 0.58 while the mean expected heterozygosity was 0.76. Analysis of molecular variance (AMOVA) revealed 13.74% variation attributed to between breeds. Pairwise $F_{st}$ values revealed that Gir and Tharparkar were genetically more differentiated (22.7%) and least differentiation (7%) was observed between Gir and Sahiwal. Breed structure and degree of admixture were assessed with STRUCTURE software. The results revealed that Gir and Tharparkar breeds grouped in their own clusters while Sahiwal cattle were separated into two distinctive cluster.

Coding region of TLR3 among various Indian native cattle breeds revealed a total of 13 variations including 4 non-synonymous with conserved polarity, whereas, TLR 7 gene revealed a total of 16 variations, including six non-synonymous. Kankrej, Hariana and Gir cattle showed maximum number of SNPs while Kangyam and Nagori cattle were least polymorphic. Ten TLRs revealed a total of 196 SNPs, of which 86 were non-synonymous and 55 were unique for Indian cattle breeds. Examination of the intragenic pattern of LD revealed 5 haplo-blocks in TLR6; 4 each in TLR1 and TLR10; 3 in TLR7 and 2 each in TLR2 and TLR3 with varying LD.

Polymorphism detection in buffalo NOD-like receptor-2 revealed presence of 42 SNPs among which 10 being non-synonymous. PCR-RFLP protocols were developed and genotypes on two SNPs, G91C in CARD domain and A1135G in NOD domain of buffalo Nod-like receptor 2, have been generated. SNP A1135G has shown significant variations in allelic frequencies across clinical mastitis affected and non-affected buffaloes. Besides, NOD-like receptor-1 has shown transcription of two splice variants in buffalo mammary gland, which could play important role in local immune response.

A total of 20 SNPs were observed to be spread across the 3.4 Kb region of the IFN-γ gene in 40 indicine cattle of Tharparkar, Rathi, Sahiwal, Hariana and Kankrej breeds. A microsatellite repeat $(GTTT)_n$ in the intron-1 of the gene has been identified.

Polymorphism present across the complete TNF β gene (3.5Kb) in the 40 animals of *Bos indicus* (Hariana, Tharparkar, Kankrej, Sahiwal and Rathi) breeds was studied. Overall 31 SNPs were observed across 3.5 Kb long region. The SNP 1412(A>G) in exon2 resulted in amino acid change Gly>Asp. The observed heterozygosity (0.1588±0.1225) for all the loci for SNPs was almost the same as the expected heterozygosity (0.1555±0.1108). The overall negative Fis value of -0.1958 indicated little level of inbreeding. The Fst value of 0.1354 was observed.

Previously reported polymorphic regions of the ovine GH, GHR, TTN, CAST and DGAT1gene loci were screened for possible SNPs in Bandur, Chokla, Deccani, Ganjam, Madgyal, Magra, Malpura, Muzzafarnagri, Nali and Nellore sheep. Presence of the novel nucleotide variations in candidate genes for mutton quality in Indian sheep reflects availability of greater genetic diversity at these loci.

Genomic regions corresponding to exon 2 of DRA, DRB, DQA and DQB genes were amplified and sequenced from 37 Arunachali yaks. A total of three allelic variants of Bogr-DRA were identified. Sequence analysis of yak Bogr-DQA revealed a total of 8 alleles, corresponding to two major groups, DQA1 and DQA2. A total of five Bogr-DQB alleles were also identified and among these, three DQB alleles were newly identified in yak.

An effort was made to mine transcriptome data to identify genes that were specifically induced or repressed across three physiological stages of buffalo mammary gland. A total of 2281 transcripts were found to be differentially expressed. The whole set of genes related to milk fat metabolism were up-regulated during lactation in comparison to involution stage of buffalo mammary gland. During involution, several genes related to apoptosis, immune and oxidative stress response were also found to be up-regulated.

mRNA expression of one of the major solute carrier (involved in active transport of glucose across the plasma membrane) SLC2A1 (GLUT1) was increased within the first 3 weeks of lactation. Another major solute carrier SLC2A8 (GLUT8) showed higher expression during mid lactation period, whereas, SLC2A4 (GLUT4) expression was significantly higher at peak lactation and low during early and mid stages of lactation period in Sahiwal cows.

An attempt was made to undertake comparative evaluation of cell proliferation and heat shock protein levels as indicators of thermotolerance at varying temperature-humidity index (THI) across Sahiwal cows (Indicus cattle), Karan Fries cows (Cross-bred), Holstein Friesian cows (Exotic) and Murrah buffalo. Serum concentrations of HSPs were found comparatively higher in Holstein Friesian and Karan Friesian cows to Sahiwal cows and Murrah buffaloes. Similar trend was observed for cortisol and TNF-α.

A large buffalo reference family of 10,000 daughters of 12 sires was created. The daughters were genotyped for 79 microsatellite markers situated on 8 chromosomes. Genotyping was done on the reference population using identified microsatellite markers. The phenotypic records

obtained were verified for normal distribution. The data was subjected to analysis using single marker analysis. The meta-QTL analysis was carried out using Biomercator. The QTL positions were identified and the regions were fine mapped using a large number of SNPs.

A total of 6.54 Lakh and 1.96 Lakh SNPs were identified in buffalo using reduced representation library and RNA seq, respectively. A total of 196669 SNPs were identified in the coding part of the genome. These SNPs were then validated using a 384 SNP data set using Golden Gate assay of Illumina. In RNAseq analysis the expression of genes included more than 800 genes directly associated milk and related traits.

Yak milk was analysed for fatty acid composition. Analysis of yak (*Bos grunniens*) milk showed it having a high content of total solids (16.9–17.9%), proteins (4.9–5.9%) and fat (5.5–7.5%). These values are significantly higher than those of cow and goat milk, but relatively similar to those of buffalo.

NBAGR is providing consultancy service of cytogenetic screening of breeding males to various agencies throughout the country with the aim to check the spread of chromosomal defects and to keep the herds free of such genetic defects as per the policy of Government of India. During the year a total of 372 breeding bulls were screened for their cytogenetic parameters.

Candidate genes for reproductive traits viz. KiSS1, GPR54, INHBB, JY-1 and AA-NAT were analyzed for identification of SNPs across nine indigenous goat breeds differing in reproductive traits and geographic distribution. Sixteen SNPs were found in the candidate genes. PCR-RELP protocol was standardized for five SNPs in KiSS1 gene and one SNP was found to be associated with litter size in Black Bengal goats.

Tetra-ARMS PCR and PCR-RFLP were standardized for genotyping mutations in BMPR1B, GDF9 and BMP15 genes in 391 pedigreed goat samples belonging to seven breeds (Black Bengal, Barbari, Beetal, Jhakrana, Osmanabadi, Sangamneri and Ganjam). Association of 4 novel SNPs was identified in different breeds of Indian goats in different parities.

At Core Lab, Chennai, genes with respect to draught parameters (IGF-1, ADRB2, GPX-1, VEGF-A, ACE- I, BDKRB2) were characterized in *Bos indicus* cattle- Kangayam, Umblachery, Pulikulam, Barghur, Hallikar and Ongole. A large number of SNPs were identified. Few SNPs from these candidate genes were found to exhibit association with different phenotypes recorded in draft cattle breeds.

At Core Lab, AAU, Khanapara, molecular characterization based on 25 microsatellites of three cattle populations from Assam, Manipur and Arunachal Pradesh was completed. All the 3 populations were distinct and totally unrelated from each other.

At Core Lab, Anand, candidate genes related to milk quality/ composition and milk yield in indigenous camel breeds were explored.

In the Bureau library, 43 journals (12 foreign and 31 Indian journals) were subscribed to keep track of the current scientific / technical developments.

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

At present 18 research projects including 4 externally funded and one National Fellow project are going on.

Total 8 patents were filed to the Patent Office, Delhi. Three patent applications, already filed in 2011 were published in the Indian Patent Office.

Technology "A Kit for parentage verification in Indian Ruminant Livestock" was commercialized.

Scientific findings were published through 33 research papers in national and international journals of high impact factor. Apart from this, 3 monographs and leaflets were also published.

Three scientists were deputed for overseas training under NAIP-HRD. Many scientists attended the workshops, symposia and conferences within the country.

A sports contingent of 34 members participated in ICAR Zonal Sports Meet (North Zone-2014) held at Indian Institute of Pulses Research, Kanpur (Uttar Pradesh) from 20th-23rd March, 2014. Volleyball smashing and basketball teams won gold and silver medals respectively. One silver and one bronze medals were also bagged for individual performance.

30th Foundation Day of Bureau, Biodiversity day, Republic Day and Independence Day were celebrated at NBAGR campus.

NBAGR in collaboration with Society for Conservation of Domestic Animal Diversity (SOCDAB), Karnal, organized a National Symposium on "Harmonizing Phenomics and Genomics for sustainable management of livestock for upliftment of rural masses" from 6-7th February, 2014 at NBAGR Karnal.

Bureau participated in various livestock and Dairy Fairs and installed exhibitions to showcase their activities.

A number of distinguished persons visited the Institute. His Excellency Lyonpo Yeshey Dorji, Minister for Agriculture & Forests, Royal Government of Bhutan interacted with scientists during their visit.

NBAGR scientist was conferred a prestigious award "Biotech Product and Process Development and Commercialization Award 2013" by Honourable President of India.

NBAGR scientists taught various courses in DCB and BAC Divisions of NDRI and also guided the students for masters degree.

At present, 30 scientific, 18 technical, 19 administrative and 5 skilled staff persons are working at the Bureau. Two persons including newly selected Director joined the Bureau. Two scientists and 4 technical persons were promoted to higher grades/posts.

Research Laboratory Wing on the first floor of the main building was inaugurated by Dr. S Ayyappan, Secretary (DARE) & DG (ICAR) on 11th February, 2014.

# History and Profile

- About Bureau
- Organogram
- Financial Outlay


NBAGR
अंतर्राष्ट्रीय जैव-विविधता दिवस समारोह
दिनांक : 22 मई 2014
स्थल : सभागार, प्रथम तल

## 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:

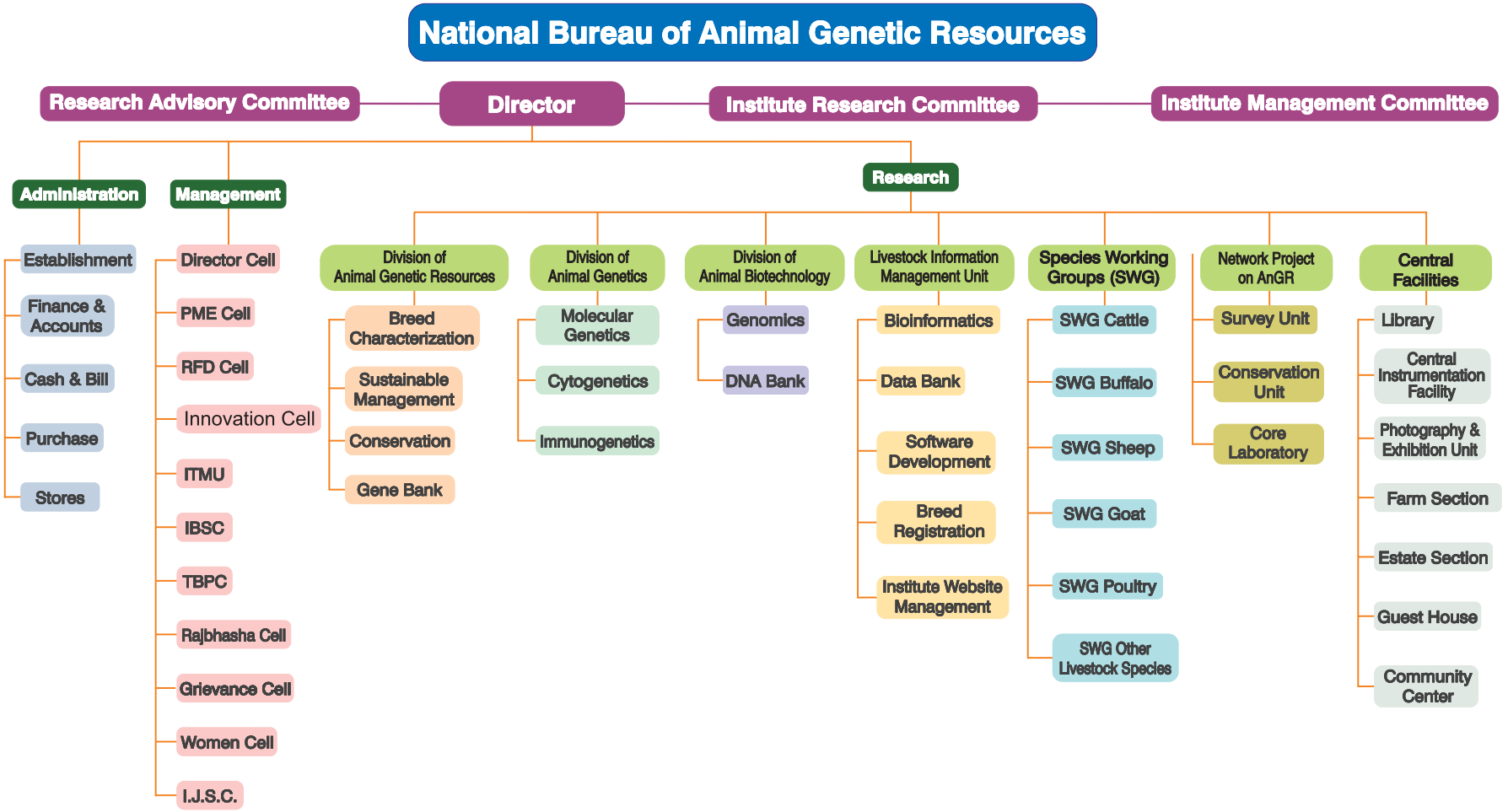
### MANDATE

**'Identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country.**

### 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.

# Organogram


National Bureau of Animal Genetic Resources
Research Advisory Committee
Director
Institute Research Committee
Institute Management Committee
Administration
Management
Research
Establishment
Finance & Accounts
Cash & Bill
Purchase
Stores
Director Cell
PME Cell
RFD Cell
Innovation Cell
ITMU
IBSC
TBPC
Rajbhasha Cell
Grievance Cell
Women Cell
I.J.S.C.
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
Species Working Groups (SWG)
SWG Cattle
SWG Buffalo
SWG Sheep
SWG Goat
SWG Poultry
SWG Other Livestock Species
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 Center

## Financial Outlay

**Budget Estimates (in Lakh) for Plan, Non-Plan & Network Project of NBAGR alongwith expenditures for the financial year 2013-14.**

| Sr. No. | HEAD | NON-PLAN | | PLAN | | Network Project | |
|---|---|---|---|---|---|---|---|
| | | Receipt | Expenditure | Receipt | Expenditure | Receipt | Expenditure |
| 01. | Capital | | | | | | |
| | i) Works | | | 41.43 | 41.43 | 0.00 | 0.00 |
| | ii) Other capital expenditure | 10.50 | 9.93 | 44.82 | 44.79 | 0.00 | 0.00 |
| | Total Capital | 10.50 | 9.93 | 86.25 | 86.22 | 0.00 | 0.00 |
| 02. | Revenue | | | | | 39.00 | 38.82 |
| | i) Establishment expenses | 621.20 | 621.09 | 0.00 | 0.00 | 0.00 | 0.00 |
| | ii) Traveling Allowance | 2.50 | 2.50 | 12.00 | 12.00 | 0.00 | 0.00 |
| | iii) Research & Operational expenses | 34.00 | 33.31 | 89.00 | 88.55 | 0.00 | 0.00 |
| | iv) Administrative Expenses | 76.24 | 76.22 | 117.00 | 116.98 | 0.00 | 0.00 |
| | v) Miscellaneous expenses | 8.00 | 8.00 | 3.00 | 2.98 | 0.00 | 0.00 |
| | Total Revenue | 741.94 | 741.12 | 221.00 | 220.51 | 39.00 | 38.82 |
| 03. | Pension & Retirement benefits | 5.00 | 4.99 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Grant Total | 757.44 | 756.04 | 307.25 | 306.73 | 39.00 | 38.82* |

* includes releases of Rs. 32.00 lakhs.

**Revenue generated (in Lakh) during the year 2013-2014**

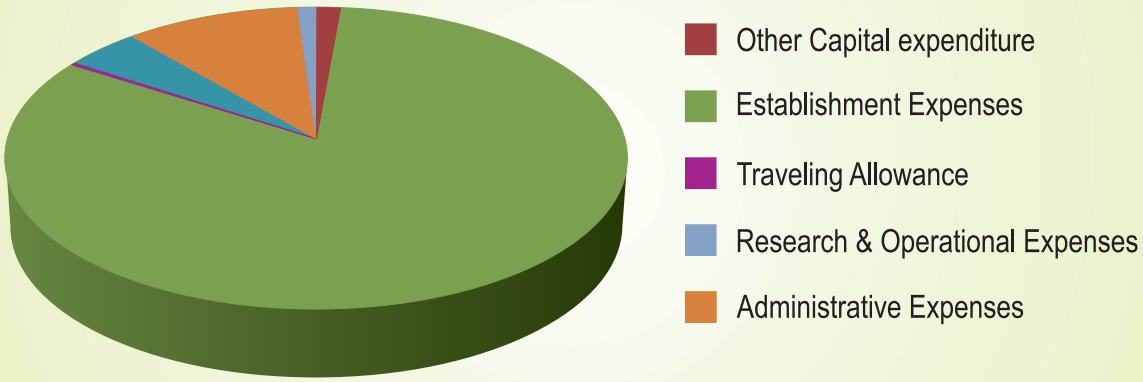
| Sr. No. | Head of Account | Amount |
|---|---|---|
| 1. | Sale of Publication & Advertisement | 0.54 |
| 2. | Licence fee | 1.70 |
| 3. | Training Programs - Income | 1.45 |
| 4. | Hostel and Guest house rent | 3.27 |
| 5. | Sale of Technology | 1.39 |
| 6. | Sale of farm Produce | 7.14 |
| 7. | Others Misc. Revenue Receipts | 17.66 |
| | Total | 33.15 |

**Revenue Target Fixed : 27.70 Lakhs**

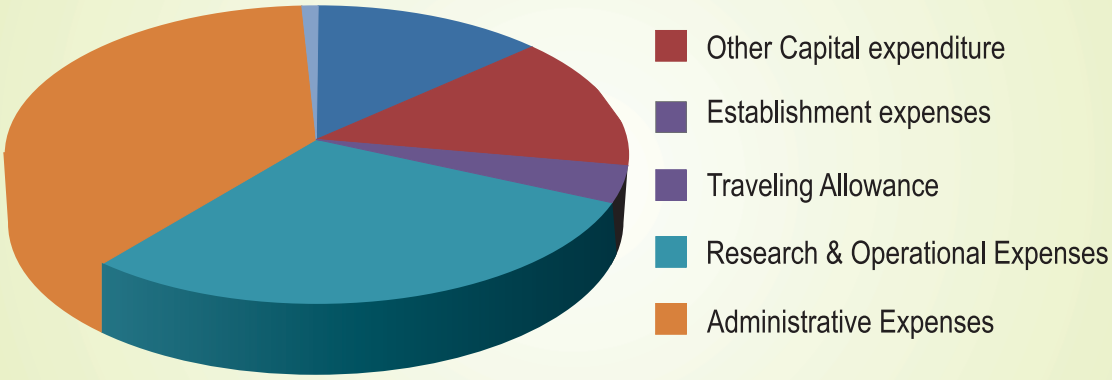
**Target Achieved : 33.15 Lakhs**

FINANCIAL OUTLAY

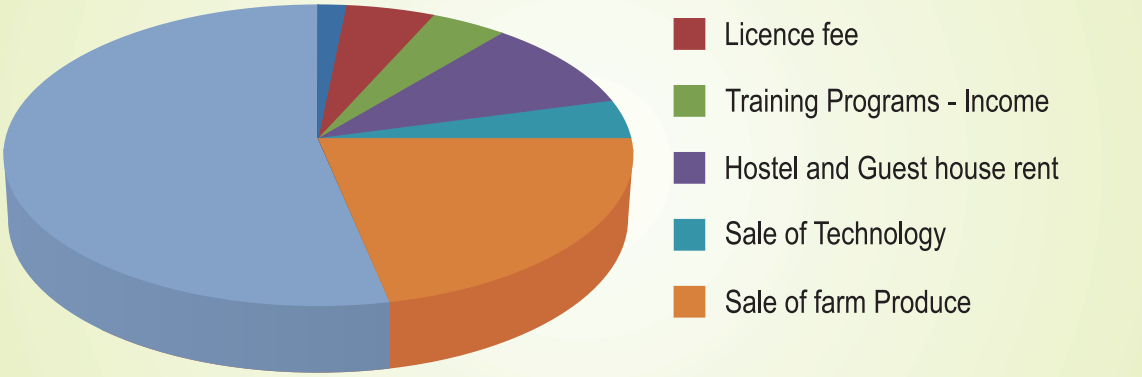
## Funds Utilization under Non-Plan




## Funds Utilization under Plan




## Revenue Generated




2013-14

# Research Accomplishments

- Livestock Information Management
- Phenotypic Characterization and Conservation
- Genetic Characterization and Functional Genomics
- Network Project on AnGR

## Livestock Information Management

**Establishment of National Agricultural Bioinformatics Grid (NAIP):** High Performance Computing (HPC) system has been installed in the Computer Center at the Institute. The system is a Linux cluster equiped with one master node, one login node, 16 compute nodes, 20 terabytes of Network attached storage and 20 terabytes of file system storage. Bioinformatics software including CLC-Bio Genomic Server, Discovery studio has been installed on the HPC for performing a number of genomic and proteomic data analysis.

**SNP density in cattle milk trait genes:** A study has been taken on evaluation of SNP density on genomic DNA of 12 genes in cow involved in milk traits that included ABCG2, APOD, BTG3, DGAT1, CSN3, CSN1S1, LEP, PRL, LTF, CLDN8, CXCL14 and GHR. Homologous genes were considered in five other mammalian species - human, mouse, pig, cow, dog and horse. Chromosome positions and genomic sequences for milk genes were retrieved from Ensembl database. Multiple sequence alignments of transcripts of the genes in 45 vertebrate species were downloaded from UCSC genome browser. Multiple sequence alignment of combination of genomic sequences of genes and transcript alignments were performed using *Kalign* tool available on NCBI website. SNPs data for the genes was retrieved for the six species from Ensembl variation databases. The data was collated using MS-Excel for calculating position of SNPs on genomic sequences of genes. Programs in C++ were executed to place the SNPs on MSA of genomic plus transcript sequences, to extract SNP positions from the MSA, and to locate start and end positions of exons in the MSA. An R-script was executed to plot the SNP positions as well as exons on the MSA. The homology based study using genomic sequences of milk genes will be helpful in focusing on SNP rich areas of the genomic DNA of livestock species.

**Comparative analysis of large phylogeny estimation methods:** Size of homologous sequence datasets has increased manifold in recent years, involving several hundreds of taxa leading to large scale phylogeny. Large phylogeny estimation is a hard optimality-criterion-based phylogeny inference, which is computationally intensive. It has application in meta-genomic studies such as animal rumen and fecal micro-biota. For the comparative analysis, software for three popular phylogeny estimation methods - RAxML, PhyML and MetaPiga were downloaded and installed on HPC system. The software were executed on simulated nucleotide benchmark datasets of size 100 taxa with long (L1), medium (M1) and short (S1) gap length. It included five instances of each dataset available at http://www.cs.utexas.edu/users/phylo/sate/public/sate_journal.html. Each dataset was having a true alignment file in fasta format and a true tree for inference in Newick format called PIMT (Potentially Inferable Model Tree) for comparison. Phylogenetic trees were compared with respect to accuracy and consistency. Results of each estimated tree were then compared with the PIMT using Ktreedist software, which calculates and compares minimum branch length score and symmetric difference (Robinson-Foulds/RF distance). K-score of 100L1 dataset for Metapiga, PhyML and RAxML programs were 1305.59, 220.15 and 223.15, respectively. The values of symmetric difference for 100S1 dataset

for the three methods were 186.4, 12.8 and 16, respectively. The study shows that phylogenies of size 100 taxa can be estimated using PhyML with little degradation in tree accuracy as compared to RAxML. Performance of MetaPiga with very high K-score and symmetric difference was poor in these experiments.

**Comparison of three phylogeny estimation methods (taxa of size 100)**

| Dataset | Phylogeny Estimation Method | Mean K-Score | Mean Symmetric difference |
|---|---|---|---|
| 100S1 | Metapiga | 830.87 | 186.4 |
| | PhyML | 220.15 | 12.8 |
| | RAxML | 120.2 | 16 |
| 100M1 | Metapiga | 1408.67 | 186.4 |
| | PhyML | 220.5 | 20.8 |
| | RAxML | 222.46 | 20.8 |
| 100L1 | Metapiga | 1305.59 | 186.8 |
| | PhyML | 220.15 | 12.8 |
| | RAxML | 223.15 | 13.2 |

**Tissue specific *in-silico* SNP mining from EST's in livestock species:** EST data for skin, spleen, mammary gland, liver tissues for pig, and spleen, intestine and mammary gland tissues of cow were retrieved from NCBI website. ESTs were processed using the online tool EGassembler, which performs all the task of quality checking as one operation. RepBase repeats library for a species was used to mask the repeats and NCBI's core vector library was used to mask the vector sequences. EST sequences were then assembled into contigs using the CAP3 tool. Contigs were analyzed for SNPs using freely available QualitySNP tool, which has the benefit that it does not require quality files and the reference sequence for SNP detection. SNPs were searched for their presence in the dbSNP database. This was performed by searching contigs in genome assembly of respective species using *blat* tool in UCSC genome browser. Aligned contigs and chromosome segment were matched for SNP positions on a chromosome. Subsequently, SNPs were searched for their availability in dbSNP database by writing Perl scripts. The number of SNPs in skin tissue of pig was 3444, of which 421 were available in dbSNP database.

**Tissue-wise SNPs in pig and cow**

| Livestock species | Tissue | Number of EST Sequences | Number of Contigs | Number of SNPs | SNPs in dbSNP database |
|---|---|---|---|---|---|
| Pig | Skin | 50410 | 6476 | 3444 | 421 |
| | Spleen | 73312 | 7575 | 5032 | 595 |
| | Mammary Gland | 23061 | 1545 | 1688 | 74 |
| | Liver | 129323 | 17941 | 17083 | 2246 |
| Cow | Mammary gland | 106150 | 8189 | 10150 | 43 |
| | Spleen | 25781 | 4890 | 3690 | 15 |
| | Intestine | 3010 | 394 | 192 | 0 |

Subsequently, a database on tissue-wise SNPs was developed using MySQL. Perl scripts were written to parse and fill the tissue-wise SNPs data in the database. Web interface was developed using PHP language. User can query the database by species name, tissue name, chromosome name and gene name. Output options are also available to filter the search. Output field settings include dbSNP-id, gene name, chromosome name, contig and contig-sequence. Records of tissue-wise SNPs are also linked to Ensembl and dbSNP databases for genes and SNPs.

## Phenotypic Characterization and Conservation

### Sanchori cattle

Sanchori cattle are mainly distributed in Sanchore, Bhinmal and Raniwada tehsils of Jalore district of Rajasthan. Physical traits were recorded on 151 cows and 19 bulls from the breeding tract. The coat colour of cows was mostly white (74.2%) or grey (23.2%) whereas for bulls, it was white (15.8%), grey (68.4%) and black (10.5%). Muzzle and tail switch were mostly black. The horn size was smaller in length as well as circumference as compared to Kankrej or Nari cattle found in that area. The horn colour was black (70.6%), creamy (15.9%) or mixed (13.5%). The orientation of horn was outward, upward and inward ending with pointing tips in majority of cases (73.5%). The orientation of ear was horizontal (75.9%) but sometimes slightly drooping (24.1%). In cows the hump was of medium size (79.5%), dewlap was large (86.1%) and naval flap was medium (59.6%). The shape of udder was either pendulous (88.6%) or round (11.4%). The teats shape was mostly cylinderical (90.9%) ending with rounded tips (77.3%). The animals were kept in open houses adjacent to the farmers' house made in the agricultural fields called '*Dhanis*'. Animals were kept on grazing for 6-8 hours in a day in the nearby agricultural fields along with the stall feeding of 2-6 kg (average 4.18 kg) concentrate, 5 to 15 kg dry fodder (average 10.33 kg) and 2-12 kg green fodder (4.13 kg) per day. Breeding was natural and a few farmers opted AI by using Kankrej semen. The average body length, height at withers, chest girth, paunch girth, face length, ear length, horn length, horn circumference, tail length and tail length without switch of cows were obtained as 129.3±0.65, 122.95±0.34, 167.03±0.75, 183.5±0.97, 44.07±0.20, 31.66±0.17, 32.01±0.60, 22.87±0.28, 117.94±0.70, 87.95±0.58 cms, respectively. Whereas in bulls/bullock the corresponding values were 137.86±0.68, 138.57±0.35, 188.7±1.02, 199±1.43, 46.85±0.18, 32.5±0.1, 42.21±0.73, 21.38±0.20, 129±0.68, 94.6±0.68 cms, respectively.

*Sanchori bull*

*Sanchori cow*

The age at first calving varies between 3-4 years (average 39.5 months) and the bull becomes sexually matured at the age of 2.5 to 3 years. The calving interval was found to be 14.5 months ranging from 12 to 20 months. In Sanchori cattle good milk production potential was observed as peak milk yield was reported to be 6-18 kg per day in a lactation period ranging from 8-15 months (average 10.16 months). Daily milk yield of 276 cows in different months and order of lactation was recorded. The overall daily milk yield was obtained as 9.08±0.16 litres per day. The cows in first to tenth month of lactation yielded an average of 9.76±0.57, 10.71±0.39, 10.64±0.30, 9.78±0.33, 9.76±0.32, 8.58±0.40, 7.40±0.28, 6.42±0.69, 6.05±0.50, 5.0±0.40 litres of milk in a day, respectively. The life span of cows was reported to be 22-25 years with lifetime calvings of 12 to 15.

Morpho-metric traits of Sanchori cattle

| Trait | Cows (153) | Bulls/ Bullock (14) | Calves (107) | Males (1-3 Y) (11) | Females (1-3 Y) (29) |
|---|---|---|---|---|---|
| Body Length (cm) | 129.3±0.65 (6.25%) | 137.86±0.68 (6.95%) | 82±0.10 (13.67%) | 104.82±0.43 (4.55%) | 113.72±0.34 (8.77%) |
| Height at withers (cm) | 122.95±0.34 (3.37%) | 138.57±0.35 (3.51%) | 88.13±0.09 (11.47%) | 108.18±0.39 (3.98%) | 114.90±0.27 (6.94%) |
| Chest Girth (cm) | 167.03±0.75 (5.56%) | 188.7±1.02 (6.49%) | 97.91±0.14 (14.76%) | 128±0.69 (5.92%) | 144.96±0.54 (10.39%) |
| Paunch Girth (cm) | 183.5±0.97 (6.53%) | 199±1.43 (8.61%) | 100.07±0.15 (16.42%) | 131.18±0.96 (8.05%) | 150.93±0.60 (11.05%) |
| Face Length (cm) | 44.07±0.20 (5.53%) | 46.85±0.18 (5.07%) | 27.73±0.06 (24.60%) | 35.09±0.37 (11.50%) | 39.45±0.12 (9.05%) |
| Ear Length (cm) | 31.66±0.17 (6.74%) | 32.5±0.1 (4.31%) | 24.28±0.03 (13.44%) | 28.27±0.24 (9.37%) | 30.10±0.09 (8.89%) |
| Horn Length (cm) | 32.01±0.60 (22.87%) | 42.21±0.73 (24.36%) | -- | 8.40±0.41 (48.99%) | 13.96±0.25 (48.63%) |
| Horn Circumference (cm) | 22.87±0.28 (14.71%) | 21.38±0.20 (11.85%) | -- | 14±0 (0%) | 19.73±0.23 (17.60%) |
| Tail Length (cm) | 117.94±0.70 (7.27%) | 129±0.68 (5.30%) | 65.72±0.12 (19.50%) | 96.27±0.49 (5.63%) | 105.96±0.45 (10.97%) |
| Tail length without switch (cm) | 87.95±0.58 (8.14%) | 94.6±0.68 (7.14%) | 55.66±0.08 (15.96%) | 75.45±0.63 (9.15%) | 79.93±0.36 (12.53%) |

## Manipuri cattle

Surveys were conducted in 13 villages of three districts (Imphal east, Imphal west and Churachandpur) of Manipur state to characterize indigenous cattle of the state. A total of 363 animals of different age, sex were included in the study.

Indigenous cattle of Manipur are non-descript type. They are of small size, well built, stout, hardy and in cylindrical shape. The different coat colours observed were dark brown (48%), light brown (28%), black (12%), grey (4%) and spotted with black or white patches on brown body (8%). The birth weight ranged from 8 to 15 kg. The estimated average body weights in cow and bullock were 176 kg and 175 kg, respectively. Daily milk production ranged from 2.0 to 4.50 kg. The average per day milk yield was 2.65±0.18 kg. A pair of bullock may plough about 1.0 acre of land in 6-8 hours. The age at first calving, lactation length, dry period, service period, calving interval, herd life and number of calving during life time ranged from 30-45 months, 120-270 days, 6-9 months, 3-9 months and 12-18 months, 12-15 years, 6-8 calving, respectively. Eight different body measurements were recorded on 363 animals of different age and sex. All the data were analyzed according to age and sex. The average body length, height at wither, heart girth, paunch girth, horn length, ear length, face length and tail length without switch in cows (176) were 100.32±0.59, 106.22±0.51, 137.69±1.01, 142.12±0.98, 11.85±0.38, 19.59±0.17, 38.06±0.2 and 74.30±0.50 cm, respectively. Herd size ranged from 2 to 20. Animals were kept mainly on extensive system of management i.e. grazing from morning to evening. Cattle were reared mainly for bullock power and manure (100%), however, around 18% farmers kept them for milk. Breeding was natural. Milking was once in a day i.e. morning. Vaccination of animals was done for HS, FMD and BQ.

## Belahi cattle

Daily milk production, growth and reproduction data for Belahi cattle was recorded under field (Ambala and Panchkula districts). Average weight at birth was estimated as 17.6 ± 0.51 kg in males and 15.2 ± 0.58 kg in females, the 3 month weights were 31.6 ± 1.22 and 33.75 ± 1.42 kgs and adult body weights were 304.8 ± 1.35 and 266.74 ± 2.15 kg in males and females, respectively. Overall average daily milk yield and 305 day milk yield were estimated as 3.25 ± 0.15 kg and 1014.43 ± 45.46 kg respectively, in 79 cows belonging to 5 herds.

*Adult female Belahi cattle with calf*

## Gojri buffalo

Survey was conducted to identify and evaluate new indigenous buffalo population under migration in Himachal Pradesh and Punjab states. Physical appearance of Gojri buffaloes include black coat colour with brown thick hairs; white patches may be present on black face, and muzzle is black in colour. Males are brownish to black in colour. Horns are medium to large sized with curved orientation which moves backwards and then towards front to complete the loop, locally called '*Pattih wale seengh*'. Udder is small round shaped but well-placed with cylindrical teats and milk vein is visible. Gujjar community rear these buffaloes and majority of them were Muslims. Livestock rearing is their primary occupation. Gojri buffaloes graze for about 6-7 hours/day among hill top and hilly terrains in Himachal Pradesh but livestock keepers from Punjab region do not migrate and their animals are stall fed. Gojri buffaloes are reared for milk, draft power and manure/dung. The males are used for agriculture and transport etc.

Biometrics estimates of 33 males and 200 females for height at withers, body length, chest girth, paunch girth, face length, face width, horn length, horn circumference, ear length, hip bone, pin bone, tail length and tail up to switch were calculated and are presented in table. The

*Adult female Gojri buffalo*

*Gojri buffaloes under migration*

average mean height, chest girth and body length reported for Murrah and Nilli Ravi, indicated that Gojri buffalo is lighter, smaller and shorter than these.

**Morphometric measurements (cms) of adult Gojri buffalo**

| Character | Male | Female |
|---|---|---|
| Height at withers | 136.63 ± 1.22 | 128.66 ± 0.32 |
| Body length | 138.91 ± 1.59 | 133.33 ± 0.35 |
| Chest girth | 203.47 ± 1.99 | 195.91 ± 0.67 |
| Paunch girth | 230.88 ± 2.48 | 213.91 ± 1.34 |
| Face length | 48.97 ± 0.44 | 48.58 ± 0.11 |
| Face width | 24.50 ± 0.36 | 22.33 ± 0.09 |
| Horn length | 35.75 ± 1.32 | 44.61 ± 0.61 |
| Horn circumference | 21.41 ± 0.48 | 19.82 ± 0.12 |
| Ear length | 29 ± 0.16 | 28.76 ± 0.09 |
| Hip bone | 55.38 ± 0.57 | 53.58 ± 0.24 |
| Pin bone | 23.63 ± 0.56 | 24.29 ± 0.29 |
| Tail length | 95.81 ± 1.44 | 90.57 ± 1.15 |
| Tail up to switch | 109.16 ± 1.31 | 104.15 ± 0.67 |

## Singharey goat of Sikkim

The goat population of Sikkim state of NEH region of India is 110120 (18th livestock census, 2007) spread in all the four districts i.e. East Sikkim (18046), West Sikkim (45232), North Sikkim (15018) and South Sikkim (31824). The males and females are almost in equal proportion (56349 and 53771, respectively).

Local goat of sikkim was characterized through survey in East and West districts of Sikkim. Information on phenotypic and biometric traits of native goats and their management was collected. Although the flocks seen consisted of black, white, brown and mixture of these colours but goats with stripes on face extending from base of horn to the muzzle mainly constituted the flocks. These goats are called as 'Singharey' by the local people. These goats have been surviving in the Himalayan terrain of Sikkim since ancient times. Singharey goats are small to medium sized having coat colour varying from tan or light brown to brown with a mixing of grey/white hair. In breeding males, black ring is present around the neck but not in castrated males.

The horns are strong orienting upward and backward. The under belly is generally light brown or white. Ears are medium, semi pendulous and have white margin. Legs are short, stout, medially black or white. Black top line is seen in many of goats. The flock size with a farmer varies from 2 to 15.

Mean body measurements for height at withers, body length, chest girth, paunch girth, face length, horn length, ear length and tail length were 54.71±0.73, 61.44±0.69, 66.75±0.66, 71.31±1.16, 15.98±0.17, 9.53±0.39, 13.05±0.31, 11.15±0.20 respectively in adult female goats (n=50). The corresponding estimates in adult male animals (n=68) were 57.78±0.90, 62.97±0.90, 72.25±0.77, 76.56±1.11, 17.50±0.22, 15.21±0.51, 13.21±0.19, 12.26±0.23 respectively. The adult body weights in female and male goats are 26.68±0.71, 32.00±0.90 kg, respectively.

*Coat colors of Singharey goat*

Singharey goats have moderately developed udder but with small teats. Milk production is approximately 300–500 ml per day. However, milking of goat is not practiced on regular basis. The gestation period ranges between 145-155 days. Twinning is very common in these goats. Breeding is through natural mating. In the border regions cross breeding with Black Bengal was observed. In majority of cases the males are castrated at younger age.

These goats are maintained on semi-extensive management by small and marginal farmers of Sikkim mainly for meat purpose. Goat houses are temporary structures and are made of bamboo sticks and wooden logs with no proper arrangement of electric and water supply. Goats are kept on local vegetation available in the jungle. Stall fed goats are kept on local grass, maize and tree leaves.

## Ecotypes of Deccani sheep

Three ecotypes (Solapuri, Madgyal and Kolhapuri) of Deccani sheep in Maharashtra were surveyed in Solapur, Sangli and Kolhapur districts, respectively. Coat colour varied from white with brown patches/spots in Madgyal to black with white patches in Solapuri. Kolhapuri sheep were mottled. Majority of Solapuri sheep were black but some animals had white patches on forehead and hind legs. Kolhapuri sheep were black mingled with varying shades of brown and off white. The head, face, belly and legs were devoid of wool. Madgyal and Solapuri ecotypes were large, tall and long as compared to Kolhapuri. All the ecotypes had a straight backline and a medium length thin tail. Madgyal and Solapuri sheep had a typical roman nose as judged against Kolhapuri. Some males were horned in Solapuri but females were polled, while some Kolhapuri ewes had thin horns. Wattles were present in some of the Solapuri sheep.

*Kolhapuri sheep*

*Madgyal sheep*

*Solapuri sheep*

Substantial sexual dimorphism was observed in Madgyal, Solapuri and Kolhapuri ecotypes. The body weight of ewes were 44.7, 37.0 and 31.8 kg respectively and the corresponding sexually dimorphism were 1.29, 1.49 and 1.36 respectively. Non significant differences between ear lengths of both sexes were observed. Presence of collinearity was indicated between 'wither height' and 'rump height' traits. Principal Component Analysis provided an objective description of the body shape and size, and concise picture of morphological structure of the Madgyal sheep

## Kajali sheep

Kajali, a lesser known sheep population is distributed in Sangrur, Barnala, Ludhiana and adjoining districts of Punjab (India) and primarily reared for mutton production. The coat colour of Kajali is primarily white but dark brown and black animals were also found. Out of total animals surveyed 84.26% animals are with white coat colour and black face and ear. The dark brown to black colour in the face and ear is spread over with varying degree even up to 95 %. The name of the breed 'Kajali' is derived from black circles around the eyes; which is the distinguishing characteristics of this breed; this black circle is even found in dark tan or brown face animals. The Kajali sheep have Roman nose, long and pendulous ears and long tail touching to ground. Both sexes are polled, however in some males, horns were also noticed. The animals are found to be large in size with well built body. The adult body weight of males and females was 55.95 ± 2.24 and 42.83 ± 2.24 kg, respectively, which varies from 30 to 70 kg in males and 26 to 58 kg in females. The average body length, height, chest girth, ear length, face length and tail length in females were 70.32 ± 0 .49, 71.52 ± 0.36, 84.00 ± 0.49, 22.15 ± 0.22, 21.27 ± 0.80 and 52.76 ± 0.92 cm, respectively and corresponding figures for males were 77.86 ± 1.12, 76.95 ± 1.19, 91.00 ± 1.34, 22.68 ± 0.43, 23.05 ± 0.37 and 58.41 ± 0.02 cm, respectively. The flock size varies from 5 to 70. Most of the farmers kept 1 to 3 breeding rams. Farmers also maintained Munjal sheep but majority of the farmers used Kajali rams for breeding. Percentage of Kajali and other breeds was 64.52 and 35.48, respectively. The animals are grazed about 6-8 hrs a day from 10 AM to 6 PM and the distance covered for grazing is 2 to 10 km. The lambing percentage was 70–80 with about 6% twining. The age at maturity in males was 12–15 months and in females it was 15 to 18 months. The preliminary results indicate that the Kajali sheep is phenotypically different from other sheep breeds of the region.

*Kajali sheep*

*Kajali lambs*

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

| Traits | Adult body weight | Body Length | Height | CG | EL | FL | TL |
|---|---|---|---|---|---|---|---|
| Overall | 45.69 ± 0.90 (101) | 71.91± 0 .54 | 72.67 ± 044 | 85.48 ± 0.56 | 22.26 ± 0.20 | 21.65± 0.19 | 53.96 ± 0.87 |
| Male | 55.95 ± 2.24 (22) | 77.86 ± 1.12 | 76.95 ± 1.19 | 91.00 ± 1.34 | 22.68 ± 0.43 | 23.05 ± 0.37 | 58.41 ± 2.02 |
| Female | 42.83 ± 0.67 (79) | 70.32 ± 0.49 | 71.52 ± 0.36 | 84.00 ± 0.49 | 22.15 ± 0.22 | 21.27 ± 0.80 | 52.76 ± 0.92 |

Figures in parentheses indicate number of observations

## Harringhata Black chicken

Performance recording was done from day old stage onwards from Harringhata Black birds maintained by 150 households in the breeding tract. Information on population of Harringhata Black, flock structure and size, management practices, disease prevalence and vaccination practices were recorded from 2509 households spread over 17 Gram Panchayats of

*Harringhata Black hen*

Haringhata and Chakdaha block in Nadia and Habra-II, Gaighata, Amdanga and Bongaon in North 24 Pargana districts. Mortality, growth, reproduction and production parameters were also recorded.

Backyard poultry in the breeding tract of Harringhata Black breed is managed mainly by women (99.7%) and is used both for meat and eggs. Birds are kept in the free range system. Small *kutcha* sheds are made to provide shelter during night. These birds scavenge in the nearby fields; eat whatever available in the form of grains, seeds, vegetation, insects, etc. This is supplemented with kitchen waste and paddy grains but no commercial feed is given.

About 34 percent of the poultry keepers were landless who owned about 35 percent of birds with a flock size of 8.17, while 48 percent had up to 0.5 acres of land and owned about 45 percent of birds with a flock size of 7.37. Average flock size was 7.9, which included 3.25 Harringhata Black birds. On an average, a flock consisted of 62% chicks, 33% hens and 5% cocks. Estimated population of Harringhata Black in the breeding tract is 63600.

Broodiness is usual but to maximize the egg production, farmers don't practice it every time. Farmers set eggs of 3-4 hens under one broody hen for hatching and other broody hens again start egg production after few days.

Plumage colour is black. Some cocks have brown feathers on neck and wings. Comb is red and mainly single. Earlobe is red or white. Beak is blackish in appearance. Wattles are small and red in color. Shank color is blackish grey or yellow. Few birds had tuft of feathers on head. Body weight at 10 months of age was 1.1 kg in hens and 1.3 kg in cocks. Average age at first egg was 5.63 months. Average laying period, incubation period and brooding period was 15, 20.36 and 63.52 days, respectively. Average number of eggs per cycle was 12.32 and annual egg production was 45 with brooding and 98 without brooding. Average number of chicks per hatch was 9.45 and hatching percentage was 77.4 on total egg basis.

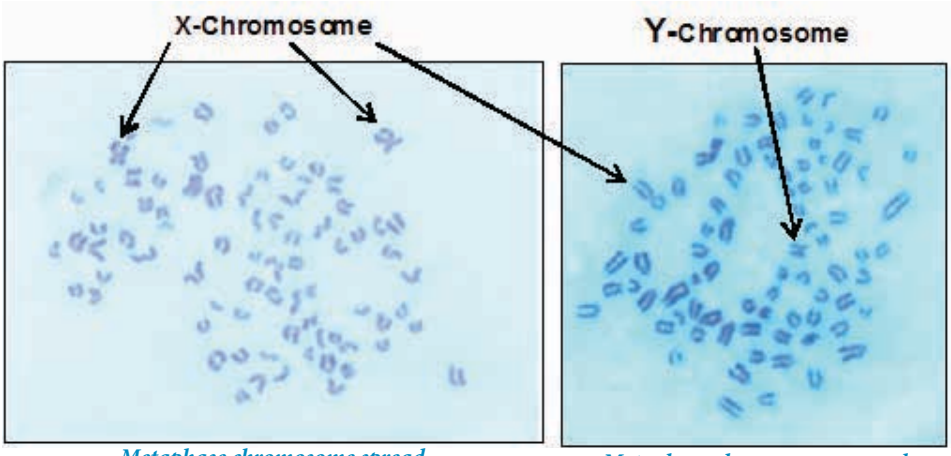
## Rajapalayam dog

The survey on Rajapalayam dog breed was conducted in Dog Breeding Unit, Chennai, Rajapalayam and villages of Rajapalayam taluk of Virudhunagar district of Tamil Nadu.

Rajapalayam dogs are medium in size with compact body, tucked-up abdomen with white coat color and pink skin, nostrils and eyelids, with semi-dropping ears, semi-curved tail and straight top-line. Eyes are golden in color and the nasal bridge is straight.

The mean height at withers, body length, chest girth, punch girth (in cms) and body weight (kg) of adult dogs (n=78) were 59.218±0.510, 56.019±0.422, 64.013±0.579, 47.308±0.646 and

*Rajapalayam- bitch*




*Metaphase chromosome spread of Rajapalayam bitch*

*Metaphase chromosome spread of Rajapalayam dog*

22.064±0.447, respectively. In bitches age at first oestrous ranges from 12- 15 months with duration of estrus ranged 13-21 days and normally mated on 9th, 11th & 13th day after estrous bleeding. The main breeding season is November to January, gestation length is 2 months, age at first whelping ranges 21-27 months with a whelping interval of 8-12 months and number of whelping in lifetime is 10 to 12. The litter size ranges from 4-10 and age at weaning is 30-45 days.

The dogs are maintained mostly with non-vegetarian food, feeding once in a day along with milk, rice and egg. The animals are hardy and reported to be resistant to communicable diseases. Breeders vaccinate the dogs regularly with seven in one mega vaccine and anti-rabies along with regular de-worming. There is high demand for Rajapalayam puppies from different sectors of the society, the price ranges from Rs 2,750 to 15,000 for a pair of puppies (one male + one female). Rajapalayam dogs are mainly used for guarding of farm and farm houses.

Chromosome analysis of Rajapalayam dog revealed common fundamental number (2n=78), with 38 pairs of acrocentric autosomes, one large sub metacentric X chromosome and a small sub metacentric Y chromosome.

## Harmonizing biodiversity conservation and agricultural intensification through integration of plant, animal and fish genetic resources for livelihood security in fragile ecosystem (NAIP)

The project was operated in Udaipur (Rajasthan), Chamba (Himachal Pradesh) and Adilabad (Andhra Pradesh) districts. Baseline survey indicated that animal production system is low-input low-output and livestock constituted important component of agriculture in all the three districts. Various activities undertaken included phenotypic characterization of AnGR, awareness generation through organization of animal biodiversity fairs cum health camps, interaction with the line department, improvement and conservation of native livestock breeds, and generation of sustainable fund. To begin with cattle, buffalo, goat, sheep and native poultry were undertaken for their improvement and conservation using native/improver breeds. Native cocks, hens and chicks were supplied to the farmers to enhance their livelihood security. Improvement of goats in all the three districts was identified as a major intervention while improvement of backyard poultry production in Udaipur, Gaddi sheep

in Chamba and local cattle in Adilabad was continued. NBAGR procured and supplied 88 Sirohi bucks, 2 Gir bulls, 180 native cocks and 1776 chicks in Udaipur district; 93 Gaddi bucks, 35 Gaddi rams and 1000 Murrah semen doses in Chamba ; and 54 native bucks, 8 native bulls, 170 chicks and 1750 semen doses in Adilabad for improvement and conservation of livestock breeds. Impact assessment was undertaken by consortium partners. Sustainable funds have also been generated under the subproject to continue conservation and improvement activities after completion of the sub project.

## Utilization of caprine cauda epididymal spermatozoa for cryopreservation

To maximize the utilization of epididymal sperms for conservation, the testis from slaughtered bucks were brought to laboratory within two hours. The epididymis were washed with normal saline and kept in a polybag at 5$^{O}$C. The epididymis was cut open and kept in a buffer solution for 20 minutes after 24, 48 and 72 hours of epididymis storage. The sperm motility (%) at these time intervals was 85, 69 and 51 respectively. The live sperm proportion (%) at these time intervals was 89, 85 and 85. The proportion of coiled tail increased during this time period, whereas cytoplasmic droplets decreased. These results indicate suitability of utilizing epididymal sperms for their conservation even after extended hours post slaughtering of bucks.

## Conservation (*Ex situ*)

A total of 15,821 frozen semen doses of 8 breeds of different livestock species have been procured and added to repository in GeneBank during this year. The National GeneBank at NBAGR now stores about 1,28,074 frozen semen doses belonging to forty one breeds of seven species -cattle, buffalo, goat, sheep, camel, equine and yak.

**Semen doses added in Gene Bank**

| Species | Breed | No. of males | Semen doses |
|---|---|---|---|
| Cattle | Tharparkar | 5 | 13,000 |
| Goat | Osmanabadi | 9 | 491 |
| | Assam Hill | 5 | 500 |
| Equine | Zanskari | 2 | 330 |
| | Marwari | 2 | 160 |
| | French Donkey | 4 | 240 |
| Yak | Arunanchali | 1 | 100 |
| Buffalo | Mehsana | 5 | 1,000 |
| Total | | 33 | 15,821 |

# Genetic Characterization and Functional Genomics

## Genetic characterization of Belahi cattle

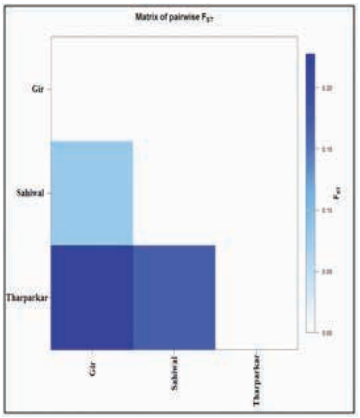
Genetic characterization of Belahi cattle was carried out using microsatellite based genotyping. Data for microsatellite markers (INRA35, ILSTS005, INRA05, INRA63, BM1824, ILSTS11, CSSM60, CSSM66, TGLA122, MM12, CSSM33, MM8, ILSTS06, CSSM8, TGLA227, HEL1) was generated on 48 samples of Belahi cattle. The mean observed and effective number of alleles were found to be 9.31 and 4.38 respectively. The candidate genes affecting the milk production traits bGH (Intron-3), PRL (Exon-3), κCN (Exon-4), $\alpha s_1$CN (5' NCR), αLA (5'region-Intron-1), βLG (Exon-4 to Intron-4), Pit1 (Exon-5 & 6), BTN1 (Exon-7), BTN3 (Exon-2- Exon-3), bCN (Exon-7) and DGAT1 (Exon-7) were PCR amplified using primers available in the literature for the candidate genes and RFLP based characterization was done in 50 samples of Belahi cattle. The gene and genotype frequencies were estimated for above 11 genes in Belahi cattle.

## Breed signature for Sahiwal, Gir and Tharparkar cattle

Data generated for 75 loci was analyzed and to prune the list of loci differentiating the populations, 51 loci were considered which were able to differentiate the 3 breeds. Across 3 cattle breeds, the observed number of alleles per locus ranged from 7 to 25 with a mean value of 15.61±0.72 and effective number of alleles ranged from 1.49 to 10.15 with an average value of 5.06±0.30. The mean observed heterozygosity was 0.58 while the mean expected heterozygosity was 0.76. Observed heterozygosity values were less than expected heterozygosity across 3 breeds.

The results of analysis of molecular variance (AMOVA) revealed 13.74% variation attributed to between breeds. Pairwise $F_{ST}$ values were estimated between each pair of breeds, which revealed that Gir and Tharparkar were genetically more differentiated (22.7%) and least differentiation (7%) was observed between Gir and Sahiwal. Pairwise $F_{ST}$ values are depicted graphically below, which showed distinction of Tharparkar from rest of the cattle breeds.

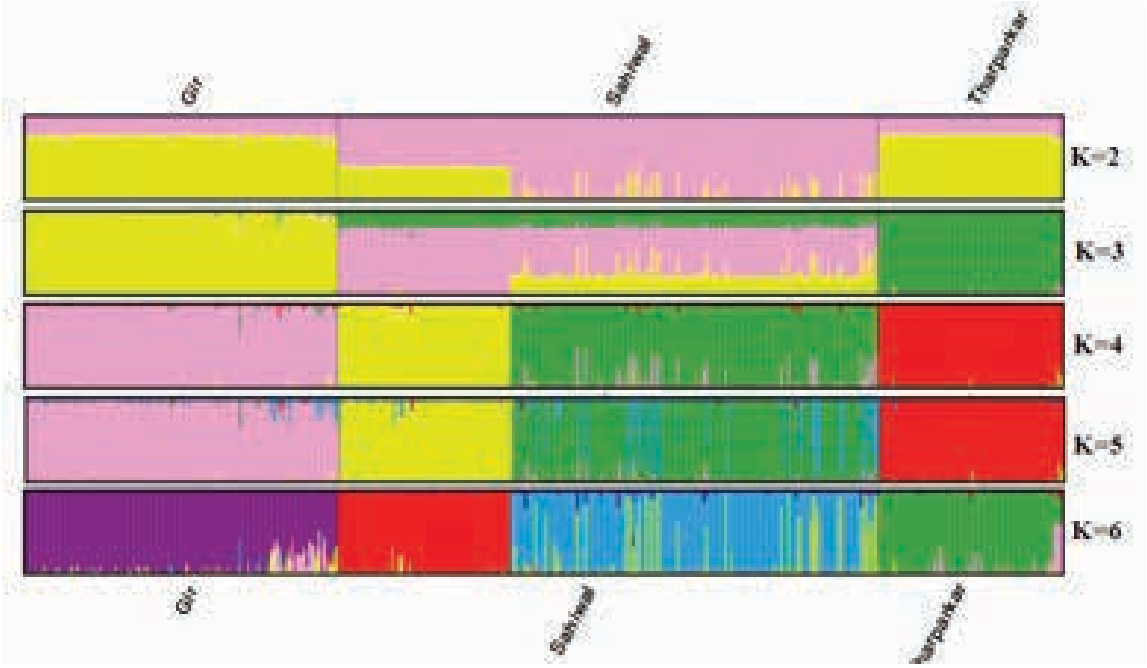
Breed structure and degree of admixture were assessed with STRUCTURE software. The analysis was carried out with 5 different runs from K = 2 to K = 6 to identify the most likely number of clusters present in the dataset. The 5 runs were clumped and the graphical clustering




*Genetic differentation of cattle breeds*

**Different genetic parameters observed in Gir, Sahiwal & Tharparkar cattle breeds**

| Breed | Sample size | No of alleles | Effective No of alleles | Observed Heterozygosity | Expected Heterozygosity |
|---|---|---|---|---|---|
| Gir | 311 | 8.53±0.48 | 3.31±0.19 | 0.59±0.03 | 0.63±0.03 |
| Sahiwal | 523 | 12.80±0.63 | 4.58±0.29 | 0.57±0.03 | 0.72±0.02 |
| Tharparkar | 182 | 11.86±0.53 | 4.60±0.30 | 0.61±0.03 | 0.72±0.03 |
| Overall | 1016 | 15.61±0.72 | 5.06±0.30 | 0.58±0.03 | 0.76±0.02 |



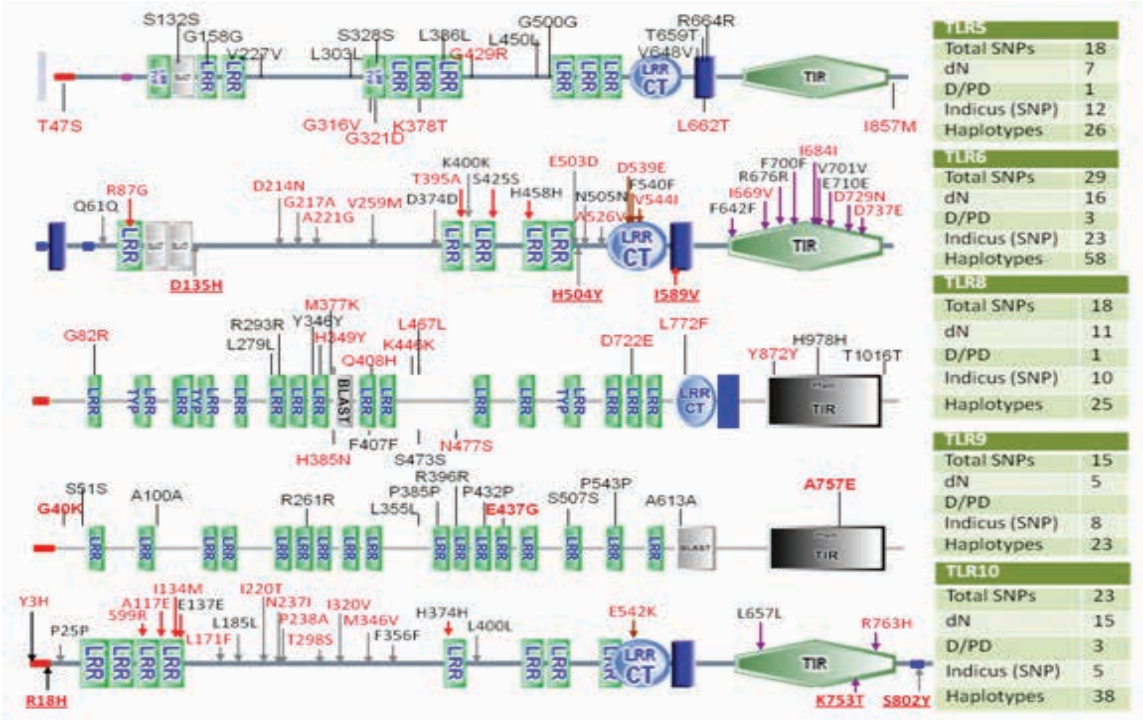

*Structure analysis of three cattle breeds from K=2 to 6*

of breeds was observed. The results revealed that Gir and Tharparkar breeds grouped in their own clusters while Sahiwal cattle were separated into two distinctive cluster at K=4.

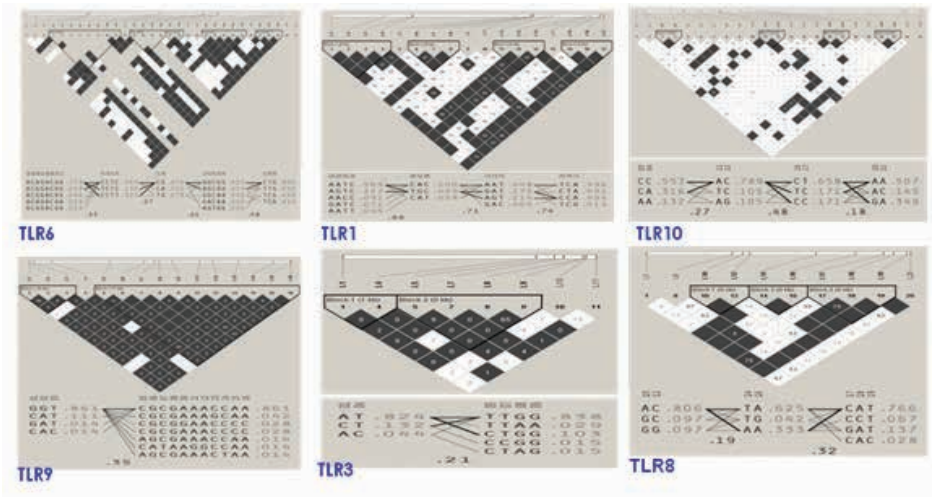
## Delineating polymorphism and evolution of Toll-like receptors in Indian native (*Bos indicus*) cattle breeds

Sequence characterization and genotyping of toll-like receptor 3 and 7 (TLR 3, 7) genes were undertaken in diverse Indian native cattle breeds to identify single nucleotide polymorphisms. Comparative sequence analysis of coding region of TLR3 in the analyzed breeds revealed a total of 13 variations. Out of these, 4 variation were non-synonymous with conserved polarity. The comparative sequence analysis of TLR 7 gene revealed a total of 16 variations. Six of these were non-synonymous, 7 were synonymous and 3 occurred in UTRs. Except few, polarities of most of amino acids were found to be conserved. Amongst the analyzed breeds, Kankrej, Hariana and Gir cattle showed maximum numbers of SNPs while Kangyam and Nagori cattle were least polymorphic. Overall, the comparative sequence analysis of ten TLRs, revealed a total of 196 SNPs, of which 86 were non-synonymous and 55 were unique for Indian cattle breeds. All the observed polymorphic nucleotide sites were biallelic, unbiased and distributed across all the domains.

Comparison of protein domain architecture of different TLR gene clusters of Indian native cattle with other mammalian species revealed regions of conservation in the TLR with variable LLR patterning. Further, using maximum likelihood approaches, positively selected codons (PSC) were found in all the TLRs studied. The number of PSC in TLR7, 8, 9 and 10 were 2, 4, 4 and 5 respectively. The diploid genotypes obtained for TLRs 1-3, 6-7 and 10 were resolved using the Baysian PHASE platform. Calculations were carried out over 1000 iterations, 10 thinning intervals and 1000 burns in iterations. Examination of the intragenic pattern of linkage disequilibrium (LD) via 95% confidence intervals constructed for D', application of the four gamete rule and estimates of recombination revealed 5 haplo-blocks in TLR6; 4 each in TLR1 and TLR10; 3 in TLR7 and 2 each in TLR2 and TLR3 with varying LD.




*Variations observed in different TLRs across different native cattle breeds*



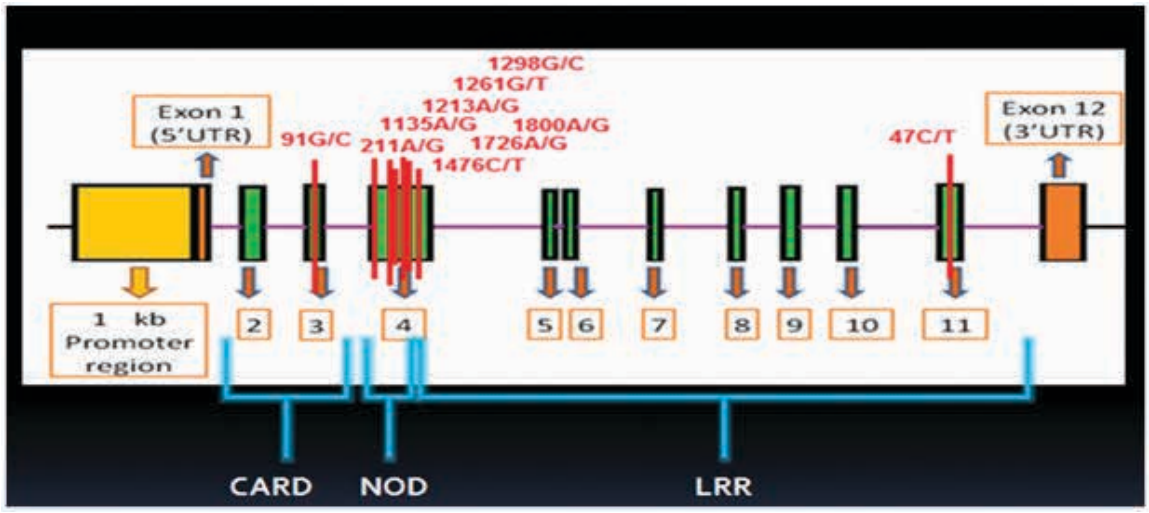

*Haplotype blocks for different TLR genes across Indian native cattle breeds*

When compared across different species, level of haplotype sharing was low and only 1-4 predominant haplotypes were observed for the majority of the investigated species. On evaluation of putative functional effects of amino acid substitutions encoded by SNPs using PolyPhen and SIFT, 19% (16/85) of SNPs were predicted to impact protein function. Overall, the study suggests the existence of substantial diversity within Indian cattle.

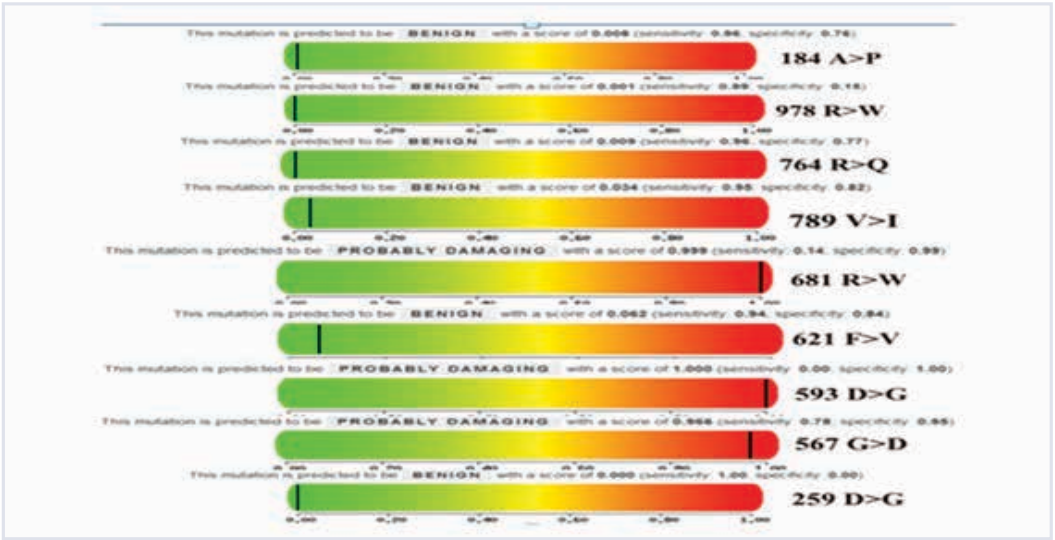
## Characterization of Nod-like receptor (NLR) genes in buffalo (NAIP)

Complete mRNA and genomic sequence data of buffalo Nod-like receptor 2 (NLR2) has been generated. Polymorphism detection in buffalo NLR2 revealed presence of 42 SNPs among which, 20 were in exonic region, 10 being non-synonymous, 7 synonymous and 3 in 5'UTR. PCR-RFLP protocols were developed and

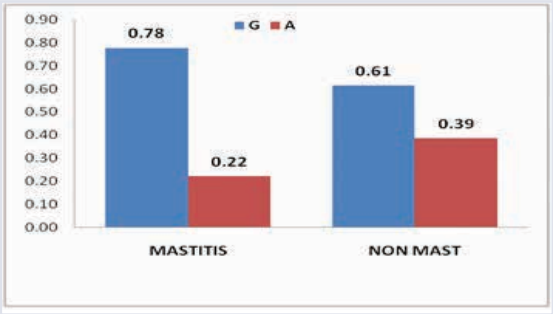
genotypes on two SNPs, G91C in CARD domain and A1135G in NOD domain of buffalo Nod-like receptor 2, have been generated on 79 calves, 31 with diarrhoea and 48 healthy, without showing any significant association with the disease incidence. Allele frequencies of same SNPs in mastitis affected and non-affected buffaloes have also been documented for association with clinical mastitis, with Exon4 1135A>G Nod-domain SNP (*SmaI*-PCR-RFLP), showing significant variation in allelic frequencies among mastitis affected and non-affected animals. Among the non-synonymous SNPs identified in buffalo Nod-like receptor 2 gene, three- 567 G>D, 593 D>G and 681 R>W have been found to be probably damaging to the structure and function of the gene by Polyphen analysis. In another experiment, cDNA amplification of Nod-like receptor 1 in buffalo mammary gland has shown presence of two transcript variants, due to splicing out of 1828 nucleotides long exon 3. Splice variants have been reported to be playing important role in regulating the expression of normal transcripts and levels of inflammation, leading to tissue damage. This is the first report on identification of transcript variants in buffalo Nod-like receptors.




*Distribution of non-synonymous SNPs across different exons in buffalo Nod-like receptor 2*



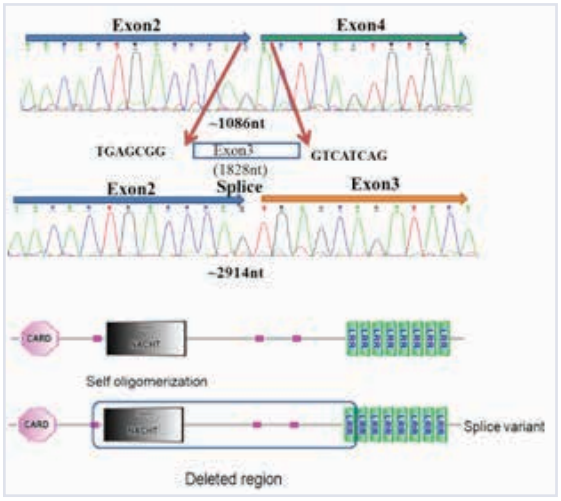

*Damaging amino acid changes arising due to non-synonymous SNPs in buffalo NLR2*




*Allelic frequencies of NOD2 Exon 4 1135A>G SNP in mastitic and healthy buffaloes. ($\chi^2$ value=4.493, Significant; Critical value $\chi^2_{0.05}$ = 3.841)*

## Genetic variability in the bovine cytokines

***Interferon- gamma gene (IFN-γ gene):*** A total of 20 SNPs were observed to be spread across the 3.4 Kb region of the IFN-γ gene in 40 *Bos indicus* animals of 5 breeds viz. Tharparkar, Rathi, Sahiwal, Hariana and Kankrej. Of the 20 variations there were 10 transitions, 8 transversions and 2 indels. The exon-1 of the gene contained an SNP (T>G) at position +176 which was non-synonymous and resulted in amino acid change from glycine to valine in the signal peptide of the molecule. This amino acid has been reported to be associated with the susceptibility to para tuberculosis infection in the *Bos taurus* populations. The exon-2 and exon-3 of the interferon gamma gene were conserved. The microsatellite repeat (GTTT) in the intron-1 of the gene exhibited a very high degree of polymorphism. The promoter region of the IFN gamma gene was found to contain transcription factor binding sites for the FOXJ2 and Evi-1 transcription factors at positions c.1672 and c. 1697, respectively. The completely conserved sequences of the exonic regions suggest that the structure of the interferon gamma protein needs to be conserved in order to perform its biological function in the cell.




*Detection of splice variants in buffalo Nod-like recptor-1, showing splicing out of complete exon3*

***Tumour necrosis factor (TNF) gene:*** Polymorphism present across the complete TNF-β gene (3.5Kb) in the 40 animals of *Bos indicus* Hariana, Tharparkar, Kankrej, Sahiwal and Rathi breeds was analysed. Overall 31 SNPs and 3 small insertion/deletion polymorphisms were observed across the complete gene region. Two SNPs were present in exon 2 at positions 1412(A>G) and 1485(C>T); two SNPs were present in exon3 at positions 1925(C>T) and 2027(C>T). The SNP 1412(A>G) in exon2 resulting in amino acid change Gly. Asp. The other SNPs were synonymous. The lowest minor allele frequency was that of the T allele at position 2447(C>T) of 0.0125. The promoter region had 23 putative transcription factor binding sites. Using PHASE, forty six most probable haplotypes of the gene were observed. All the 34 SNP loci were polymorphic. The observed heterozygosity (0.1588±0.1225) for all the loci was almost the same as the expected heterozygosity (0.1555±0.1108) which suggested the genotypes at these SNP positions to be almost in Hardy-Weinberg equilibrium. The overall negative Fis value of -0.1958 indicated little level of inbreeding. The Fst value of 0.1354 was observed.

All the SNPs observed have not been previously reported in any of the *Bos taurus* breeds and may be considered to be putative novel SNPs.

## Nucleotide diversity in candidate genes for mutton quality traits in Indian sheep

Nucleotide sequence variations were assessed in candidate genes associated with mutton quality traits in sheep. Previously reported polymorphic regions of the ovine growth hormone (*GH)*, growth hormone receptor *(GHR),* Titin (*TTN*) calpastatin *(CAST)* and diacylglycerol acyltransferase 1 *(DGAT1)* gene loci were screened for possible SNPs across a panel of 10 indigenous sheep breeds namely Bandur, Chokla, Deccani, Ganjam, Madgyal, Magra, Malpura, Muzzafarnagri Nali and Nellore. Sequence alignments, comparisons and haplotype data analyses were carried out using various genetic software. Allele and genotype frequencies were estimated for the identified SNPs.

All the loci had more than 98% identity with homologous regions in the ovine reference sequence (Oar3.1). Analysis of the aligned sequence data with reference sequence revealed several singleton variations in exon 4 and 5 of *GH* gene. Two SNPs (g.1674A>T and g.1792A>C) were identified in the exon 5, both of which were observed to be heterozygous in nature. The allele frequency of the A allele in g.1674A>T and g.1792A>C SNPs was observed to be 0.674 and 0.860 respectively. The haplotype and nucleotide diversities were estimated to be 0.837 and 0.026 respectively for the *GH* locus. Exon 6 region of *GHR* and CDS of *TTN* revealed several singleton variations, whereas 5'UTR of *TTN* was observed to be highly conserved in the investigated sheep breeds. Several putative regulatory motifs could be identified in the 5'UTR of *TTN* gene, most of which were conserved across species. Four SNPs were identified in the intron 12 of *CAST* (c.61+131A>T; c.61+260A>G; c.61+326A>G; c.61+417A>G). Two novel SNPs g.375G>T and g.454C>G were observed in the exon 1 and intron 1 of *DGAT1* respectively. Presence of the novel nucleotide variations in candidate genes for mutton quality in Indian sheep reflects availability of greater genetic diversity at these loci.

## Allelic diversity of MHC class II genes in indigenous yak

To explore allelic diversity of yak MHC (*Bogr*) class II loci, genomic regions corresponding to exon 2 of DRA, DRB, DQA and DQB genes were amplified and sequenced from 37 Arunachali yaks. A total of three allelic variants of *Bogr*-DRA were identified, among which two variants were novel. Most common variant in yak population was completely homologous to *BoLA*-DRA*01011 allele of cattle. None of the variants of yak DRA could reveal any amino acid substitution, proving its highly conserved nature across the species. Sequence analysis of yak *Bogr*-DQA based on exon 2 region revealed a total of 8 alleles, corresponding to two major groups, DQA1 and DQA2. Alleles of both DQA groups shared less than 80% nucleotides identity, indicating presence of possible duplication of DQA loci in yak. A total of five *Bogr*-DQB alleles were also identified and among these, three DQB alleles were newly identified in yak. Among 37 yaks, a total of four yaks were found to be homozygous at DRB3 locus. Among 33 yaks with heterozygous alleles at Bogr-DRB3.2 locus, seven animals exhibited low nucleotides variation between alternate alleles, whereas in other 26 yaks nucleotides variation between the alleles was very high. Among three *Bogr*-DRB3.2 alleles identified in yak, one allele was

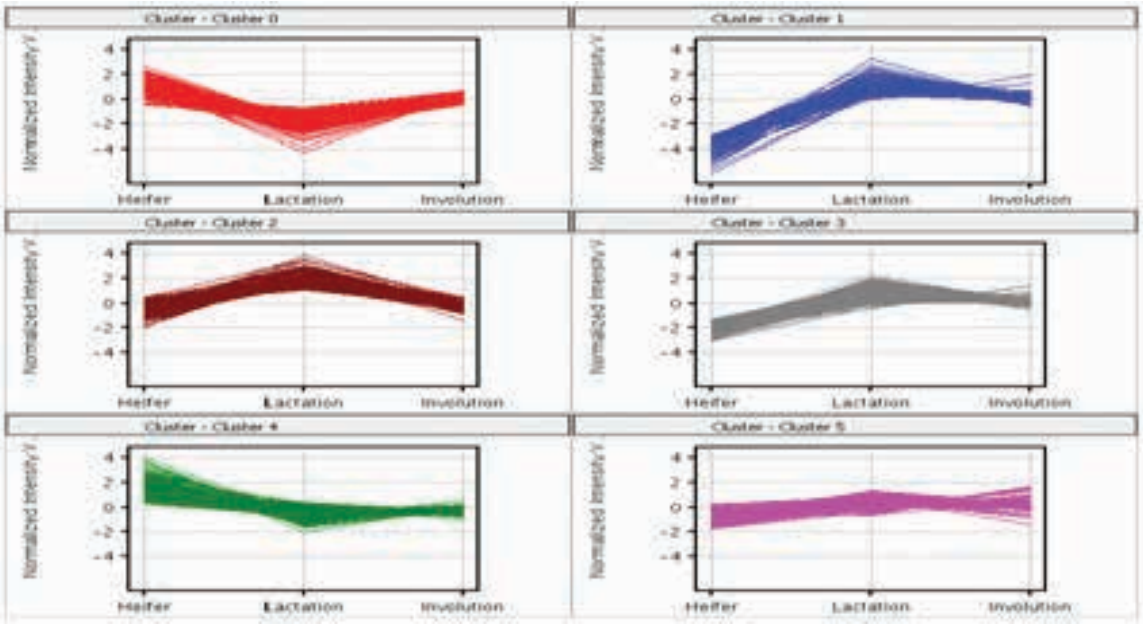
novel. Preliminary results revealed expectedly high allelic diversity at DQA, DQB and DRB3 loci in indigenous Arunachali yak, indicating population having higher fitness level.

## Mining of microarray based transcriptome data of buffalo mammary gland (NAIP)

An effort was made to mine transcriptome data to identify genes that were specifically induced or repressed across three physiological stages of buffalo mammary gland. The heterologous bovine specific microarray chip was successfully utilized to delineate transcriptome profile of buffalo mammary tissue from different physiological stages (heifer, lactating, and involution). A total of 2281 transcripts were found to be differentially expressed ($p<0.05$). Further with cutoff criteria of signed fold change ≥2-or ≤2, a total of 1808 genes were found to be significantly differentially expressed across the three stages. The grouping of differentially expressed genes through hierarchical clustering algorithms clearly indicated distinct transcriptomic signature during each of the three stages. The k-means clustering yielded a total of 6 major clusters. These clusters helped to identify Differentially Expressed Genes on the basis of their expression pattern *vis-a-vis* physiological stages of buffalo mammary gland.

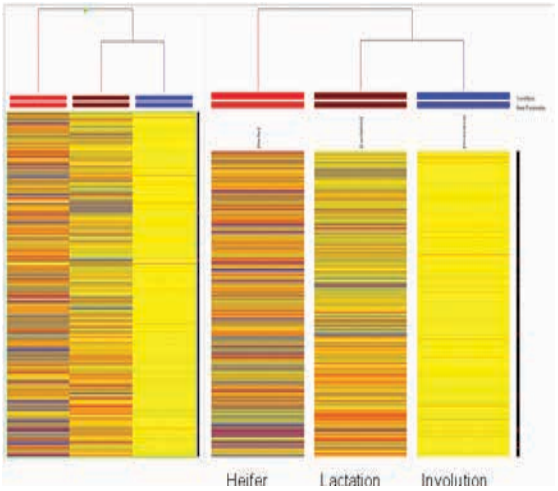
As expected, the whole set of genes related to milk fat metabolism; ATP binding casette, subfamily G member 2 (*ABCG2)*, Butyrophilin subfamily 1, member A1(*BTN1A1*), Fatty acid binding protein 3 (*FABP3*), Glycerol-3 phosphate acyltransferase (*GPAM*), Xanthene dehydrogenase(*XDH),* Fatty acid synthase (*FASN*), Sterol CoA desaturase (*SCD*) etc., milk protein synthesis; beta casein (*CSN2*), kappa casein (*CSN3*), and genes like Lipoprotein lipase (*LPL*), Prolactin (*PRL*), Mucin 1 cell surface associated (*MUC1*), *SLC2A1/GLUT1*, BCL2-associated arthanogene 3 (*BAG3*), Lipin1 (*LPN1*) *etc.* were up-regulated during lactation in comparison to involution stage.

On the other hand, during involution, several genes related to apoptosis, immune and oxidative stress response *viz.*, Interleukin 10 receptor-beta




*Normalized expression profile of DEG across different physiological stages of location*

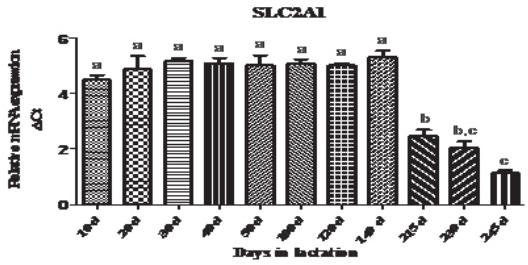
(*IL10R*), interleukin 18 (*IL-18*), chemokine C-X-C motif ligand 10 (*CXCL10*), defensin-beta1 (*DEFB1*), major histocompatibility complex, classII, DRB3 (*BOLA-DRB*), lyzozyme (*Lyz*), lipase A (*LPA*), lipopolysaccharide binding protein (*LBP*), matrix metallopeptidase 19 (*MMP19*), serpine peptidase clade E (*SERPINE1*), transforming growth factor beta receptor III (*TGFBR3*), transforming growth factor beta III (*TGFB*), insulin like growth factor binding protein 3 (*IGFBP3*), retinol binding protein 4 (RBP4), cathespin Z (*CTSZ*), cathespin S (*CTSS*), fibronectin type III domain containing 4 (*FNDC4*) were found to be up-regulated.



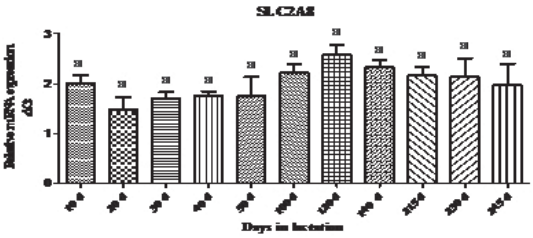

*Dendrogram view of hierarchical clustering of significantly DEGs across heifer, lactating and involution stage buffalo mammary gland*

## Expression profiling of solute carrier/ glucose transporter (SLC2A/GLUT) genes in mammary epithelial cells of Sahiwal cows (NAIP)

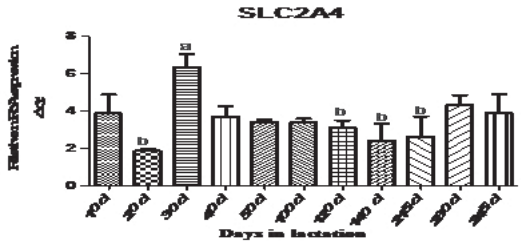
Solute carriers (SLC2A/ GLUT) are one of the major types of transporter superfamily that have been predominantly involved in active transport of glucose across the plasma membrane. Therefore, present study was undertaken to assess relative mRNA expression of major solute carriers (SLC2A/GLUTs) viz., SLC2A1 (GLUT1), SLC2A (GLUT4), SLC2A8 (GLUT8), SLC2A12 (GLUT12) genes in milk purified mammay




**Relative mRNA level of *SLC2A1* gene in Sahiwal MEC during different lactation stages. Values are expressed as means± SE. Different letters indicate significant differences between tissues (p<0.05)**




**Relative mRNA level of *SLC2A8* gene in Sahiwal MEC during different lactation stages. Values are expressed as means± SE. Different letters indicate significant differences between tissues (p<0.05)**



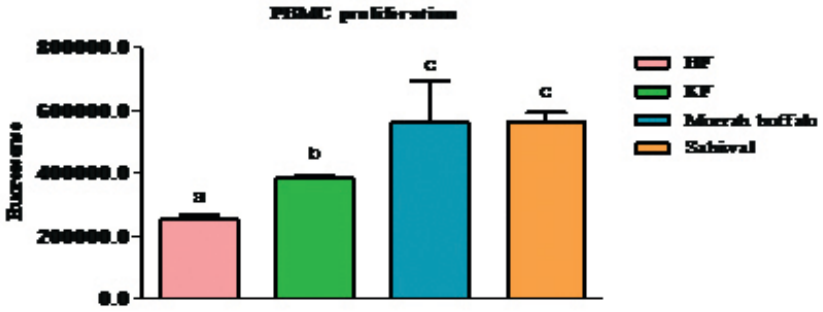

**Relative mRNA level of *SLC2A4* gene in Sahiwal MEC during different lactation stages. Values are expressed as means± SE. Different letters indicate significant differences between tissues (p<0.05)**

epithelial cells of Sahiwal cows during different lactation stages. For this study, a total of 16 healthy multiparous Sahiwal cows based on their previous three years lactation history maintained at NDRI, Karnal were selected. The mRNA expression of one of the major solute carrier SLC2A1 (GLUT1) was found to be increased immediately within the first 3 weeks following initiation of lactation (10-20 days in lactation and remained increased at peak/mid lactation period (30-140 days in lactation). Another major solute carrier SLC2A8(GLUT8), showed higher expression during mid lactation period (100-140 days) in comparison to late lactation

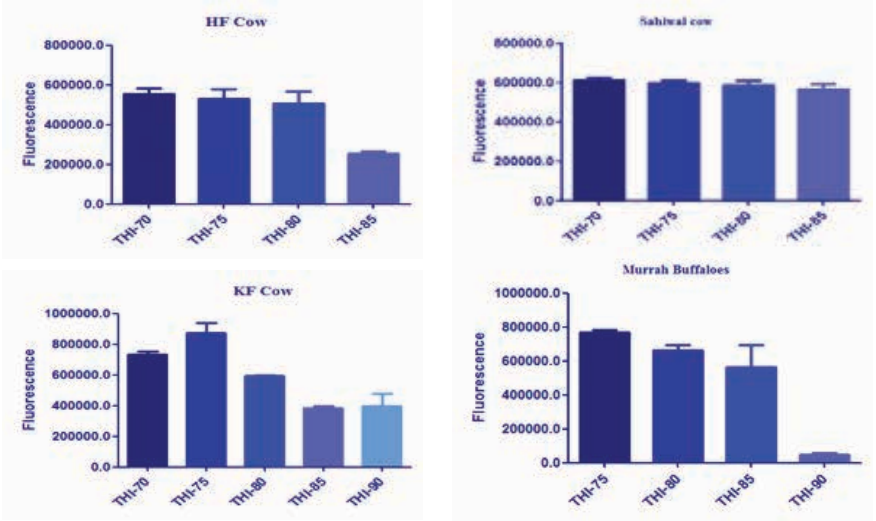
period, whereas, SLC2A4 (GLUT4) expression was significantly ($p<0.05$) higher at peak lactation and low during early and mid stages of lactation period. Our expression data indicated SLC2A1,SLC2A4 and SLC2A8 to be the major solute carriers in Sahiwal MEC. These results provide the knowledge and understanding of expression pattern the major facilitative glucose transporter genes indicating their role in regulating glucose uptake in mammary epithelial cells of Sahiwal cows.

## Evaluation of cellular proliferation rate and heat shock protein level in cattle and Buffaloes during summer stress (National Fellow Project)

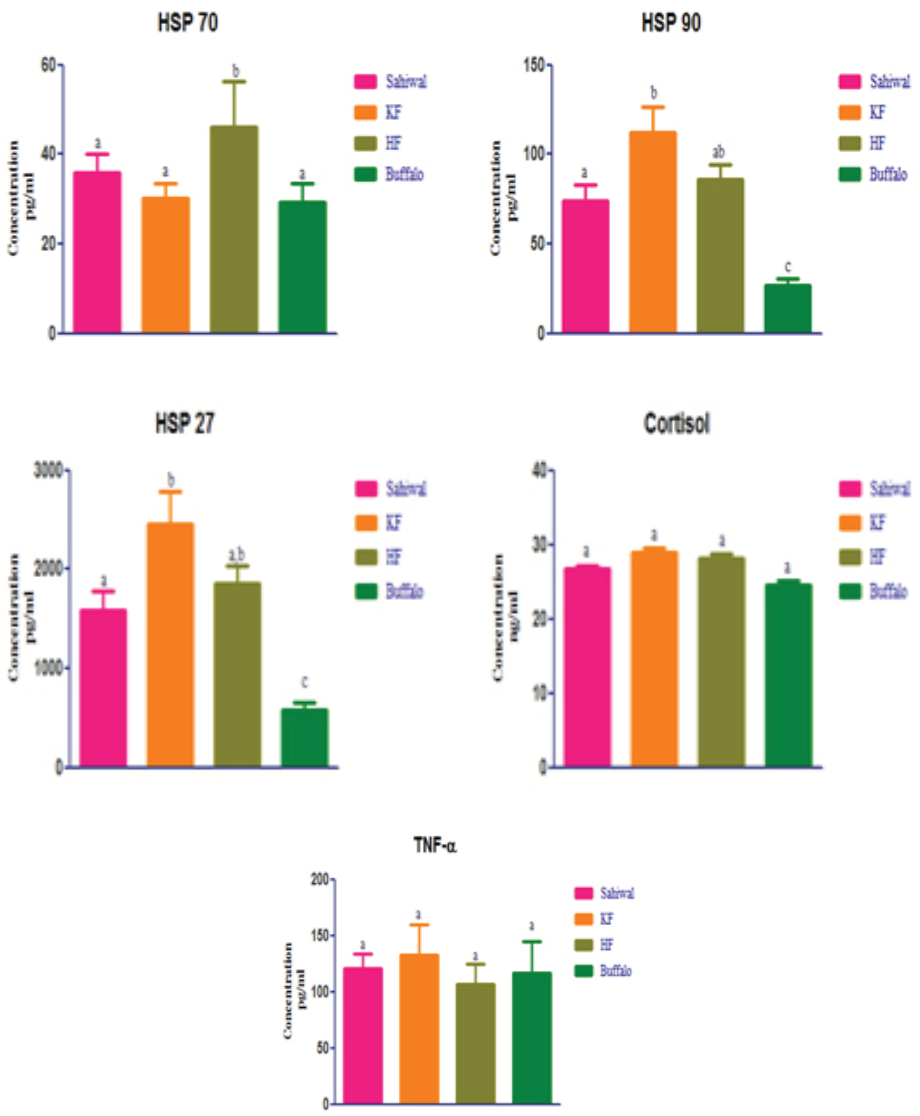
An attempt was made to undertake comparative evaluation of cell proliferation and heat shock protein levels as indicators of thermotolerance at varying temperature-humidity index (THI) across Sahiwal cows (*Bos indicus*), Karan Fries cows (Cross-bred), Holstein Friesian cows (*Bos taurus*) and Murrah buffaloes (*Bubalus bubalis*). For this study, a total of 10-12 healthy animals each of Sahiwal, Karan Fries, HF cows and Murrah Buffaloes were included. Peripheral blood mononuclear cells (PBMCs) and a total of 170 serum samples were isolated from blood samples collected at different temperature humidity index (THI) i.e., 70, 75, 80, 85 and 90. The data indicated significant ($p<0.05$) inhibition of cell proliferation in Holstein and Karan Fries PBMCs as compared to Sahiwal cows and Murrah buffaloes at THI-85. Unlike other animal types, Sahiwal cows, showed no significant reduction in the cell proliferation rate at higher THI. Additionally, during the month of August, at THI ≥ 85, the serum samples of 48 heifer




*Comparative cell proliferation rate at THI-85*




*PBMCs proliferation rate in cattle and buffaloes across different THI*

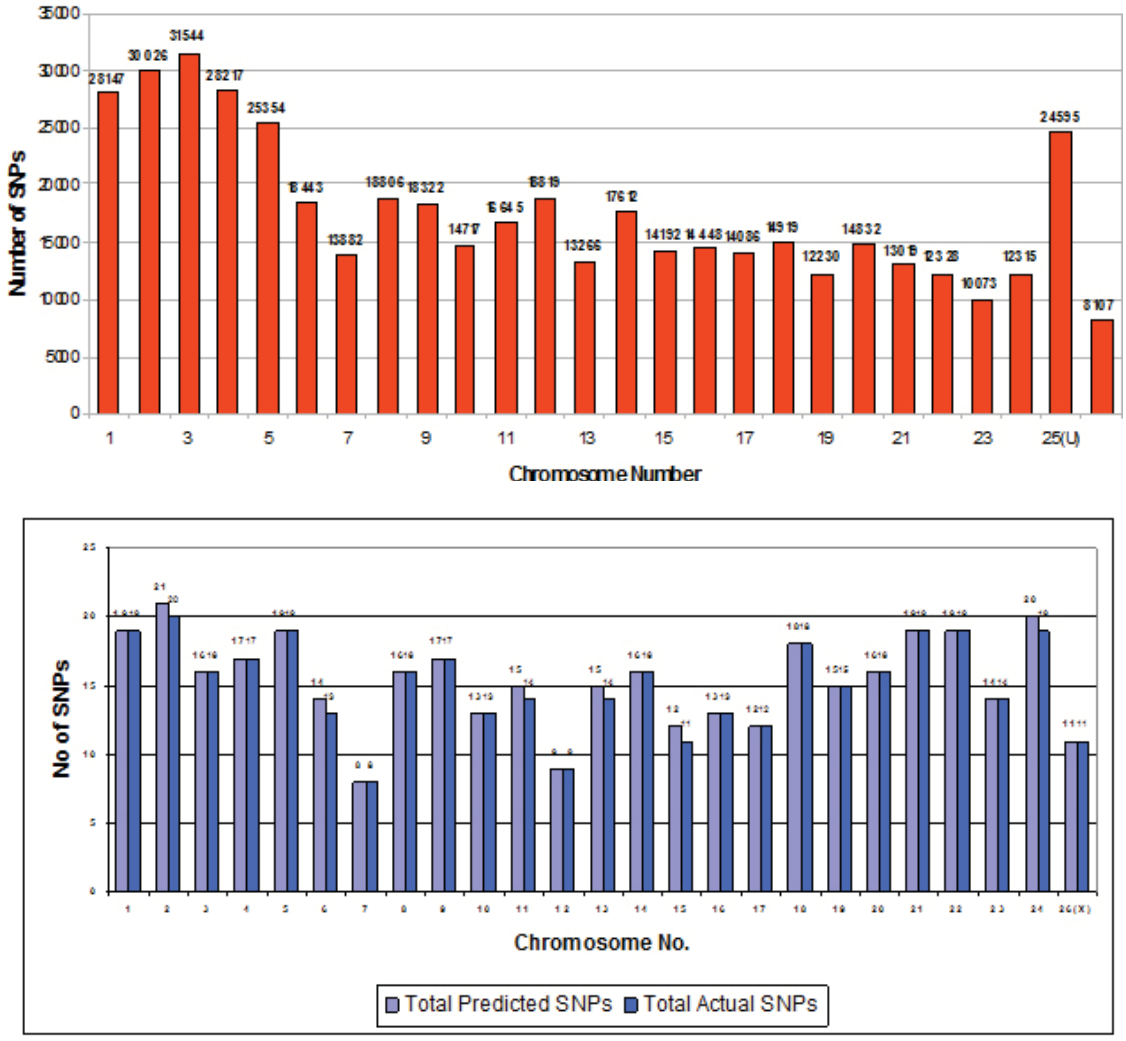



*Comparative level of stress and inflammatory proteins in serum of cattle and buffaloes at 85-THI*

animals were assayed for three major chaperons (HSP70, HSP90 and HSP27) of heat shock protein family along with cortisol and TNF-α using enzyme-linked immune-sorbent assay. The analysis revealed that serum concentrations of HSPs were comparatively higher in Holstein Friesian and Karan Fries cows in comparison to Sahiwal cows and Murrah buffaloes. Similar trend was observed for cortisol and TNF-α. The data presented here provides initial evidence that Sahiwal cows have better cellular tolerance than exotic, crossbred cows and buffaloes to summer stress and warrant further studies in this area.

## Identification of QTL for milk yield, fat and protein percentage in buffaloes (NAIP)

A large reference family of 10,000 daughters of 12 sires was created. The parentage of these daughters was verified using DNA markers. The daughters were recorded for body weights, reproductive parameters and were artificially inseminated at maturity. On calving the recording for milk yield, fat and protein percentage and also somatic cell count were recorded during first lactation. The daughters




*Number of SNPs generated on each of the buffalo chromosome using Next Generation Sequencing*

were genotyped for 79 microsatellite markers situated on 8 chromosomes. Eight selected chromosomes were BTA1 (q arm of BBU1); BTA2 (q arm of BBU2); BTA3 (BBU6); BTA4 (BBU8); BTA6 (BBU7); BTA7 (BBU9); BTA9 (BBU10) and BTA14 (BBU15). Genotyping was done on the reference population using identified microsatellite markers. The phenotypic records obtained were verified for normal distribution. The data was subjected to analysis using single marker analysis using QTL Cartographer, interval mapping using R/qtl. The meta-QTL analysis was carried out using Biomercator. The QTL positions were identified and the regions were fine mapped using a large number of SNPs.

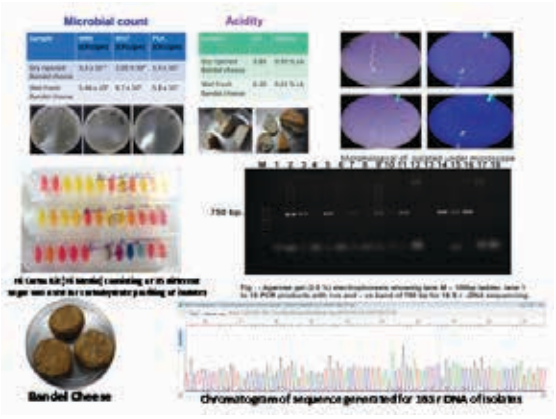
SNPs were identified using Reduced representation library and RNA seq. A total of 6.54 Lakh SNPs were identified. The chromosome wise distribution of SNPs is shown below in graphs. A total of 196669 SNPs were identified in the coding part of the genome. These SNPs were then validated using a 384 SNP data set using Golden Gate assay of Illumina. The call rate of SNP chip was 98.5% which is quite high. In RNAseq analysis the expression of genes included more than 800 genes directly associated milk and related traits. There were in all 66912 transitional changes from A/G while 67023 were C/T transitions. There were 63578 transversions -12869(A/T), 18770(C/G), 15838 (A/C) and 16041 (T/G). A total of 5572 changes were complex in nature.

## Profiling of milk constituents, identification of SNPs and their association with milk traits in non-traditional dairy animals

Milk analysis was carried out for Yak. Analysis of fatty acid composition was carried out according to ISO-IDF (2001). Fatty acid methyl esters (FAME) were prepared by base catalyzed methanolysis (KOH in methanol) according to ISO-IDF (2002). 1uL FAME was analyzed using a gas chromatograph equipped with ionizations detector. Analysis of yak (*Bos grunniens*) milk showed a high content of total solids (16.9–17.9%), proteins (4.9–5.9%) and fat (5.5–7.5%). These values are significantly higher than those of cow (*Bos taurus*) and goat (*Capra hircus*) milk, but relatively similar to those of buffalo (*Bubalus bubalis*). A total of 50 yaks from the Himachal Pradesh in India were genotyped at the alpha-casein locus using the protocol developed in the present study. A polymorphism of alpha-casein gene exon 4 has been identified by evaluating genomic DNA. The polymorphic site consists of a single nucleotide substitution G-->C at position 362 of the exon 4. Lipoprotein lipase (LPL), a major candidate gene for in lipid deposition was also analysed. A polymorphic nucleotide site (SNP)-C→T (nt19913) was identified to be located in exon 7 in the coding region of the LPL gene, which led to an amino acid substitution (Phe>Ser).

## Application of Microorganisms in Agriculture and Applied Sectors

Indigenous samples of dry ripened Bandel cheese and wet fresh Bandel cheese were procured from local market of Kolkata, West Bengal. Microbial analysis showed that wet cheese had more microbial load (5.8 x 10 CFU/gm) in comparison with dry cheese (1.4 x $10^7$ CFU/gm). Lactobacilli were found to proliferate in both cheese samples and a total of 31 isolates were initially selected on the basis of morphology under microscope.These presumptive isolates were further characterized phenotypically specially by Sugar fermentation profiling and finally 19 isolates were found to be lactobacilli. These isolates were further confirmed to be Lactobacilli by genus specific PCR. These isolates can further be screened for their technological and probiotic properties for industrial use as better starter cultures.




*Isolation of microorganisms from fermented dairy foods and sequencing of 16 S rDNA for strain identification*

## Cytogenetic screening of bovine bulls for chromosomal defects

NBAGR is providing consultancy service for cytogenetic screening of breeding males to various agencies throughout the country. The aim is to check the spread of chromosomal defects and to keep the herds free of such genetic defects as per the policy of Government of India. During the year, a total of 372 breeding bulls were screened for their cytogenetic parameters. The details of the bulls investigated are as follows:

**Numbers of bulls cytogenetically screened for chromosomal abnormalities**

| Agency | Bulls | | Total |
|---|---|---|---|
| | Buffalo | Cattle | Total |
| Uttarakhand LDB Rishikesh | 9 | 17 | 26 |
| Kerala LDB Dhoni | 11 | 55 | 66 |
| Kerala LDB Dhoni | 0 | 5 | 5 |
| Germplasm Station Narwa, Jodhpur, RCDF | 10 | 21 | 31 |
| Haryana LDB Hisar | 10 | 3 | 13 |
| Haryana LDB Gurgaon | 9 | 1 | 10 |
| LDB Jammu | 7 | 5 | 12 |
| UPLDB Chak Ganjaria | 0 | 80 | 80 |
| KLDB Mattupatty | 0 | 18 | 18 |
| Animal Breeding Centre Salon, UP | 29 | 61 | 100 |
| Milkfed Khanna | 0 | 6 | 6 |
| Network Project CIRB Hisar | 15 | 0 | 15 |
| Total | 100 | 272 | 372 |

All the bulls, except 2, were found to have a normal karyotype, representative of the respective species. The cattle bulls possessed a typical zebu/taurine type karyotype (60, XY) and the buffalo bulls, 50, XY. One buffalo bull (50, XX/50, XY) and one cattle bull (60, XX/60, XY) were sex chromosome chimeric, though no record was available with the concerned agency whether it was born single or twin. All other investigated buffalo bulls/male calves had a normal karyotypic complement (50, XY).

*Female (50, XX, left) and male (50, XY, right) cells obtained in the same buffalo bull , showing sex chromosome chimerism*

*Dr. S. Ayyappan taking keen interest in laboratory activities at NBAGR*

## Network Project on AnGR

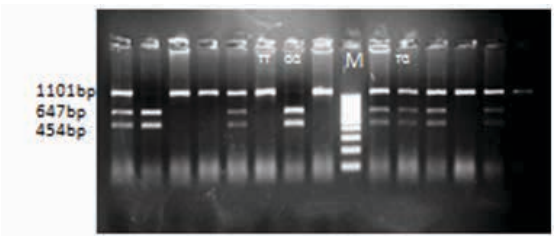
### Core Lab, NBAGR, Karnal

**Candidate genes for sexual precocity in indigenous goats:** Candidate genes for reproductive traits viz. KiSS1, GPR54, INHBB, JY-1 and AA-NAT genes were PCR amplified, sequenced and analyzed for identification of SNPs across nine indigenous goat breeds (Barbari, Beetal, Black Bengal, Malabari, Jhakrana, Osmanabadi, Sangamneri, Sirohi and Ganjam) differing in reproductive traits (prolificacy and precocity) and geographic distribution. Nine SNPs in KiSS1 (Intron 1: G296C, T455G, T505A, T693C, T950C; Intron 2: T1125C, A2510G, C2540T, A2803G), two novel SNPs, one each in exon 1 (C1122T) and intron 1 (T1830C) of GPR54 gene, two novel synonymous SNPs (G693A and C840T) in exon 2 of INHBB gene, a single SNP (C-15329T) in 3'UTR region of JY-1 gene and two synonymous SNPs (C825T in exon 2 and C1249T in exon 3) of AA-NAT gene were identified. Three putative transcription factor binding sites (*HNF-4, COMP1, Oct-1*) were identified in promoter of GPR54 of cattle whereas two were identified in goats. This was due to a variation (T to C) resulting in the loss of putative transcription factor binding site for *HNF-4* in goats.

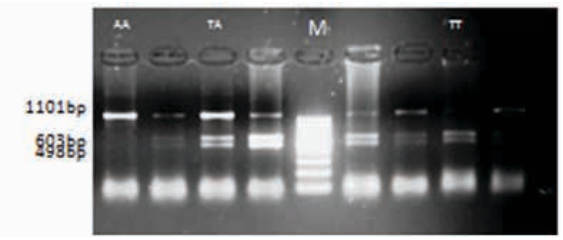
The novel SNPs in KiSS1 gene were explored for specific restriction enzyme (RE) cutting sites arising due to change of nucleotide (SNP). RE sites were identified for the SNPs of KiSS1 gene and PCR-RFLP protocol was designed and standardized for G296C, T455G, T505A, T950C and T1125C polymorphisms.

Association analysis of different loci in KiSS1 gene with litter size and age at sexual maturity in 158 animals of Black Bengal goat breed indicated that T1125C SNP of KiSS1 gene was associated ($p<0.05$) with litter size (first parity) and female goats with TT genotype had higher litter size than other two possible genotypes at this locus. However, no association of identified mutations was detected with the age at sexual maturity. Further research on a large number of animals of different breeds is required to confirm the link of SNP with increased prolificacy in goats.

**Analysis and identification of allelic variants of fecundity genes in indigenous goats:** Improvement of reproductive traits in goats has become of increasing interest, where small increase in litter size can equal large gains in profit. In recent years, many studies on the genetics of prolificacy in small ruminants have highlighted the importance of candidate genes for fecundity in affecting ovulation rate and litter size through different mechanisms. Four candidate genes for reproductive traits were sequence characterized in nine indigenous goat breeds (Barbari, Beetal, Black Bengal, Malabari, Jhakrana, Osmanabadi, Sangamneri, Sirohi and Ganjam) differing in prolificacy and geographic distribution. A total of 8 SNPs were identified in the studied genes.




*Electrophoresis patterns obtained after digestion with SacII endonuclease at T455G locus of KiSS1 gene in goat*

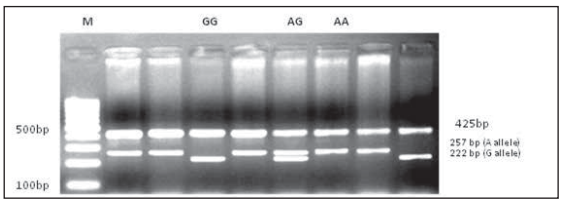



*Electrophoresis patterns obtained after digestion with DraIII endonuclease at T505A locus of KiSS1 gene in goat*

**SNPs identified in candidate fecundity genes of goat**

| Gene | Region | SNP |
|---|---|---|
| BMPR1B | Promoter | T(-242 )C<br>G(-623)A |
| BMP15 | Exon II | G735A<br>C808G |
| GDF9 | Exon II | C818T<br>A959C<br>G1189A |
| BMP4 | Exon II | G1354A |

These novel polymorphisms need to be associated with prolificacy trait for identification of molecular markers that can be used to identify high prolific animals at an early stage of life using robust and less costly genotyping techniques. Therefore Tetra-ARMS PCR was designed for genotyping G1189A (GDF9), G735A (BMP15) and T(-242)C (BMPR1B) mutations and PCR-RFLP was standardized for genotyping C818T and A959C (GDF9) and C808G (BMP15) mutations. Representative samples from each set were also typed in parallel with direct sequencing for each SNP, to assess the accuracy of the assays. The scored genotypes were 100% in accordance with direct sequencing.

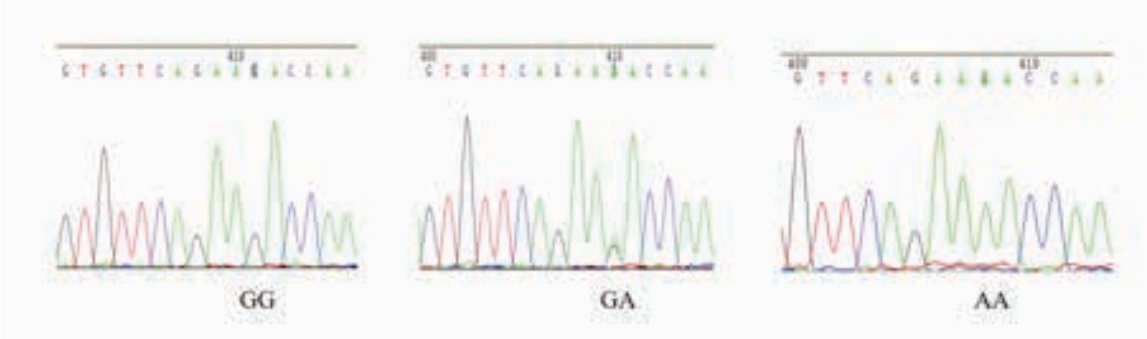



*PCR product of tetra-primer ARMS PCR for G735A locus of BMP15 gene in goat*

Using these approaches, 391 pedigreed goat samples belonging to seven breeds (Black Bengal, Barbari, Beetal, Jhakrana, Osmanabadi, Sangamneri and Ganjam) were genotyped to find out association of identified SNPs with reproductive traits. The fixed effect model was employed for analysis of litter size in different goat breeds and least square means were used for multiple comparisons in litter size among the different genotypes. Association of 4 novel SNPs; C818T (GDF9), T-242C (BMPR1B), C808G and G735A (BMP15) was identified in different breeds of Indian goats in different parities. Locus A959C of GDF9 associated with fecundity in exotic goats was also found to be associated.

## Core Lab, TANUVAS, Chennai

Six genes were characterized with respect to draught parameters in *Bos indicus* cattle, in a panel of 6 cattle breeds (Kangayam, Umblachery, Pulikulam, Barghur, Hallikar and Ongole) and a large number of SNPs were identified. Phenotypes on endurance power such as pulling power, speed of the animal, stride length, respiration rate, rectal temperature and heart rate were recorded. Few SNPs from these candidate genes were found to exhibit association with different phenotypes recorded in draft cattle breeds. The genes studied were, Insulin-like growth factor – 1 gene (IGF-1), $\beta_2$ adrenergic receptor gene ($ADRB_2$), Glutathione peroxidase




*Genotypes for G735A mutation of BMP15 gene confirmed by direct DNA sequencing in goat*

– 1 gene (GPX-1), Vascular endothelia growth factor – A gene ( VEGF-A), Angiotensin I converting enzyme gene (ACE- I), Bradykinin $\beta_2$ receptor gene ($BDKRB_2$).

## Core Lab, AAU, Anand

Candidate genes related to milk quality/ composition and milk yield in indigenous camel breeds were studied. Primers used in this study were designed on the basis of homologous genes of Bos taurus to sequence the exonic regions and to identify SNPs. Few SNPs showed association with various recorded traits like milk production, protein yield, fat yield, etc. The candidate genes studied were α-casein, β-casein, κ-casein, Growth Hormone, Leptin, Lactoferrin and Lactoperoxidase.

## Core Lab, AAU, Khanapara

Molecular characterization based on 25 microsatellites of three cattle populations from Assam, Manipur and Arunachal Pradesh was undertaken. All the 3 populations investigated were distinct populations and totally unrelated with each other, which was also indicated by phylogenetic analysis, principal component analysis and AMOVA test. The phylogenetic clusters of studied cattle populations revealed that geographically adjacent populations are more genetically related. The populations studied do have moderate amount of heterozygosity, indicating scope for further improvement of genetic variation among the individual animals. No bottleneck was observed in the studied genetic groups.

*Cattle of Assam*

*Cattle of Arunachal Pradesh*

*Cattle of Manipur*

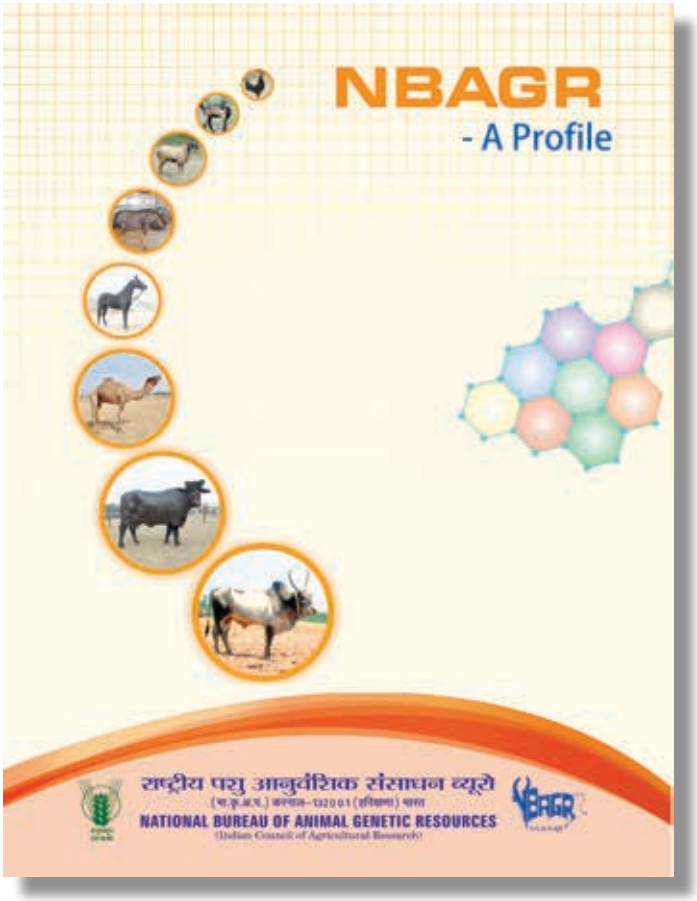
**Different parameters recorded in cattle populations**

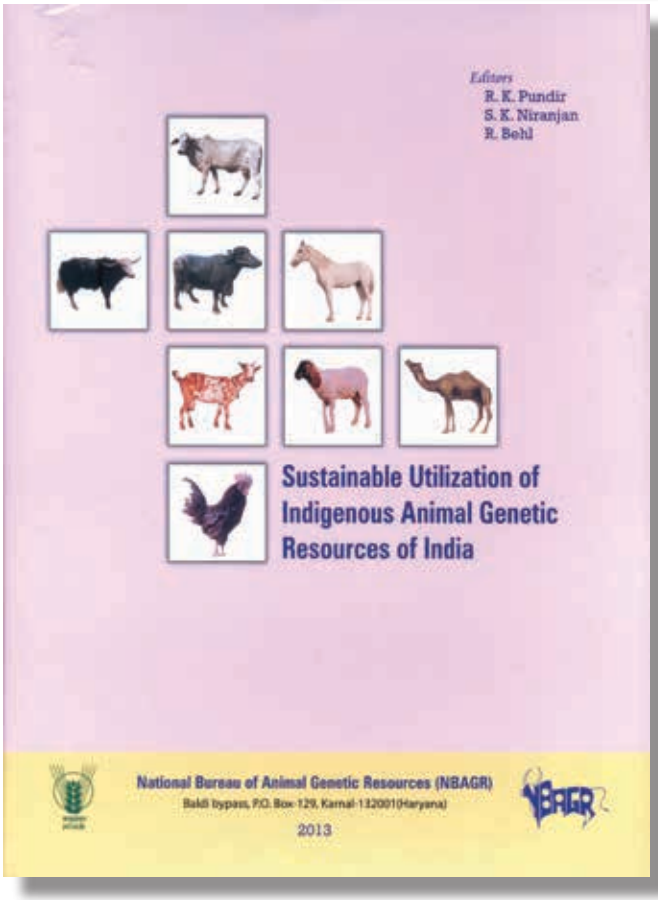
| Populations | Total Alleles | Parameters | | | |
|---|---|---|---|---|---|
| | | Average number of alleles | Effective number of alleles | Observed Heterozygosity | Expected Heterozygosity |
| Assam | 118 | 4.92±0.069 | 1.88±0.084 | 0.45±0.023 | 0.48±0.024 |
| Arunachal Pradesh | 80 | 3.33±1.274 | 2.16±0.077 | 0.63±0.233 | 0.69±0.165 |
| Manipur | 102 | 4.857±1.79 | 2.034±0.311 | 0.54±0.248 | 0.58±0.187 |
| Mean± SE | 300 | 4.37±0.052 | 2.03±0.008 | 0.54±0.005 | 0.58±0.006 |


NABARD
XIth National Symposium
ONIZING PHENOMICS & GENOMICS FOR SUSTAINABLE
ENT OF LIVEST R UPLIFTMENT OF RURAL MASSES
7, 2014
by
Conservati ic Animal Biodiversity (SOCDAB)
Natio al Genetic Resources
132001
MAJ. GEN. SHRI KANT
CHIEF GUEST
DR. G. S. JAKHAR
GUEST OF HONOUR

# Research Projects & Publications

- Research Projects
- Publications
- Patents and Technologies


NBAGR
- A Profile
राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो
NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES


Editors
R. K. Pundir
S. K. Niranjan
R. Behl
Sustainable Utilization of Indigenous Animal Genetic Resources of India
National Bureau of Animal Genetic Resources (NBAGR)
2013


INSIGHTS INTO COAT COLOURS IN HORSES
RAHUL BEHL, R.K. PUNDIR, JYOTSNA BEHL,
R.K. VIJH & B.K. JOSHI

# Research Projects

## Completed Research Projects

### Institute Funded

1. Characterization and evaluation of Sanchori and Nari cattle of Rajasthan - PK Singh, RK Pundir, DK Sadana and HS Rathore (LPPS, Sadri).

2. Characterization and evaluation of indigenous cattle germplasm in Northern Eastern (Tripura, Mizoram and Manipur) states of India -RK Pundir, PK Singh and DK Sadana.

3. Phenotypic characterization of Harringhata Black breed of chicken- PK Vij, MS Tantia and S Pan (WB Univ., Kolkota).

4. Study of the genetic variability in the Bovine Cytokines (*Bos-indicus*) - Jyotsna Behl, Rahul Behl and NK Verma.

5. Delineating polymorphism and evolution of Toll-like receptors in Indian native *Bos indicus* cattle breeds - Monika Sodhi and and M Mukesh (BP Mishra upto 24.02.2011).

6. Nucleotide diversity in candidate genes for mutton quality traits in Indian sheep- Reena Arora and DK Yadav (S Bhatia upto Feb., 2012).

7. Characterization of Gojri buffalo and Belahi cattle populations under migration in Foot Hills and Sub-Himalayan regions of Northern India -Vikas Vohra, SK Niranjan and AK Mishra (w. e. f. Sept., 2012).

8. Candidate gene analysis and identification of allelic variants of fecundity in indigenous goat - Sonika Ahlawat and Rekha Sharma.

9. Characterization of candidate genes for sexual precocity in indigenous goats - Rekha Sharma, Sonika Ahlawat, Manoranjan Roy (AH & VS WB) and Sanjay Mandakmale (MPKV, Rahuri).

### Externally Funded

1. Application of microorganisms in agriculture and applied sectors (ICAR Funded Project) Sub-Project: Isolation of microorganisms from fermented dairy foods and sequencing of 16 S rDNA for strain identification - Karan Veer Singh (w.e.f. 18.05. 2012) and SK Tomar (NDRI) (Dinesh Kumar-BT-upto 18.05. 2012, Rameshwar Singh upto 03.09.2012).

2. Identification of SNP's in QTL region in Indian goats and their association with milk quality traits for healthfulness - SP Dixit, M Mukesh and Rajesh Kumar and AK Tyagi (DBT).

3. Identification of Quantitative Trait Loci for Milk yield, Fat and Protein Percent in Buffaloes - RK Vijh, MS Tantia upto 30.06.2011, PK Vij upto 30.06.2011, SB Gokhale, DN Shinde and RL Bhagat (NAIP).

4. Toll-like receptors in farm animals- Evolutionary lineages and application in disease resistance - RS Kataria, (BP Mishra upto 24.02.2011 and P Kathiravan upto 9th Sept., 2011) SK Niranjan (w.e.f. 24.09.2011) and Sanjeev Singh (w.e.f. 24.09.2011) (NAIP).

## On-Going Research Projects

### Institute Funded

1. Phenotypic and genetic characterization of Koraput sheep - Sanjeev Singh, KN Raja, Reena Arora, Indrajit Ganguly and Sanat Mishra, CEO, OLRDS, Bhubaneswar - April, 2012 to March, 2014 (extended upto September, 2014).

2. Classification of ecotypes of Deccani sheep - Dinesh Kumar Yadav, Reena Arora and Anand Jain - April, 2012 to March, 2016.

3. Characterization of Kajali sheep in its native tract - AK Mishra, KN Raja, V Vohra and Yashwant Singh (GADVASU-Bathinda) - April, 2013 to March, 2015.

4. Characterization of non-descript goat genetic resources of Rohilkhand Region of Uttar Pradesh and Uttarakhand - SP Dixit, PS Dangi, RS Barwal, Neel Kant (GBPUAT) and VikasVohra (w.e.f. 14.07. 2011). - January, 2010 to December, 2012, extended upto March, 2014, extended upto September, 2014.

5. Characterization of Sikkim goats - NK Verma, RAK Aggarwal, Rekha Sharma and PS Dangi- April, 2013 to March, 2015.

6. Assessment of cattle genetic introgression in the domestic yak populations - Jayakumar S and Karan Veer Singh - April, 2012 to March, 2014, extended upto September, 2014.

7. Characterization of indigenous dog breeds of Tamil Nadu - KN Raja, PK Singh, AK Mishra, Indrajit Ganguly and P Devendran (TANUVAS) - April, 2013 to March, 2015.

8. Utilization of cauda epididymal spermatozoa for cryopreservation of caprine genetic biodiversity - RAK Aggarwal and D Mallakar (NDRI) - April, 2011 to March, 2014, extended upto March, 2015.

9. Development of breed signature for Sahiwal, Gir and Tharparkar cattle - MS Tantia and Monika Sodhi (w.e.f. 01.4.2013) - April, 2012 to March, 2015.

10. Identification of allelic diversity of MHC class II DR and DQ genes in domesticated indigenous Yak (*Bos grunnieons*) and Mithun(*Bos frontalis*) - SK Niranjan, RS Kataria, Jyotsana Behl, TK Biswas (NRC-YAK), Taba Heli (KVK Pampumpare) - April, 2013-March, 2016.

11. Development and validation of human tissue plasminogen activator gene construct in mammalian cell culture system - Indrajit Ganguly and Sanjeev Singh - April, 2012 to September, 2014, extended upto March, 2015.

12. Profiling of milk constituents, identification of SNPs and their association with milk traits in non-traditional dairy animals (NTDA) - Karan Veer Singh and Jayakumar S - April, 2012 to March, 2015.

13. Network Project on Animal Genetic Resources - Arjava Sharma (w.e.f. 01.10.2013), Project coordinator and MS Tantia, Incharge 1992- Contd.

### Externally Funded

1. Analysis of mammary gland transcriptome and proteome during lactation and involution in indigenous cattle and buffalo for identification of probable mammary biomarkers - M Mukesh, (BP Mishra upto 24.02.2011), RS Kataria and Monika Sodhi (w.e.f. January, 2012) - July 2008 to March 2012, extended upto 31st May, 2014 (NAIP).

2. Bio-prospecting of genes and allele mining for abiotic stress tolerance - RK Vijh - April, 2009 to March, 2012, extended upto 30th June, 2014 (NAIP).

3. Establishment of National Agricultural Bioinformatics Grid (NABG) in ICAR -

Avnish Kumar, DK Yadav, Dinesh Kumar BT (upto 18.05.2012), B Prakash and PK Vij - April, 2010 to March, 2012, extended upto 30th June, 2014 (NAIP).

4. Harmonizing Biodiversity conservation and Agricultural Intensification through Integration of plant Animal and fish genetic resources for livelihood security in fragile ecosystem - BK Joshi (up to 30.09.2013) Arjava Sharma (w.e.f. 01.10.13), Anand Jain, MS Tantia (up to 30.09.2011), PK Vij, NK Verma, RAK Aggarwal KN Raja and Vikas Vohra (w.e.f.10.07.2012) September 2009 to June 2013, extended upto June, 2014. (NAIP).

### National Fellow Project

1. Genome data mining to unravel molecular basis of thermo-tolerance and adaptation to diverse environment in native cattle and buffaloes - Manishi Mukesh - May, 2011 to 2016.

## Publications

1. Ahlawat S, Sharma R, Maitra A, Tantia, MS, Roy M and Mandakmale S (2014) New genetic polymorphisms in Indian goat BMPR1B gene. *Indian Journal of Animal Sciences* 84 (1): 39–44.

2. Behl Dhingra Jyotsna, Sharma A, Kataria RS, Verma NK, Kimothi SP, Bhatia AK, Sodhi M, Behl R, Joshi BK (2014) Genetic polymorphisms in the Bovine Toll-like receptor 4 (TLR4) and Monocyte Chemo attractant protein-1(CCL2) genes: SNPs distribution analysis in *Bos indicus* Sahiwal cattle breed. *Animal Biotechnology*, 25(4):250-265.

3. Dangi, PS, Singh, R, Pundir, RK, Singh, A, Chaudhary, V and Verma, NK (2013). Study of various performance traits in Rathi cattle. *Indian Journal of Animal Research*, 47(4):321-326.

4. Dubey PK, Goyal S, Kumari N, Mishra SK, Arora R, Kataria RS (2013). Genetic diversity within 5'upstream region of Toll-like receptor 8 gene reveals differentiation of riverine and swamp buffaloes. *Meta Gene,* 1:24–32.

5. Dubey PK, Singh S, Yadav NK, Kathiravan P, Mishra BP and Kataria RS (2014). PCR-SCCP and sequence analysis of leptin gene reveals novel polymorphism in intron 1 and allele fixation in exon 2 of Indian buffaloes (*Bubalus bubalis*). *Indian Journal of Biotechnology* 13: 47-51.

6. Goyal S, Dubey PK, Kumari N, Niranjan SK, Kathiravan P, Mishra BP, Mahajan R and Kataria RS (2014). Caprine Toll-like receptor 8 gene sequence characterization reveals close relationships among ruminant species. *International Journal of Immunogenetics* 41:81-89.

7. Goyal S, Dubey PK, Sahoo BR, Mishra SK, Niranjan SK, Singh S, Mahajan R, Kataria RS (2014). Sequence based structural characterization and genetic diversity analysis across coding and promoter regions of goat Toll-like receptor 5 gene. *Gene*, 540: 238–245.

8. Goyal S, Dubey PK, Kathiravan P, Mishra BP, Mahajan R and Kataria RS (2013). Expression analysis of viral nucleic acid recognizing toll-like receptor-7 and 8 genes across caprine tissues. *Indian Journal of Animal Sciences,* 83: 1068-1070.

9. Jamuna V, Chakravarty AK, Patil, CS, Mahajan AC, Dash S and Vohra V (2013).

Decline in Reproductive performance in High producing Murrah Buffalo. *Journal of Animal Research*, 3(2):203-208.

10. Janjanam J, Jamwal M, Singh S, Kumar S, Panigrahi AK, Hariprasad G, Jena MK, Anand V, Kumar S, Kaushik JK, Dang AK, Mukesh M, Mishra BP, Srinivasan A, Reddy VS, Mohanty AK (2013). Proteome analysis of functionally differentiated bovine (*Bos indicus*) mammary epithelial cells isolated from milk. *Proteomics*, 13(21):3189-204.

11. Kapila N, Kishore A, Sodhi M, Sharma A, Mohanty AK, Kumar P and Mukesh M (2013). Temporal changes in mRNA expression of heat shock protein genes in mammary epithelial cells of riverine buffalo in response to heat stress in vitro. *International Journal of Animal Biotechnology*, l 3: 5-9

12. Kishore A, Sodhi M, Kumari P, Mohanty AK, Sadana DK, Kapila N, Khate K, Shandilya U, Kataria RS and Mukesh M (2013). Peripheral blood mononuclear cells: a potential cellular system to understand differential heat shock response across native cattle (*Bos indicus*), exotic cattle (*Bos taurus*), and riverine buffaloes (*Bubalus bubalis*) of India. *Cell Stress and Chaperones* DOI:10 1007/s12192-013-0486-z.

13. Kishore A, Sodhi M, Mukesh M, Mishra BP, Sobti RC (2013). Sequence analysis and identification of new variations in the 5'-flanking region of αS2-casein gene in Indian zebu cattle. *Moleculor Biology Reports*, 40(7):4473-81.

17. Maitra A, Sharma R, Pandey AK, Singh LV, Mandakmale SD and Mishra BP (2013). Preliminary identification and characterization of Leptin gene polymorphism in Indian goats. *Journal of Applied Animal Research*. http://dx.doi.org/10.1080/09712119.2013.79589.

18. Malakar AK, Pallavi Singh KV and Srivastava S (2013). Review on DNA Microarrays: A Novel Tool for Identification and Exploitation of Fish conservation in Aquaculture. *World Journal of Fish and Marine Sciences*, 5 (1): 26-34.

19. Manuja A, Manuja BK, Kataria RS, Sethi RK and Singh RK (2013). Comparative Analysis of Molecular Structure, Function and Expression of Buffalo (*Bubalus bubalis*) Toll-Like Receptor 9. *Journal of Buffalo Science*, 2:63-71.

20. Mishra P, Ali AS, Kuralkar, SV, Dixit SP, Aggarwal RAK, Dangi PS and Verma NK (2013). Analysis of genetic diversity in Berari goat population of Maharashtra state. *Iranian Journal of Applied Animal Sciences*, 3(3):553-559.

21. Patil, CS, Chakravarty, AK, Singh A, Kumar V, Valsalan J and Vohra V (2014). Development of predictive model for daughter pregnancy rate and standardization of voluntary waiting period in Murrah buffalo. *Tropical Animal Health and Production*, 46(1): 279-284.

22. Sharma A, Dutt G, Jayakumar S, Verma NK, Singh MK, Pathodiya OP, Khadda BS and Dixit SP (2013). Novel SNPs in IGF1, GHR and IGFBP-3 genes reveal significant association with growth traits in Indian goat breeds. *Small Ruminant Research*, 115: 7– 14.

23. Sharma A, Jigyasa A, Sodhi M, Kishore A, Mishra BP, Mohanty AK, Kataria RS, Kaushik JK, Mukesh M (2014). Stage Specific Expression of ATP-Binding Cassette and

Solute Carrier Superfamily of Transporter Genes in Mammary Gland of Riverine Buffalo (*Bubalus bubalis*). *Animal Biotechnology,* 25: 200-209.

24. Sharma R, Ahlawat S, Maitra A, Roy M, Mandakmale S, Tantia MS (2013). Polymorphism of BMP4 gene in Indian goat breeds differing in prolificacy. *Gene*, 532: 140–145.

25. Sharma R, Maitra A, Singh PK and Tantia MS (2013). Genetic diversity and relationship of cattle populations of East India: distinguishing lesser known cattle populations and established breeds based on STR markers. *Springer Plus*, **2**: 359-368.

26. Sharma R, Maitra A, Pandey AK, Singh LV and Mishra BP (2013). Single nucleotide polymorphisms in caprine calpastatin gene. *Russian Journal of Genetics (Genetika).* 49 (4): 441-447.

27. Sharma R, Maitra A, Singh LV and Tantia MS (2013). Identification of Novel Single Nucleotide Polymorphisms in Meat Quality Candidate Genes of Indian Goats. *Indian Journal of Dairy Science,* 66(4): 309-316.

28. Sharma R, Singh PK, Maitra A, Pandey AK, Mukesh M, Singh SR and Kumar B (2013). Molecular characterization, body parameters and management practices of Purnea cattle. *Indian Journal of Animal Sciences*, 83(5): 536-541.

29. Singh LV, Sharma A, Singh N, Kaur N, Jayakumar S, Dixit SP, Gupta N and Gupta SC (2013). Comparative sequence analysis in the exon 5 of growth hormone gene in the various livestock species of India. *Animal Biotechnology,* 25(1): 69-72.

30. Sodhi M, Mukesh M, Kishore A, Mishra BP, Kataria RS, Joshi BK (2013). Novel polymorphisms in UTR and coding region of inducible heat shock protein 70.1 gene in tropically adapted Indian zebu cattle (*Bos indicus*) and riverine buffalo (*Bubalus bubalis*). *Gene*, 25; 527(2):606-15

31. Yadav DK, Arora R and Jain A (2014). Exploring Deccani sheep ecotypes of Maharashtra: Are these autonomous breeds? *Indian Journal of Small ruminants,* 20(1):91-94.

32. Yadav P, Singh DD, Mukesh M, Kataria, RS Yadav A, Mohanty AK and Mishra BP (2014). Expression Profiling of Glucose Transporter 1 (GLUT1) and Apoptotic Genes (BAX and BCL2) in Milk Enriched Mammary Epithelial Cells (MEC) in Riverine Buffalo during Lactation. *Animal Biotechnology*, 25(3): 151-159.

## Technical/popular article:

1. Joshi BK and Monika Sodhi (2013) Biodiversity: the lifeline of mankind. *Saadar India*. Pp: 22-27.

2. निरंजन एसके, काथिरवन पी, सिंह एस एवं कटारिया आरएस (2013) टोडा भैंस–नीलगिरि पहाड़ो की विशिष्ट नसल. पशुधन प्रकाश, 4:3–6.

3. सिंह पीके एवं असिजा के (2013) भारत में गोवंश विविधता एवं दूध उत्पादन में उनका योगदान. दुग्ध–गंगा (एनडीआरआई) करनाल

4. Singh S and Ganguly I (2013) RNAi technology: Implications and applications-A review. *Agricultural Review,* 34 (1):60-70.

5. सिंह एस एवं गांगुली आई (2013) भारत की मांस उत्पादन करने वाली भेड़ की नस्ल तथा मांसाहारी भोजन का महत्व. पशुधन प्रकाश, 4:65–67.

6. सिंह एसपी एवं सिंह एस (2013) पशु चिकित्सा हेतु घरेलु औषधियाँ और उनका प्रयोग. पशुधन प्रकाश, 4:57–59.

7. तोमर एके, चोपड़ा ए, मिश्रा एके एवं नकवी एसएमके (2013). देश में अग्रणी राजस्थानी भेड़ सम्पदा. पशुधन प्रकाश, 4:17–22.

8. विज पीके, निरंजन एसके, टाटिया एमएस एवं जोशी बीके (2013) पशुधन नस्ल पंजीकरणः राष्ट्रीय सम्पदा की सुरक्षा. पशुधन प्रकाश 4:84–90.

9. Vohra V, Sadana DK and Kataria RS (2014). Documentation of farm animal genetic Resource - Kalahandi Buffalo E-pub./vv2014/3 March 27, 2014. http://www.scribd.com/doc/215029475/Breed-Descriptor-Kalahandi-Epub

10. Vohra V, Niranjan SK, Mishra AK and Sadana DK (2014) Documentation of farm animal genetic resource – Gojri Buffalo. Online publication Epub/vv/2014/05/28 March, 2014. http://www.scribd.com/doc/215030309/

11. Vohra V, Kataria RS and Sadana DK (2014). Documentation of farm animal genetic resource – Niliravi Buffalo E-pub./vv2014/4 March 27, 2014 http://www.scribd.com/doc/215029869/Breed-Discriptor-Nilli-Ravi-Epub

12. Vohra V, Niranjan SK and Kataria RS (2013). Detection and genotyping of single nucleotide polymorphism. E-pub./vv2013/1 September 5, 2013. http://www.scribd.com/doc/165650161/Detection-and-Genotyping-Single-Nucleotide-Polymorphism

## Books

1. Raja KN, Kathiravan P, Sharma R and Joshi B K. 2013. Genome analysis in farm animals. Jaya publishing house, Delhi, ISBN: 978-93-82471-15-8.

2. Pundir RK, Niranjan SK, and Behl R, 2013. Sustainable Utilization of Indigenous Animal Genetic Resources of India. National Bureau of Animal Genetic Resources, Karnal, Haryana, India, 209 pp. *ISBN: 978-93-85537-08-2.*

3. Behl R, Pundir RK, Behl J, Vijh RK, and Joshi BK 2013. Insights in to coat colours in horses. Glam Media, Karnal, pp 98. *ISBN: 978-93-85537-09-9.*

4. Sadana DK, Singh PK, Pundir RK, Vohra V. Country Report-2 on State of World Animal Genetic Resources, FAO, Rome.

## Book chapters

1. Mishra AK (2013) Contributed in "Poultry breeding" in *Hand book of Animal Husbandry* published by ICAR New Delhi.

2. Vij PK (2013). Registration of Livestock and Poultry Breeds in India. In '*Sustainable Utilization of Animal Genetic Resources of India*'. Eds. R K Pundir, S K Niranjan and R Behl. NBAGR, Karnal. *ISBN: 978-93-85537-08-2*. pp: 140-45.

3. Ganguly I, Ganguly A, Singh S and Raja KN (2013) DNA sequence analysis in *Genome analysis in farm animals*, Narendra Publishing house, Delhi.

4. Singh S, Ganguly I and Singh SP (2013) Biodiversity and conservation of small ruminants. In *conservation agriculture: the new paradigm* Biotech books, New Delhi.

5. Kataria RS and Niranjan SK (2013). Molecular markers for characterization and conservation of livestock biodiversity. In

*Sustainable Utilization of Indigenous Animal Genetic Resources of India.* NBAGR, Karnal.

- Verma N K (2013). Status and characterization of goat genetic resources of India. In *Sustainable Utilization of Indigenous Animal Genetic Resources* NBAGR, Karnal.
- Vohra V and Niranjan SK (2013). Documentation of Belahi Cattle conserved by Gurjar Pastoral communities from Haryana in Livestock Keepers Profile for Breed Savior Awards 2012 Sponsored by National Biodiversity Authority of India in collaboration with SEVA, LIFE Network and NBAGR, Karnal (Haryana)

## Leaflets & Pamphlets

1. NBAGR Profile 2014, NBAGR Karnal
2. सिंह पीके, मिश्रा एके एवं वोहरा वी (2013) भारतीय पशुधन सम्पदा, एनबीएजीआर, करनाल
3. वोहरा वी, मिश्रा एके एवं निरंजन एसके (2013) प्रसवोपरान्त भैंसों की देखभाल, एनबीएजीआर, करनाल

# Patents and Technologies

## Patents

Total eight patents were filed to the Indian Patent Office, New Delhi during this financial year.

**Patents filed to the Indian Patent Office, Delhi**

| Application No. | Patent Title | Inventors | Type of application | Date of filing patents |
|---|---|---|---|---|
| 1889/DEL/2013 | QTLs for milk yield in buffaloes | Dr. Ramesh Kumar Vijh, Priyanka Banerjee, Jyoti Joshi, Upasna Sharma | Complete | 26-Jun-13 |
| 1890/DEL/2013 | QTLs for somatic cell count in buffaloes | Dr. Ramesh Kumar Vijh, Priyanka Banerjee, Jyoti Joshi, Upasna Sharma | Complete | 26-Jun-13 |
| 2426/DEL/2013 | QTLs for milk fat percent in buffaloes | Dr. Ramesh Kumar Vijh, Priyanka Banerjee, Jyoti Joshi, Upasna Sharma | Complete | 16-Aug-13 |
| 2427/DEL/2013 | QTLs for milk protein percent in buffaloes | Dr. Ramesh Kumar Vijh, Priyanka Banerjee, Jyoti Joshi, Upasna Sharma | Complete | 16-Aug-13 |
| 3717/DEL/2013 | A kit for molecular traceability of meat in livestock and poultry species | Dr. Ramesh Kumar Vijh, Jyoti Joshi, Priyanka Banerjee, Upasna Sharma | Provisional | 20-Dec-13 |
| 3718/DEL/2013 | Traceability of Buffaloes to their breed/ geographical location of origin | Dr. Ramesh Kumar Vijh, Jyoti Joshi, Priyanka Banerjee, Upasna Sharma | Provisional | 20-Dec-13 |
| 3719/DEL/2013 | Traceability of Goat to their breed/geographical location of origin | Dr. Ramesh Kumar Vijh, Jyoti Joshi, Priyanka Banerjee, Upasna Sharma | Provisional | 20-Dec-13 |
| 3720/DEL/2013 | Traceability of Camel to their breed/geographical location of origin | Dr. Ramesh Kumar Vijh, Jyoti Joshi, Priyanka Banerjee, Upasna Sharma | Provisional | 20-Dec-13 |

Three patent applications, already filed in 2011 viz. "A Kit for Parentage Verification in Zebu Cattle (Bos Indicus); A Kit for Parentage Verification in Camels (Single and Double Hump); A Kit for Parentage Verification in Buffaloes (Bubalus Bubalis)", were published in the Indian Patent Office Journal on 28th June 2013 and first examination request of these three patent applications were submitted to the Indian Patent Office, New Delhi on 16th August 2013.

### Commercialization of technology

National Agricultural Innovation Project (NAIP) of the Indian Council of Agricultural Research (ICAR) organized a two-day Agri-Tech Investors Meet, to promote the agro-technologies developed during the NAIP period (2006-13). The meet was held at the NASC Complex, New Delhi on 18-19 July 2013. During this event MoU was signed between M/s Sandor Proteomics Pvt. Ltd. Hyderabad and NBAGR for commercialization of the technology entitled "A Kit for parentage verification in Indian Ruminant Livestock" on 18th July 2013.

# Other Activities

- Library
- Infrastructure Development
- Important Meetings
- Exhibitions
- Celebrations
- Trainings / Workshops
- Awards & Recognition
- Deputation
- Sports
- National Symposium
- Distinguished Visitors


Brainstorming Workshop on
Strategy related to Conservation and

## 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 the guiding force in the management of the library issues pertaining to purchase of scientific books/journals etc. The Bureau LAC was reconstituted on 9th July, 2013. The composition of LAC is as follows:

| | |
|---|---|
| Director | Chairman |
| I/c AGR | Member |
| I/c AG | Member |
| I/c DNAFU | Member |
| Dr. Reena Arora(P.S.) | Member |
| A.O. | Member |
| FAO | Member |
| I/c Purchase | Member |
| I/c Library | Member |

Books and journals worth Rs. 10,13,297 were procured in the library during the period. Twelve foreign journals and thirty one Indian Journals have been subscribed for the benefit of scientific readers.

| | |
|---|---|
| Total collection | 3997 |
| Books added | 132 |
| Indian Journals subscribed | 31 |
| Foreign journals subscribed | 12 |
| News papers subscribed | 07 |

## Infrastructure Development

### Inauguration of High Performance Computing (HPC) system

Dr. KML Pathak, Deputy Director General (Animal Sciences), ICAR inaugurated the High Performance Computing (HPC) system installed at the Computer Center of NBAGR, Karnal on

*Dr. KML Pathak inaugurating HPC system*

2nd September, 2013. The HPC system consists of Linux Cluster with 16 nodes, 20 Terabytes of Network Attached Storage (NFS server), 20 Terabytes of Parallel File System based Storage and 64 bit Linux Operating System. The system will be used for animal genomics and proteomics studies in the National Agricultural Research System.

### Inauguration of Research Laboratory Wing

Research Laboratory Wing on the first floor of the main building was inaugurated by Dr. S Ayyappan, Secretary (DARE) & DG (ICAR) on 11th February, 2014. Dr. KML Pathak, DDG (AS) ICAR and Dr. AK Srivastava, Director, NDRI, Karnal also graced the occasion.

*Dr S.Ayyappan inaugurating the Research Laboratory Wing*

## Important Meetings

### IMC meeting

Institute Management Committee meeting was held on 8th July, 2013 under the chairmanship of Director, NBAGR.

*IMC meeting in progress*

### IJSC meeting

Institute Joint Council meeting was held on 20th July, 2013 under the chairmanship of Director to discuss the various matters related with welfare of the staff.

### ITMC meeting

Six meetings of ITMC of NBAGR, Karnal were held to finalize different issues pertaining to IPR and commercialization of technology during the period under report.

ITMC meetings were held with the agenda of discussion on six patent applications submitted by Dr. RK Vijh and others and issue of commercialization of the technology "PCR based DNA test for the differentiation of cattle and buffalo meat and milk" submitted by Dr. RS Kataria and others.

### DBT-Task Force meeting

NBAGR organized the Task Force Meeting of DBT on 16th-17th May, 2013.

### IRC meeting

Institute Research Committee (IRC) meeting was held on 29th-30th October, 2013 under the Chairmanship of Dr. Arjava Sharma, Director, NBAGR. Progress of the on-going research projects was reviewed.

*IRC meeting in progress*

### RAC meeting

Research Advisory Committee (RAC) meeting was held on 12th March, 2014 under the Chairmanship of Dr. R Prabakaran. The progress of the research activities for the year 2013-14 was reviewed and recommendations were made for the betterment of research.

*RAC meeting in progress*

## Exhibitions

Photography and Exhibition Unit of the Bureau organized exhibitions on farm animal genetic resources at different places / states during Kissan Melas / Dairy Melas /Pashumela and field days.

**Exhibitions / fairs organized by Photo Exhibition Unit, NBAGR**

| S. No. | Occasion | Dates | Place |
|---|---|---|---|
| 1 | AnGR Exhibition | 27th April 2013 | NBAGR, Karnal (Haryana) |
| 2 | KisanMela | 15th October 2013 | Directorate of Wheat Research |
| 3 | KisanMela | 5th February 2014 | Sugarcane breeding Institute, Karnal |
| 4 | Foundation Day Celebrations | 21st September 2013 | NBAGR, Karnal (Haryana) |
| 5 | Dairy Mela | 25-27th February 2014 | National Dairy Research Institute |
| 6 | National Livestock Championship | 8th to 12th January 2014 | Muktsar Mela, Punjab |

*NBAGR exhibition at DWR, Karnal*

## Celebrations

### International Biodiversity Day

The Bureau celebrated International Biodiversity Day on 22nd May, 2013 at the Bharoli Kalan village of Pathankot (Punjab). Pashu Mela-cum-Animal Genetic Resource Exhibition was organized by team of scientists from National Bureau of Animal Genetic Resource Karnal, (ICAR) in collaboration with Animal Husbandry Directorate (Punjab) and Krishi Vigyan Kendra, Gurdaspur (Punjab). Traditional Gojri buffalo Keepers of Gujjar Community were praised for their contribution in livestock sector on this occasion. Various breed competitions were held on 20th and 21st May, 2013 among the Gojri buffalo keepers of more than 10 villages of Pathankot tehsil and winners for different categories were awarded. The program was coordinated by Dr. Vikas Vohra, Dr. SK Niranjan and Dr. AK Mishra.

*Glimpse of International Biodiversity Day*

### Independence Day

NBAGR celebrated 67th Independence Day of India on 15th August, 2013. Dr BK Joshi, Director, addressed the staff and their families on this occasion. Cultural program presented by the children made the day even more special.

*Independence Day celebration*

### 30th Foundation Day

NBAGR celebrated its Foundation Day on 21st September, 2013. Dr. Gurbachan Singh, Chairman, Agricultural Scientists Recruitment

Board (ASRB) was the chief guest and delivered the Foundation Day lecture. Dr. AK Srivastava, Director National Dairy Research Institute graced the occasion as guest of honor. A poster exhibition was held to mark the occasion.

To promote competitive spirit for excellence in working, best workers in technical, administrative and supporting staff were also recognized with awards. Smt. Anita Chanda, PA (Administrative category), Dr. PS Dangi, Assistant Chief Technical Officer and Sh. Subhash Chander, Senior Technical Assistant (Technical category), Sh. Deepak, Skilled Supporting Staff (Supporting Staff) category were falicitated on this occassion. Fourth edition of hindi journal "पशुधन प्रकाश" was also released on the occasion.

## Vigilance Day

NBAGR staff members took the oath against corruption on 28th October, 2013 to commemorate the Vigilance Day.

## Republic Day

The NBAGR staff and families celebrated the Republic Day on 26th January, 2014. Dr. Arjava Sharma, Director, NBAGR hoisted the tricolor and addressed the staff and family members on this occasion.

*Republic Day celebration*

*Dr. P. S. Dangi, (Technical category)*

*Smt. Anita Chanda, PA (Administrative category)*

*Sh. Subhash Chander, (Technical assistant category)*

*Sh. Deepak (Supporting Staff category)*

## Trainings and Workshops

- Dr. NK Verma, Incharge PME and Dr. SK Niranjan attended the *"MDP workshop on PME of Agricultural Research Projects"* at NAARM, Hyderabad on during 18th-22nd June, 2013.
- Short Course on *"Sustainable Utilization of Indigenous Animal Genetic Resources of India"* sponsored by Education Division, Indian Council of Agricultural Research, New Delhi was organised during 17th-26th July, 2013 at NBAGR, Karnal. Dr. RK Pundir was Course Director and Dr. SK Niranjan was Course Coordinator. Thirteen participants from different states participated in this training programme.
- Workshop on 'Animal Bioinformatics and Genomics Research Programs' under National Agricultural Bioinformatics Grid (NABG) was held at National Bureau of Animal Genetic Resources, Karnal on 2nd September, 2013. It was attended by Dr. KML Pathak DDG (Animal Sciences) as Chief Guest. Dr. BK Joshi, Director, NBAGR, Dr. Arjava Sharma, Project Director, PDC, Dr. Anil Rai, IASRI, Dr. V Bhasin, Principal Scientist, ICAR, and other scientists from IASRI, NBAGR, NDRI, IVRI, CIRB, GADVASU, and LLRUVAS. The workshop deliberated on research programs to be taken in the areas of Animal Bioinformatics and Genomics to be proposed under the Network Project on Computational Biology and Agricultural Bioinformatics during XII Plan (2012-17).

- Dr. PK Singh, I/c ITMU, Dr. AK Mishra, Principal Scientist, Dr. RS Kataria, Principal Scientist, Dr. Vikas Vohra, Senior Scientist, Dr. KN Raja, Scientist, Mrs. Karuna Asija, Research Associate, ITMU attended one day Awareness Programme and Workshop on *"IPR for Agriculture & Allied Sciences"* organized at NDRI, Karnal on 18th October, 2013.
- Dr. RK Pundir attended training on *"Management Development Programme on Leadership Development (Pre RMP Cadre)"* held from 26th November to 07th December, 2013 at NAARM, Hyderabad.
- Training on *"Computational Tools for Animal Genome Resource Data Analysis"* under NAIP Subproject "Establishment of National Agricultural Bioinformatics Grid (NABG) in ICAR" was held at NBAGR, Karnal from 2nd-13th December, 2013. The training was coordinated by Dr. Avnish Kumar and Dr. Karan Veer Singh.

*Dr. KML Pathak addressing the participants of the workshop*


*Brain storming workshop at New Delhi*

- Brain storming workshop on *"Strategies related to conservation and productivity enhancement of farm animal genetic resources"* was organized by NBAGR and Trust for Advancement of Agricultural Sciences (TAAS) at NASC complex, New Delhi on 10th January, 2014. Dr. Arjava Sharma was organizing secretary.


*Brain Storming Session at Imphal, Manipur*

- Brain Storming Session on *"Animal Genetic Resources of Manipur"* was organized on 5th March, 2014 at Imphal, Manipur.
- Dr. Vikas Vohra acted as Joint Coordinator of ICAR sponsored 21 days National Training Programme (Centre of Advanced Faculty Training in AGB) on *"Advanced Breeding and Allied Technologies for Enhancing Livestock Productivity"* held at DCB Division, NDRI, Karnal during 5th -25th March, 2014.
- Dr. PK Singh, I/c ITMU, Dr. AK Mishra, Principal Scientist, Dr. RS Kataria, Principal Scientist, Dr. Vikas Vohra, Senior Scientist, Dr. KN Raja, Scientist, Mrs. Karuna Asija, Research Associate, ITMU attended one day Awareness Programme and Workshop on "IPR for Agriculture & Allied Sciences" organized at NDRI, Karnal on 18th October 2013.

## Awards & Recognitions

- **Hon'ble President of India** conferred the prestigious ***"Biotech Product and Process Development and Commercialization Award 2013"*** upon **Dr Ramesh Kumar Vijh** on Technology Day (11th of May, 2013) at Vigyan Bhawan New Delhi for his outstanding research contribution for the development of parentage verification kits for livestock species. The award carried a certificate, a trophy and prize money of Rs 2.0 Lakhs.


*Dr R.K.Vijh receiving award from Hon'ble President of India*

- Dr. PG Nair award 2013 was awarded to Dr. RK Vijh for outstanding scientific contributions made during last three years.

*Dr R.K.Vijh receiving Dr. P. G. Nair award*

- NBAGR received Best Stall Award at Kisan Mela organized at Directorate of Wheat Research, Karnal on 15th October, 2013.

*Best stall award to NBAGR*

- M Mukesh, Amit Kishore, Parvesh Kumari, Preeti Verma, Sandeep Mann and M Sodhi received best poster award at XIth National Symposium on "Harmonizing Phenomics and Genomics for Sustainable Management of Livestock for Upliftment of Rural Masses" of Society of Conservation of Domestic Animal Biodiversity (SOCDAB) held at NBAGR, Karnal on 6th-7th February, 2014 for the research presentation: *"SNP mining to unravel diversity and evolution of immune responsive genes"*.

- Dinesh Kumar Yadav, Reena Arora and Anand Jain received second best poster award at XIth National Symposium on "Harmonizing Phenomics and Genomics for Sustainable Management of Livestock for Upliftment of Rural Masses" of Society of Conservation of Domestic Animal Biodiversity (SOCDAB) held at NBAGR, Karnal on 6th-7th February, 2014 for the research presentation *"Morphological structure of Madgyal sheep as revealed by principal component analysis of body measurements"*.

- Monika Sodhi, Ankita Sharma, Amit Kishore, MS Tantia, RS Kataria, Inderjeet Ganguly, AK Mohanty, Parvesh Kumari, Pradeep Jatav and M Mukesh received second best poster award at XIth National Symposium on "Harmonizing Phenomics and Genomics for Sustainable Management of Livestock for Upliftment of Rural Masses" of Society of Conservation of Domestic Animal Biodiversity (SOCDAB) held at NBAGR, Karnal on 6th-7th February, 2014 for the research presentation: *"Understanding biochemical and transcriptomic changes during pre and post partum stages of native cattle and buffaloes"*.

- Sonika Ahlawat, Rekha Sharma, A. Maitra and M. S. Tantia received young scientist award at XIth National Symposium on "Harmonizing Phenomics and Genomics for Sustainable Management of Livestock for Upliftment of Rural Masses" of Society of Conservation of Domestic Animal Biodiversity (SOCDAB) held at NBAGR, Karnal on 6th-7th February, 2014 for her research presentation on "*Designing of Tetra-ARMS PCR and PCR-RFLP based methods for genotyping novel mutations in Fec genes*".

- A K Mishra, K N Raja, V Vohra and Yashwant Singh received second best poster award at XIth National Symposium on "Harmonizing Phenomics and Genomics for Sustainable Management of Livestock for Upliftment of Rural Masses" of Society of Conservation of Domestic Animal Biodiversity (SOCDAB) held at NBAGR, Karnal on 6th-7th February, 2014 for the research presentation: *Kajali sheep: an unexplored mutton type sheep of Punjab.*

- P K Singh, R K Pundir, D K Sadana, and K Asija received best poster award at XIth National Symposium on "Harmonizing Phenomics and Genomics for Sustainable Management of Livestock for Upliftment of Rural Masses" of Society of Conservation of Domestic Animal Biodiversity (SOCDAB) held at NBAGR, Karnal on 6th-7th February, 2014 for the research presentation: *Physical Traits, Management and Performance of Sanchori cattle in its breeding tract.*

- Meenakshi Arora, Avnish Kumar Bhatia and Dinesh Kumar Yadav received best poster presentation award at National Symposium on -Emerging Trends in Agri-Bioinformatics (ETAB-2013) held at Directorate of Wheat Research, Karnal during 16th-17th December,

2013 for the presentation: *Comparative analysis of large scale phylogeny estimation softwares.*

- Rekha Sharma, A Maitra, Manishi Mukesh, Monika Sodhi, P K Singh, Sonika Ahlawat and M S Tantia received best oral paper presentation award in the International Conference on "Biodiversity, Bioresources and Biotechnology" held at, Mysore, Karnataka (India) on 30th-31st January, 2014 for the research presentation: "*Indian cattle population structure: new insights from microsatellite and mitochondrial polymorphisms*".
- BIOVED Fellowship 2014 in the field of Animal Genetics and Breeding to Dr. R. K. Pundir, BIOVED Research Institute of Agriculture and Technology, Allahabad.
- Fellow of National Academy of Dairy Science (India) was conferred to Dr. P.K. Singh, Principal Scientist, AGR Division.
- Dr. P. K. Singh nominated as member of RAC for NRC on Yak, Dirang (Arunachal Pradesh) for a period of three years.
- Dr. P.K. Singh attended six meetings of ITMC at NDRI, DWR, Karnal to finalize different issues pertaining to IPR and commercialization of technology as an expert member of the committee.

*Dr. P. K. Singh receiving the fellowship award*

- Vigyan Parishad Shatabdi Samman (2012-13) to Dr. A. K. Mishra by Vigyan Parishad Pryag (branch Chitrakoot).
- For the quality management of research and training related with mandate, the Bureau has obtained ISO 9001: 2008 Certificate.

## Deputations

International training under HRD programme of NAIP (Component 1) was awarded to the following scientists of Bureau:

- Dr. Sanjeev Singh, Senior Scientist – Iowa State University, Ames, USA, from 28th August to 18th November, 2013, in the area of allele mining.
- Dr Jayakumar S, Scientist - University of Sydney, Australia from 30th August to 26th November, 2013, in the area of Marker Assisted Selection.
- Dr. Indrajit Ganguly - College of Veterinary Medicine & Biomedical Sciences, Texas A & M University, Texas, USA from 6th January 2014 to 25th March 2014, in the area of allele mining.

## Sports

A sports contingent of 34 members participated in ICAR Zonal Sports Meet (North Zone-2014) held at Indian Institute of Pulses Research, Kanpur, (Uttar Pradesh) from 20th-23rd March, 2014. The Bureau excelled in three events:

- The institute volleyball smashing and basketball teams won gold and silver medals respectively.
- Shri. Yoginder bagged silver medal in 400 meters running (men) event.
- Shri Moti Ram bagged bronze medal in cycle race (men).

*Sports Contingent with Director, NBAGR*

*Inauguration of National Symposium*



## National Symposium

National Bureau of Animal Genetic Resources (NBAGR) in collaboration with Society for Conservation of Domestic Animal Diversity (SOCDAB), Karnal, organized a National Symposium on *"Harmonizing Phenomics and Genomics for sustainable management of livestock for upliftment of rural masses"* from 6th-7th February, 2014 at NBAGR campus Karnal. Maj. Gen. Shri Kant, SM, VSM (Retd.) and Vice Chancellor, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar, presided over the inaugural function. Dr. SPS Ahlawat, former VC, Vikram University, Ujjain, and Dr. GS Jakhar, Director General, Animal Husbandry and Dairying, Haryana were the Guests of Honour. Dr. NK Verma, Principal Scientist and Dr. SK Niranjan, Senior Scientist acted as Organizing and Co-Organizing Secretary, respectively. A Compendium of 239 pages compiled and edited by Dr. DK Sadana, Dr. NK Verma, Dr. RK Pundir, Dr. PK Singh, Dr. RS Kataria, Dr. Vikas Vohra and Dr. SK Niranjan was released on this occasion. 166 delegates from different parts of the country participated in this symposium and presented their research work.

*Compendium of the conference being released by the dignitaries*

## Distinguished Visitors

- Dr. Sipke Joost Hiemstra, Head, Animal Genetic Resources Group, Centre for Genetic Resources, The Netherland visited on 21.05.2013.
- Prof. KML Pathak, DDG(AS), Dr. SC Gupta, ADG(AP&B), Dr. BS Prakash, ADG (ANP) ICAR visited on 15.06.2013.

*Dr. B. K. Joshi interacting with the visitors*

- The participants of Summer School on "Technological innovations for shaping future agriculture in salt affected areas" organized at CSSRI, Karnal visited NBAGR on 15.06.2013.
- Livestock Farmers from Barmer (Rajasthan) visited on 27.06.2013.
- Mr. Allan Mustard, Minister-Counsellor for Agricultural Affairs alongwith Dr. Santosh Singh, Sr. Agricultural Specialist, Embassy of United States of America visited on 09.07.2013.
- The participants of Agriculture Exposure Visit Programme of Jharkhand State Agriculture Department organised by Centre for Agriculture and Rural Development, New Delhi visited on 12.08.2013.
- The Secretary, Dept. of Animal Husbandry, Dairying and Fisheries, New Delhi visited on 22.08.2013.
- Dr.KML Pathak, Deputy Director General (AS), ICAR visited on 02.09.2013.

*Director, NBAGR welcoming Dr. KML Pathak (DDG, AS)*

- Dr. Gurbachan Singh, Chairman, Agricultural Scientists' Recruitment Board, New Delhi visited on 21.09.2013.
- Students of B.Sc. Biotechnology from DAV College, Amritsar visited on 07.11.2013.
- A group of 50 female farmers from F.T.C. Godhra Distt. Panchmahal (Gujarat) visited NBAGR on 21.12.2013.
- A group of 50 farmers from F.T.C. Godhra Distt. Panchmahal (Gujarat) visited NBAGR on 11.01.2014.

*Farmers from Barmer*

- His Excellency Lyonpo Yeshey Dorji, Minister for Agriculture & Forests, Royal Government of Bhutan accompanied by three officers visited on 03.02.2014.

*His Excellency Lyonpo Yeshey Dorji interacting with the scientists*

- Maj. Gen. Shri Kant, SM, VSM (Retd), & Vice Chancellor, Lala Lajpat Rai University of Vety. & Animal Sciences, Hisar visited on 06..02.2014.

- Dr. SPS Ahlawat, Former Director, NB AGR, IVRI and Vice-Chancellor, Vikram University visited on 06.02.2014.
- Dr. GS Jakhar, Director General, Animal Husbandry & Dairying, Haryana visited on 06.02.2014.
- Dr. SC Gupta, Former ADG (AP&B), ICAR visited on 6-7.02.2014.
- Dr. RS Gandhi, ADG (AP&B), ICAR visited different labs of NBAGR on 07.02.2014.
- Dr. S Ayyappan, Secretary (DARE) & DG (ICAR), Dr. KML Pathak, DDG (AS) ICAR and Dr. AK Srivastava, Director, NDRI, Karnal visited on 11.02.2014.
- Sh. Arvind R. Kaushal, Additional Secretary (DARE) and Secretary (ICAR) and Dr.K.M.L.Pathak, DDG(AS), ICAR visited on 14.02.2014.
- The students of MSc (Integrated) Bioanalytical Sciences from Ramnarain Ruia College, Mumbai visited on 06.03.2014.
- Dr. RS Rana, Former Director, NBPGR, New Delhi visited on 13.03.2014.

*Dr. S. Ayyappan DG, ICAR addressing the Bureau staff*

*Sh. Arvind R Kaushal's visit to NBAGR*

- A batch of 17 students (M.Sc. Integrated) alongwith two faculty members from Kurukshetra University, Kurukshetra visited on 13.03.2014.
- The students from Hansraj College, Delhi University visited on 19.03.2014.

# Personnel

- Bureau Staff
- Promotions
- Joining/Training
- Superannuation
- Joinings/Transfers


11 मई 2013, नई दिल्ली
Day
S Jaipal Red
T Ramasam
Anil Gupta

## Bureau Staff

| Sr. No. | Name of Scientist | Designation |
|---|---|---|
| 1. | Dr. BK Joshi | Director (up to 30.09.2013) |
| 2. | Dr. Arjava Sharma | Director (w.e.f. 01.10.2013) |
| 3. | Dr. DK Sadana | Pr. Scientist |
| 4. | Dr. B Parkash | Pr. Scientist |
| 5. | Dr. RK Vijh | Pr. Scientist |
| 6. | Dr. Anand Jain | Pr. Scientist |
| 7. | Dr. MS Tantia | Pr. Scientist |
| 8. | Dr. PK Vij | Pr. Scientist |
| 9. | Dr. NKVerma | Pr. Scientist |
| 10. | Dr. RAK Aggarwal | Pr. Scientist |
| 11. | Dr. PK Singh | Pr. Scientist |
| 12. | Dr. RK Pundir | Pr. Scientist |
| 13. | Dr. RS Kataria | Pr. Scientist |
| 14. | Dr. Anil Kumar Mishra | Pr. Scientist |
| 15. | Dr. Monika Sodhi | Pr. Scientist |
| 16. | Dr. Jyostna Behl | Pr. Scientist |
| 17. | Dr. Satpal Dixit | Pr. Scientist |
| 18. | Dr. Dinesh Kr. Yadav | Pr. Scientist |
| 19. | Dr. Manishi Mukesh | Pr. Scientist & National Fellow |
| 20. | Dr. Reena Arora | Pr. Scientist |
| 21. | Dr. Avnish Kumar | Pr. Scientist |
| 22. | Dr. Rahul Behl | Sr. Scientist |
| 23. | Dr. Rekha Sharma | Sr. Scientist |
| 24. | Dr. Vikas Vohra | Sr. Scientist |
| 25. | Dr. Saket Kr. Niranjan | Sr. Scientist |
| 26. | Dr. Indrajit Ganguly | Sr. Scientist |
| 27. | Dr. P Kathiravan | Sr. Scientist |
| 28. | Dr. Sanjeev Singh | Sr. Scientist |
| 29. | Dr. Karan Veer Singh | Scientist (S.S) |
| 30. | Dr. KN Raja | Scientist |
| 31. | Dr. Jayakumar S. | Scientist |
| 32. | Dr. Sonika Ahlawat | Scientist |

## Technical

| S. No. | Name | Designation |
|---|---|---|
| 1. | Dr. PS Dangi | ACTO |
| 2. | Sh. SK Jain | ACTO |
| 3. | Dr. PS Panwar | STO |
| 4. | Sh. Sanjeev Mathur | STO |
| 5. | Sh. Moti Ram | TO |
| 6. | Sh. Harvinder Singh | TO |
| 7. | Sh. Sat Pal | TO |
| 8. | Sh. Jamer Singh | TO |

| S. No. | Name | Designation |
|---|---|---|
| 9. | Smt. Pravesh Kumari | TO |
| 10. | Sh. Naresh Kumar | TO |
| 11. | Sh. Ramesh Kumar | STA |
| 12. | Sh. Subhash Chander | STA |
| 13. | Sh. Rakesh Kumar | STA |
| 14. | Sh. Ashok Kumar | STA |
| 15. | Sh. Mahavir Singh | STA |
| 16. | Sh. Vijay Singh | STA (up to 01-08-2013) |
| 17. | Sh. Om Prakash | STA |
| 18. | Sh. Ramesh Chand | STA |
| 19. | Sh. Balvinder Singh | Technician (T-1) |

## Administrative

| S. No. | Name | Designation |
|---|---|---|
| 1. | Sh. Jagtar Singh | AO |
| 2. | Sh. Sunil Kumar | F&AO |
| 3. | Sh. Karambir | PS to Director |
| 4. | Sh. Balkar Singh | AAO |
| 5. | Sh. Pawan Kr. Gupta | AF&AO |
| 6. | Sh. Ramesh Behl | Assistant |
| 7. | Smt. Anita Chanda | PA |
| 8. | Smt. Amita Kumari | PA |
| 9. | Smt. Indu Bala, Steno | Steno Gr.III |
| 10. | Sh. Jita Ram | Assistant |
| 11. | Smt. Shashi Bala | Assistant |
| 12. | Sh. Yoginder | Assistant |
| 13. | Sh. Sopal | UDC |
| 14. | Sh. Satish Kumar | UDC |
| 15. | Sh. Shiv Chander | LDC |
| 16. | Sh. Rajnish Kumar | LDC |
| 17. | Smt. Neerja Kaul | LDC |
| 18. | Sh. Naresh Kumar | LDC |
| 19. | Sh. Babu Ram | LDC |

## Skilled Supporting staff

| S. No. | Name | Designation |
|---|---|---|
| 1. | Sh. Krishan Lal | SSS |
| 2. | Sh. Sewa Ram | SSS |
| 3. | Sh.Ram Sagar | SSS |
| 4. | Sh. Deepak | SSS |
| 5. | Sh. Satbir | SSS |

## Promotions

- Smt. Pravesh Kumari, Senior Technical Assistant has been promoted to the next higher grade of Technical Officer w.e.f. 01.07.2012.
- Sh. Naresh Kumar, Senior Technical Assistant has been promoted to the next higher grade of Technical Officer w. e. f. 16.03.2013.
- Sh. Om Prakash, Technical Assistant has been promoted to the next higher grade of Senior Technical Assistant w.e.f. 10.06.2013.
- Sh. Ramesh Chand, Technical Assistant has been promoted to the next higher grade of Senior Technical Assistant w.e.f. 16.09.2013.
- Dr. Avnish Kumar has been promoted to the next higher post of Principal Scientist w.e.f. 06.02.2013.
- Dr. Manishi Mukesh has been promoted to the next higher post of Principal Scientist w.e.f. 09.09.2012.

## Joinings/Transfers

- Sh. Balvinder Singh (Technician) joined NBAGR on 01.08.2013 upon transfer from Regional Centre, NBSS & LUP, New Delhi.
- Sh. Vijay Singh, Sr. Technical Assistant has been transferred from NBAGR, Karnal to Regional Centre, NBSS & LUP, New Delhi on 01.08.2013.
- Dr. Arjava Sharma joined NBAGR, Karnal as Director on 01.10.2013 (F.N.)

## Superannuation

- Dr. B. K. Joshi superannuated on 30.09.2013 after serving as Director, NBAGR for about six years.

*Dr. B. Prakash felicitating Dr. B. K. Joshi*

*Dr. Arjava Sharma, Director, NBAGR felicitating Dr. B. K. Joshi, former Director, NBAGR during the Officers Club function*


ANIMAL GENETIC RESO
GRICULTURAL RESEA
BORATORY WING
NTED BY
APPAN
CTOR GENER
NCE OF
THAK
ANIMAL S
R. ARJAV

# हिन्दी खण्ड

- प्राक्कथन
- कार्यकारी सारांश
- हिन्दी अनुभाग की गतिविधियाँ

# प्राक्कथन

मुझे राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो की वार्षिक रिपोर्ट 2013–14 प्रस्तुत करने में अत्यंत प्रसन्नता हो रही है। यह दस्तावेज ब्यूरो के वैज्ञानिकों द्वारा किए गए कार्यों के साथ अन्य परिधीय गतिविधियों की मुख्य विशेषताओं की एक झलक प्रस्तुत करता है। संस्थान के अधिदेशानुसार, वर्ष 2013–14 के दौरान हमने स्वदेशी पशुओं की कुछ कम ज्ञात आबादी का लक्षणीकरण पूरा किया जिसमें सांचौरी, मणिपुरी एवं बिलाही गोवंश, गोजरी भैंस और हरिंनघट्टा ब्लेक कुकुट शमिल हैं। सिंधारी बकरी, दक्कनी के इकोटाइप, कजली भेंड़ एवं राजपालयम कुत्ता का लक्षणीकरण चल रहा है। एक्स सीटू संरक्षण हेतु, जीन बैंक में थारपारकर गाय, मेहसाना भैंस, उस्मानाबादी एवं आसाम हिल बकरी, जंसकारी एवं मारवाड़ी घोड़ा फ्रैंच गधा एवं अरूणांचली याक की कुल 15,821 वीर्य खुराक हिमसंग्रहित की गई हैं।

जीन लक्षणीकरण एवं कार्यात्मक जिनोमिक्स पर काम करते हुए बकरियों की उर्वरता एवं प्रजनन सम्बन्धित जीनों जैसे बीएमपीआर1बी, जीडीएफ9, बीएमपी15, आईएनबीबी, जेवाई1 एवं एए–एनएटी को लक्षणीकृत कर नए एसएनपी तथा उनका लक्षणों से सम्बंध का पता लगाया गया है।

विभिन्न जलवायु परिस्थियों के लिए अनुकूलन सभी पशुधन प्रजातियों की उत्तरजीविता एवं प्रदर्शन क्षमता को बनाए रखनें के लिए महत्वपूर्ण है। स्वदेशी गोवांश एवं भैंसों में विभिन्न तापमान नमी सुचकांकों पर उष्मीय सहनशीलता का अध्ययन किया गया है। देशी, विदेशी गोवंश एवं भैंसो में विभिन्न उष्मीय आघात के लिए हीटशॉक प्रोटीन का सामायिक प्रोफाइल निधार्रित किया गया। हमने सफलतापूवर्क दो एनएआई परियोजनाओं को पूरा किया। इन परियोजनाओं के तहत किए गए अनुसंधान से 14 पेटेंट दाखिल किए गए और 4 प्रौद्योगिकियों का व्यावसायीकरण किया गया। ब्यूरों ने प्रजनक सांडों की साईटोजैनेटिक स्क्रीनिंग के लिए परामर्श सेवाएं प्रदान की जिसमें इस साल 372 सांडों की गुणसूत्रीय जांच की गई।

संस्थान में चल रही अनुसंधान परियोजनाओं की प्रगति का मूल्यांकन करने के लिए आईआरसी की बैठकें समय पर आयोजित की गई। जनमानस में पशुअनुवांशिक सम्पदा पर जागरूकता उत्पन्न करने के लिए बुद्धिशीलता सत्र, व्याख्यान एवं प्रदर्शनी आयोजित की गई। पशुधन संरक्षण पर दो बुद्धिशीलता सत्र दिल्ली एवं इम्फाल (मणीपुर) में आयोजित किए गए। वैज्ञानिकों ने राष्ट्रीय एवं अंन्तराष्ट्रीय

ख्याति प्राप्त वैज्ञानिक पत्रिकाओं में अपने शोध पत्रों को प्रकाशित किया। उनके उत्कृष्ट योगदान के लिए उन्हें विभिन्न मंचों पर सम्मानित भी किया गया। ब्यूरों की उपलब्धियों की जानकारी के लिए एनबीएजीआर प्रोफाईल का नया संस्करण प्रकाशित किया गया। ब्यूरों ने अपनी उत्कृष्ट सेवाओं के लिए आईएसओ 9001:2008 प्रमाण पत्र भी प्राप्त किया। इसके अलावा ब्यूरों के कर्मचारियों ने भारतीय कृषि अनुसंधान परिषद के खेलों में भाग लिया और उत्कृष्ट प्रदर्शन किया। ब्यूरों में फरवरी महीने में एसओसीडीएबी के सहयोग से ग्रामीण जनता के उत्थान के लिए पशुधन के सतत प्रबंधन के लिए जीनोमिक्स और फीनोमिक्स के तालमेल पर एक राष्ट्रीय संगोष्ठी की मेजबानी की जिसमें देश के विभिन्न हिस्सों से 166 प्रतिनिधियों ने भाग लिया और अपना शोध प्रस्तुत किया।

इसके अलावा विदेश व देश के विभिन्न गणमान्य व्यक्तियों ने संस्थान का दौरा किया और वैज्ञानिकों से बातचीत की। प्रयोगशालाओं के लिए एक और विंग जोडकर ब्यूरो का इंफ्रास्ट्रक्चर मजबूत किया गया। पशुधन सूचना प्रबंधन इकाई की समृद्धि के लिए संस्थान में एक उच्च निष्पादन कम्प्यूटिंग (एचपीसी) सिस्टम लगाया गया। श्री अरविंद कौशल, सचिव भारतीय कृषि अनुसंधान परिषद ने भी संस्थान का दौरा किया और कर्मचारियों को सम्बोधित किया।

मैं माननीय डा. एस अय्यपन, सचिव डीएआरई एवं महानिदेशक, भारतीय कृषि अनुसंधान परिषद एवं डा. के एम एल पाठक, उप–महानिदेशक (एएस) को उनके समर्थन और मार्ग दर्शन के लिए धन्यवाद देता हूँ। साथ ही इस संस्थान की प्रसिद्धि लाने के लिए प्रयास कर रहे अपने पूरे स्टाफ का आभारी हूँ। सुधार के लिए आपके सुझाव सदा आमंत्रित हैं।

(आर्जव शर्मा)
निदेशक

## कार्यकारी सारांश

राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो और राष्ट्रीय पशु आनुवंशिकी संस्थान, राष्ट्रीय डेरी अनुसंधान संस्थान के क्षेत्रीय केन्द्र बंगलौर में दिनांक 21 सितम्बर, 1984 को स्थापित किये गए। वर्ष 1985 में ब्यूरो तथा संस्थान को रा.डे.अ.सं. करनाल परिसर में अस्थाई रूप से स्थानान्तरित किया गया। वर्ष 1994 में इसे वर्तमान मकरमपुर कैम्पस स्थानांतरित कर दिया गया। वर्ष 1995 में इन दोनों संस्थानों का विलय राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो के रूप में हुआ। यह ब्यूरो भारत में पालतू पशु व कुक्कुट संसाधनों की पहचान, मूल्यांकन, गुण निर्धारण, संरक्षण और उनके सतत उपयोग के अधिदेश हेतु देश की एक अग्रणी संस्था है। ब्यूरो निम्न उद्देश्यों की प्राप्ति हेतु कार्यरत है:

- पालतू पशु व कुक्कुट आनुवंशिक संसाधनों के गुण निर्धारण, मूल्यांकन तथा सूचीबद्ध करने के लिए व्यवस्थित सर्वेक्षणों का संचालन और राष्ट्रीय आंकड़ा कोष की स्थापना करना।
- पशु आनुवंशिक संपदा के सर्वोत्तम उपयोग, एक्स–सीटू संरक्षण तथा इन–सीटू प्रबंधन के लिए तकनीकों का विकास करना।
- आणविक जीव विज्ञान की आधुनिक तकनीकों के प्रयोग से आनुवंशिक गुण निर्धारण पर अध्ययन करना।
- पशु व कुक्कुट आनुवंशिक संसाधनों के मूल्यांकन, गुण निर्धारण और उपयोग से संबंधित प्रशिक्षण, कार्यक्रमों का संचालन करना।

वित्तीय वर्ष 2013–14 के दौरान गैर योजना और योजना के तहत कुल प्राप्ति रूपये 1064.69 लाख और कुल व्यय रूपये 1062.77 लाख था। इस अवधि में नेटवर्क परियोजना के अन्तर्गत प्राप्त रू 39 लाख में से रू 38.82 लाख खर्च हुए। वर्ष 2013–2014 के दौरान प्राप्त राजस्व 33.15 लाख रहा जो कि 27.70 लाख के निर्धारित लक्ष्य से अधिक था।

उच्च निष्पादन कंप्यूटिंग (एचपीसी) सिस्टम को संस्थान में कंप्यूटर सैंटर में स्थापित किया गया हैं। एचपीसी प्रणाली एक मास्टर नोड, एक लॉगिन नोड, 16 गणना नोड्स, नेटवर्क संलग्न संग्रहण की 20 टेराबाइट और फाइल भंडारण का 20 टेराबाइट के साथ लिनक्स क्लस्टर है। जैव सूचना विज्ञान सॉक्टवेयर एचपीसी पर स्थापित कर दिया गया है। इनमें जीनोमिक और प्रोटिओमिक डेटा विश्लेषण के लिए सीएलसी जैव जीनोमिक सर्वर, और प्रोटिओमिक्स पढ़ाई के लिए डिस्कवरी स्टूडियों शामिल हैं।

एक अध्ययन में दूध लक्षण में शामिल गाय में 12 जीन की जीनोमिक डीएनए पर एसएनपी घनत्व का मूल्यांकन किया गया है। छह प्रजातियों के जीन के लिए एसएनपी डेटा इनसेम्बल भिन्नता डेटाबेस से प्राप्त किया गया। जीन की जीनोमिक दृश्यों पर एसएनपी की स्थिति की गणना के लिए एम एस–एक्सल का उपयोग किया गया। सी++ में प्रोग्राम से एम एस ए से एसएनपी स्थितियों को निकालने के लिए, एम एस ए में ऐक्सोन के शुरू और अंत की स्थिति का पता लगाने के लिए, जीनोमिक के साथ साथ प्रतिलेख दृश्यों की एम एस ए पर एसएनपी स्थान के लिए निष्पादित किया गया। एक आर–स्क्रिप्ट का एम एस ए पर एसएनपी की स्थितियों के साथ ही ऐक्सोन प्लॉट करने के लिए निष्पादित किया गया।

तुलनात्मक विश्लेषण के लिए, तीन लोकप्रिय फाइलोजेनी आकलन के तरीकों – RAxML, PhyMLऔर MetalPiga के लिए सॉफ्टवेयर उच्च निष्पादन कम्प्यूटिंग सिस्टम पर डाउनलोड और स्थापित किए गए। सॉफ्टवेयर के साथ 100 taxa की सिम्युलेटेड न्यूक्लियोटाइड बेंचमार्क डेटासेट आकार लंबा, (एल 1), मध्यम (एम 1) और छोटी (एस1) अंतर लंबाई पर निष्पादित किया गया। Metapiga, PhyML और RAxML प्रोग्रामों के लिए 100L1डाटासेट की K=स्कोर, क्रमशः 1.305.59, 220.15 और 223.15थे। अध्ययन दिखाता है कि आकार 100 टैक्सा की

फाइलोजनी RAxML की तुलना में PhyML का उपयोग कर ट्री सटीकता में थोड़ा गिरावट के साथ अनुमान लगाया जा सकता है। बहुत उच्च K-स्कोर और सुडौल अंतर के साथ MetaPiga का प्रदर्शन खराब था।

एन सी बी आई से पुनर्प्राप्त ईएसटी के ऊतक विशेष इन–सिलिको खनन सुअर और गाय की विभिन्न ऊतकों के लिए किया गया है। सुअर के लिए त्वचा, तिल्ली, स्तन ग्रंथि , जिगर के ऊतकों और गाय के लिए तिल्ली, आंत, स्तन ग्रंथि के ऊतकों के लिए ईएसटी डेटा डाउनलोड किया गया। ऑनलाइन उपकरण Egassembler का उपयोग ईएसटी को संसाधित और CAP3 के उपयोग से कंटिग में इकट्ठे किए गए। एसएनपी को डीबीएसएनपी डेटाबेस में उनकी उपस्थिति के लिए खोजा गया। सुअर का 4ऊतकों में एसएनपी की संख्या 27,247 थी और गाय क 3 ऊतकों में एसएनपी की संख्या 14,032 थी। ऊतक के लिहाज से एसएनपी पर डेटाबेस MySQL का उपयोग कर विकसित किया गया। पर्ल स्क्रिप्ट डेटाबेस में ऊतक वार एसएनपी डेटा पार्स करने और भरने के लिए लिखा गया। वेब इंटरफेस PHP भाषा का उपयोग कर विकसित किया गया।

राजस्थान की सांचोरी गाय का बाह्य गुण निर्धारण किया गया। सांचोरी गोपशु राजस्थान के जालौर जिले के सांचोर, भीनमाल तथा रानीवाड़ा तहसीलों में पाए जाते हैं। प्रजनन क्षेत्र से 151 गाय और 19 बैलों के शारीरिक माप प्राप्त कर इनका गुण निर्धारण पूर्ण किया गया। इन गायों की दूध उत्पादन क्षमता अच्छी है। विभिन्न ब्यांत महीनों एवं ब्यांत क्रमों की 276 गायों के अभिलेखों के आधार पर यह पाया गया कि इन गायों का कुल मिलाकर दैनिक दूध उत्पादन 9.08±0.16 लीअर है। सांचौरी गायों का दुग्ध काल 8–15 माह एवं अधिकतम दैनिक दूध उत्पादन 6–18 लीटर पाया गया।

मणिपुर के स्वदेशी गोपशुओं का गुण निर्धारण राज्य के पूर्वी इम्फाल, पश्चिमी इम्फाल और चुराचांदपुर जिलों के 13 गांवों में सर्वेक्षण कर पूर्ण किया गया। ये गोपशु छोटे आकार के साथ मोटे और बेलनाकार शरीर के होते हैं। अधिकतर जानवरों का रंग गाढ़ा भूरा होता है। दैनिक दूध उत्पादन 2 से 4.50 किलो होता है जबकि औसतन 2.65±0.18 किलो होता है। एक जोड़ी बैल 6–8 घंटों में एक एकड़ भूमि की जुताई कर सकते हैं।

बिलाही गोपशुओं में औसत प्रतिदिन दुग्ध उत्पादन तथा 305 दिन दुग्ध उत्पादन क्रमशः 3.25±0.15 एवं 1014.43±45.46 किग्रा पाया गया।

हिमाचल प्रदेश और पंजाब में पाई जाने वाली एक नई भैंस की नस्ल 'गोजरी' की पहचान करने के पश्चात उसका गुण निर्धारण किया गया। गोजरी भैंस का रंग काला व शरीर पर भूरे मोटे बाल होते हैं। सींग मध्यम से लेकर बड़े आकार के होते हैं और वक्रित उन्मुखीकरण के साथ पहले पीछे जाते हैं व फिर आगे की तरफ मुड़े होते हैं। इन भैंसों को दूध, भार ढ़ोने और खाद के लिए पाला जाता है। व्यस्क नर कृषि कार्य और परिवहन में उपयोग में आते हैं। मुर्राह और नीली–राबी की तुलना में गोजरी भैंस छोटी व पतली होती है।

सिक्किम राज्य के पूर्वी और पश्चिमी जिलों में सिंधारी बकरी का गुण निर्धारण किया गया। यह बकरी छोटे से लेकर मध्यम आकार और विभिन्न रंगों की होती है। अधिकतर बकरियों के चेहरे पर सींग से लेकर थूथन तक पट्टियाँ होती हैं। प्रजनन के लिए उपयुक्त व्यस्क नरों में गर्दन के चारों तरफ काला छल्ला होता है। प्रतिदिन लगभग 300–500 मि.ली. दूध उत्पादन होता है। एक बार में दो बच्चों का जन्म काफी आम है।

डक्कनी भेड़ के तीन ईकोटाईप्स–सोलापुरी, मडग्याल और कोलहापुरी का सर्वेक्षण महाराष्ट्र के सोलापुर, सांगली और कोलहापुर जिलों में किया गया। गुण निर्धारण हेतु बाह्य शारीरिक मापों, उत्पादन एवं प्रजनन क्षमता, आर्थिक व सामाजिक स्थिति और वर्तमान में नस्ल की विशेषता के आकड़े एकत्रित किया गया। मडग्याल भूरे धब्बों के साथ सफेद रंग की होती है व सोलापुरी सफेद धब्बों के साथ काले रंग की होती है। कोलहापुरी में काले, भूरे और सफेद रंग का मिश्रण होता है। सभी ईकोटाईप्स में सीधी कमर और मध्यम

लम्बाई की पतली पूँछ होती है। रोमन नाक मडग्याल और सोलापुरी भेड़ों की विशेषता है। तीनों ईकोटाईप्स में पर्याप्त यौन द्विरूपता पाई गई।

कजली पंजाब की भेड़ एक कम ज्ञात नस्ल है जिसके गुण निर्धारण हेतु संगरूर, बरनाला, लुधियाना और आसपास के जिलों का सर्वेक्षण किया गया। यह भेड़ मुख्यतः मास के लिए पाली जाती है। कजली भेड़ का रंग मुख्य रूप से सफेद है, लेकिन गहरे भूरे और काले रंग के जानवर भी पाए जाते हैं। आंखों के आसपास काले घेरे के कारण इस भेड़ का नाम कजली पड़ा है और यही इस नस्ल की पहचान का मुख्य गुण है। इस भेड़ में रोमन नाक, लंबे कान व जमीन तक पहुँचती हुई पूँछ होती है। दोनों लिंग सींग रहित होते हैं परन्तु कुछ नरों में सींग पाए जाते हैं। प्रारंभिक परिणामों से यह संकेत मिलता है कि यह भेड़ क्षेत्र की अन्य नस्लों से अलग है।

पश्चिम बंगाल के नादिया और उत्तरी 24 परगना जिलों के 17 ग्राम पंचायतों का सर्वेक्षण कर हरिनघट्टा ब्लैक चिकन के झुंड संरचना, आकार तथा प्रबंधन प्रथाओं के आंकड़े एकत्रित किये गये। प्रजनन क्षेत्र में इनकी अनुमानित संख्या 63600 है व औसत झुंड आकार 7.9 होता है। कुछ मुर्गों के गर्दन और पंखों पर भूरा रंग होता है। कलगी लाल और मुख्य रूप से एकल है। ईयरलोब लाल अथवा सफेद व चोंच काली होती है। दस महीने की उम्र में शरीर का भार मुर्गियों में 1.1 किलो व मुर्गो में 1.3 किलो होता है। पहला अंड़ा देने की औसत आयु 5.63 महीने होती है और मुर्गी एक चक्र में औसतन 12.32 अंडे देती है। वार्षिक अंडा उत्पादन ब्रूडिंग के साथ 45 व बिना ब्रूडिंग के 98 होता है।

तमिल नाडू के विरूधुनगर जिले के राजपलयम् तालुक में कुत्तें की राजपलयम नस्ल का सर्वेक्षण किया गया। राजपलयम कुत्ते मध्यम आकार, सुगठित शरीर, सफेद रंग, गुलाबी रंग की त्वचा नाक, आईलिड, झुके हुए कान, अर्द्ध वक्र पूँछ और सीधी टॉप लाइन के होते हैं। आँखों का रंग सुनहरा व नाक सीधा होता है। ये कुत्ते मुख्यतः रखवाली के लिए इस्तेमाल होते हैं।

एक्स सीटू संरक्षण कार्यक्रम के अंतर्गत जीन बैंक में 5 प्रजातियों की 8 नस्लों की अति हिमीकृत वीर्य खुराक शामिल की गई। वर्तमान में राष्ट्रीय जीन बैंक में 7 पशुधन प्रजातियों (गाय, भैंस, बकरी, भेड़, ऊँट, घोड़े और याक) की 40 नस्लों की 1,28,074 अति हिमीकृत वीर्य खुराक संग्रहित हैं।

माइक्रोसेटेलाइट आधारित जीनोटाइपिंग से बिलाही गाय (48) का आनुवंशिक लक्षण निर्धारण किया गया। प्राप्त और प्रभावी अलील औसतन 9.31 और 4.38 पाए गए। दूध उत्पादन को प्रभावित करने वाली कैंडीडेट जीन्स का पी सी आर आर एफ एल पी से लक्षण निर्धारण किया गया।

साहीवाल, गिर और थारपारकर गोवंशीय नस्लों के स्वमान विकसित करने के प्रयास में यह पाया गया कि 75 में से 51 लोसाई उपयोगी हो सकते हैं। औसत प्राप्त और प्रभावी हेटरोजाइगोसिटी 0.58 और 0.76 पाई गई। अमोवा से पता चला कि भिन्नता में नस्लों के बीच की भिन्नता का 13.74% योगदान है। एफ एस टी के आधार पर गिर व थारपारकर आनुवंशिक रूप से अधिक विभेदित (22.7%) और गिर व साहीवाल कम विभेदित (7%) पाए गए। स्ट्रक्चर सॉफ्टवेयर से नस्ल संरचना और मिश्रण का अध्ययन किया गया। गिर और थारपारकर अपने समूहों में वर्गीकृत हुए जबकि साहीवाल दो विशिष्ट समूहों में विभाजित हुए।

विभिन्न भारतीय देशी पशु नस्लों के बीच टीएलआर3 जीन के कोडिंग क्षेत्र में 13 विविधताओं का पता चला जिसमें संरक्षित पोलारिटी के साथ 4 गैर पर्याय सहित, जबकि टीएलआर7 जीन में 6 गैर पर्याय सहित 16 विविधताओं का पता चला। कांकरेज, गिर और हरियाणा गायों में सबसे अधिक एसएनपी का पता चला जबकि कांगयाम एवं नागोरी गाय सबसे कम बहुरूपी थी। दस टीएलआर में 196 एसएनपी का पता चला जिसमें 86 गैर पयार्य थी और 55 भारतीय पशु नस्लों के लिए अद्वितीय थी। एलडी की इन्ट्राजेनिक पैटर्न से टीएलआर6 में5 हपलो–ब्लॉक का ज्ञात हुआ; इसके साथ ही 4 प्रत्येक टीएलआर1 और टीएलआर10 में; 3 टीएलआर7 में और 2 प्रत्येक टीएलआर2 और टीएलआर में बदलती एलडी के साथ प्राप्त हुए।

भैंस के नोड–लाइक रिसेप्टर–2 में बहुरूपता का पता लगाने के लिये किये गए अध्ययन से 42 बहुरूपकों की उपस्थिति का पता चला, जिनमें से दो बहुरूपकों A1135G (नोड डोमेन) तथा G91C (कार्ड डोमेन) के लिए पी. सी. आर. –आर. ऍफ. एल. पी. जीनोटाइपिंग विधि विकसित की गयी। इनमें से बहुरूपक A1135G की एलिलिक आवृत्तियों में बदलाव का असर नैदानिक स्तन की सूजन प्रभावित और गैर प्रभावित भैंसों में महत्वपूर्ण पाया गया इसके अलावा, पहली बार, नोड–लाइक रिसेप्टर–1 के सप्लाइस वैरिएंट्स की अभिव्यक्ति भैंस की स्तन ग्रंथि में देखी जा सकी है, जिसकी इस अंग की प्रतिरक्षा प्रणाली में महत्वपूर्ण भूमिका हो सकती है।

थारपारकर, राठी, साहीवाल, हरियाना और कांकरेज नस्ल की 40 गायों में आई एन एफ गामा जीन का अध्ययन किया गया। 3.4 के बी. क्षेत्र में 20 एस एन पी पाए गए। जीन के इन्ट्रोन 1 में माइक्रोसेटेलाइट रिपीट पाया गया।

हरियाना, थारपारकर, कांकरेज, साहीवाल, राठी, गाय की नस्लों में टी एन एफ बीटा जीन का लक्षण निर्धारण किया गया। कुल 31 एन एन पी 3.5 के बी के क्षेत्र में पाए गए। एक एस एन पी नॉन सिनॉनिमस था। सभी लोसाई पर प्राप्त और प्रभावी हेटेरोजाइगोसिटी लगभग बराबर थी। एफ आई एस के नकारात्मक मूल्य (–0.1958) से अंतः प्रजनन का संकेत मिला। एफ एस टी मूल्य 0.1354 देखा गया।

भेड़ की जी एच, जी एच आर, टी टी एन, सी ए एस टी और डी जी ए टी जीन के पहले रिपोर्ट किए गए लोसाई को बन्डूर, चोकला, डक्कनी, गन्जम, मडग्याल, मागरा, मालपूरा, मुजफ्फरनगरी, नाली और नेलौर भेड़ों में जाँचा गया। भारतीय भेड़ों में मांस (मटन) की गुणवत्ता के लिए कैंडीडेट जींस में पाई गई नई भिन्नताएँ आनुवंशिक विविधिता की उपलब्धता को दर्शाती हैं।

डी आर ए, डी आर बी, डी क्यू ए, डी क्यू बी, जीन्स के एक्सॉन–2 का विश्लेषण 3.7 अरूनाचली याक में किया गया। डी आर ए में 3 एलीलिक वेरिएन्ट मिले। डी क्यू ए के अनुक्रम विश्लेषण से 8 एलील मिले, जो कि दो समूहों में विभाजित थे। डी क्यू बी में पाँच एलील की पहचान की गई जिसमें से 3 एलील नए थे।

भैंस स्तन ग्रंथि के तीन शारीरिक चरणों में विशेष रूप से इन्ड्यूस्ड तथा रिप्रैसड जीन की पहचान करने के लिए ट्रांसक्रिपटोम डेटा बनाने का एक प्रयास किया गया। कुल 2281 ट्रांसक्रिप्ट्स विभिन्न पाए गए। दूध वसा चयापचय से संबंधित जीन के पूरे सेट भैंस स्तन ग्रंथि की स्तनपान के चरण में ऊपर विनियमित हुए। इन्वोलुशन, अपॉप्टोसिस, प्रतिरक्षा और ऑक्सीडेटिव तनाव प्रतिक्रिया से संबंधित कई जीन्स का भी विनियमित ऊपर होना पाया गया।

साहीवाल गायों में एसएलसी2ए1 (प्लाज्मा झिल्ली में ग्लूकोज की सक्रिय परिवहन में शामिल) जीन की एमआरएनए अभिव्यक्ति स्तनपान के पहले 3 सप्ताह के भीतर अधिक होने का पता चला। एक अन्य प्रमुख पदार्थ वाहक एसएलसी2ए8 का मध्य स्तनपान की अवधि के दौरान उच्च अभिव्यक्ति का पता चला। जबकि, एसएलसी2ए4 जीन की एमआरएनए अभिव्यक्ति अधिक दूध देने के समय काफी अधिक थी और स्तनपान की शुरुआती तथा मध्य चरणों में यह कम पायी गयी।

अलग अलग तापमान नमी सूचकांक पर थर्मो–टॉलरेंस के संकेतक के रूप में साहीवाल गायों (इंडिकस पशु), करण फ्रीज़ गायों (संकर), होल्सटीन फ्रिसियन गायों (विदेशी) और मुर्राह भैंसों में सेल प्रोलीफ्रेशन और हीट शॉक प्रोटीन के स्तर का तुलनात्मक मूल्यांकन का एक प्रयास किया गया। एचएसपी की सीरम सांद्रता साहीवाल गाय और मुर्राह भैंसों की तुलना में होल्सटीन फ्रिसियन और करण फ्रीज़ गायों में अपेक्षाकृत अधिक पायी गयी। इसी प्रकार की प्रवृत्ति कोर्टिसोल और टीएनएफ–अल्फा में भी प्राप्त हुई।

बारह नए भैंसों का उपयोग कर एक बड़ी संदर्भ आबादी (10,000 मादा संततियों) का सृजन किया गया है। इन मादाओं को आठ गुणसूत्रों पर निर्धारित 79 माईक्रोसेटेलाइट मार्कर द्वारा जीनोटाईप किया गया।

इसके अतिरिक्त मेठा–क्यूटीएल विश्लेषण करने पर क्यूटीएल स्थानों को चिन्हित किया गया तथा उनका पुष्टीकरण अनेक एसएनपी द्वारा किया गया।

कुल 6.54 लाख एसएनपी का पता रिड़यूस्ड रिप्रसेन्टेशन लाइब्रेरी द्वारा तथा 1.96 लाख एसएनपी की पहचान आरएनए अनुक्रम विश्लेषण द्वारा प्रतिवेदन अवधि के दौरान की गई। कुल मिलाकर अब तक 1,96,669 एस एन पी की पहचान जीनोम के कोडिंग भाग में की गई ही। इल्यूमीना प्लैटफार्म पर आधारित गोल्डन गेट ऐस्से द्वारा चिन्हित एसएनपी को मान्यकृत किया गया है। आरएनए अनुक्रम विश्लेषण द्वारा अभिव्यक्त होने वाले जींस का पता चला जिनमें से 800 जीन विभिन्न दुग्ध मापदण्डों से संबंधित पाए गए।

याक के दूध का फैटी एसिड की संरचना के लिए विश्लेषण किया गया जिससे कुल ठोस (16.9–17.9%), प्रोटीन (4.9–5.9%) और वसा (5.5–7.5%) का पता चला। ये परिमाण गाय और बकरी की तुलना में काफी अधिक हैं, लेकिन भैंस से अपेक्षाकृत समान हैं। ऊँट के दूध के नमूने का भी विश्लेषण किया गया।

एन.बी.ए.जी.आर. विभिन्न विभागों को प्रजनन सांडो की साईटोजेनेटिक और गुणसूत्र विकृतियों की जाँच के लिए परामर्शी सेवाएं उपलब्ध करा रहा है। ऐसा करने से भारतीय सरकार की नीति के अनुरूप आनुवंशिक दोषों को देश में फैलने से रोका जा सकता है। इस वर्ष 372 प्रजनन सांडों की गुणसूत्र विकृतियों के लिए जाँच की गई।

प्रजनन लक्षण में भूमिका वाले जीन (किस1, जीपीआर54, इन्हिबिन बीटा, जेवाई–1 तथा एए–एनएटी) का विश्लेषण स्वदेशी बकरियों की नौ नस्लों में किया गया। विश्लेषण द्वारा 16 एसएनपी पाए गए। पासीआर–आरएफएलपी विधि द्वारा जीनोटाइपिंग उपरान्त एक एसएनपी को ब्लैक बंगाल बकरियों में उपरोक्त लक्षण से संबंधित पाया गया।

टेट्रा–आरम्स पीसीआर तथा पीसीआर–आरएफएलपी विधि को बीएमपीआर 1 बी, जीडीएफ 9 तथा बीएमपी 15 जीनों में पाए जाने वाले उत्परिवर्तनों की जीनोटाइपिंग के लिए मानकीकृत किया गया। इनके द्वारा सात बकरियों की नस्लों के विश्लेषण से चार एसएनपी को प्रजनन लक्षण से संबंधित पाया गया।

कोरलैब, चिन्नई (तमिलनाडु) द्वारा भारवाही क्षमता सम्बंधित जीन्स (आई जी एफ–1, ए डी आर बी 2, जी जी एक्स–1, वी ई जी एफ–ए, ए सी ई–1, बी डी के आर बी 2) का लक्षण निर्धारण भारतीय गोवंशीय नस्लों (कंगायम, उम्बलाचैरी, पुलीकुलम, बर्गुर, हलीकर तथा ओगोंल) में किया गया तथा विभिन्न एसएनपी का पता भी चला। इनमें से कुछ एसएमपी का सम्बंध भार ढ़ोने की क्षमता के बाह्य गुणों के साथ पाया गया।

कोर लैब आनंद द्वारा भारतीय ऊंट नस्लों में दूध गुणवत्ता/संरचना एवं उत्पादकता से सम्बंधित विभिन्न जीन का अध्ययन किया गया।

कोर लैब खानापारा (असम) द्वारा माइक्रोसेटेलाईट मार्कर विश्लेषण से असम, मणीपुर तथा अरूणाचल प्रदेश की तीन गोपशु समूहों का आणविक गुण निध ारिण किया गया। इन तीनों गो पशु समूहों में भिन्नता पाई गई एवं इनमें कोई सम्बंध नहीं ज्ञात किया जा सका।

वर्तमान वैज्ञानिक एवं तकनीकी विकास की जानकारी हेतु, ब्यूरो पुस्तकालय द्वारा 43 (12 विदेशी एवं 31 भारतीय) शोध पत्रिकाओं की नियमित सदस्यता प्राप्त की गई।

अनुसंधान समितियों की बैठकों को निर्धारित समय पर किया गया। शोध परियोजनाओं की प्रगति की समीक्षा मध्यावधि संस्थान अनुसंधान समिति एवं अनुसंधान सलाहकार समितियों की बैठकों में की गई।

प्रतिवेदन अवधि के दौरान ब्यूरो में 18 शोध परियोजनाओं पर कार्य चल रहा है जिसमें चार बाह्य वित्त सहयोग से चलने वाली व एक 'नैशनल फैलो प्रोजेक्ट' शामिल है।

ब्यूरों द्वारा कुल आठ पेटेंट, भारतीय पेटेंट कार्यालय, दिल्ली में दर्ज किए गए। इसके अतिरिक्त 2011

में भेजे गए तीन पेटेंट को भारतीय पेटेंट जर्नल ने प्रकाशित किया।

ब्यूरो द्वारा भारतीय रूमंथी पशुधन के लिए एक पैतृक परीक्षण किट का व्यवसायीकरण किया गया।

वैज्ञानिक शोध परिणामों को वैज्ञानिकों द्वारा 33 शोध पत्रों के रूप में राष्ट्रीय एवं अंतराष्ट्रीय ख्याति प्राप्त शोध पत्रिकाओं में प्रकाशित किया गया। इसके अतिरिक्त तीन मोनोग्राफ/लीफ्लेटस भी ब्यूरो द्वारा प्रकाशित किये गये।

ब्यूरों के तीन वैज्ञानिकों को एन ए आई पी – एच आर डी के अर्न्तगत प्रशिक्षण हेतु विदेश भेजा गया। कई वैज्ञानिकों ने देश में आयोजित गोष्ठीयों, कार्यशालाओं इत्यादि में भाग लिया।

कानपुर (उत्तर प्रदेश) में 20–23 मार्च, 2014को आयोजित भा. कृ. अनु. प. उत्तरी जोन की अंतर संस्थान खेलकूद प्रतियोगिता में ब्यूरों की टीम ने बालीबाल (स्मेसिंग) में स्वर्ण तथा बास्केटबाल में रजत पदक हासिल किया। एकल प्रतियोगिताओं में भी एक स्वर्ण एवं एक कांस्य पदक प्राप्त हुआ।

ब्यूरो प्रांगण में ब्यूरो का 30 वाँ स्थापना दिवस, जैवविविधता दिवस, गणतंत्र दिवस और स्वतंत्रता दिवस हर्षोल्लास से मनाए गए।

ब्यूरो द्वारा पालतू पशु विविधता संरक्षण सोसायटी के सहयोग से एक राष्ट्रीय संगोष्ठी का आयोजन (6–7 फरवरी, 2014) ब्यूरो परिसर में किया।

ब्यूरों द्वारा देश के विभिन्न स्थानों पर आयोजित पशु। दुग्ध मेलों के दौरान ब्यूरों से सम्बंधित गतिविधियों को प्रदर्शित किया गया।

वर्ष के दौरान कई विशिष्ट व्यक्तियों ने ब्यूरो की प्रयोगशालाओं का दौरा किया। भूटान के कृषि एवं वन विभाग मंत्री ने ब्यूरों के वैज्ञानिकों से विचार विमर्श किया।

ब्यूरों के वैज्ञानिक को प्रतिष्ठित "बायोटेक प्रोडक्ट तथा प्रोसेस डेवलप्मेन्ट तथा कोमर्सिएलाइसेशन अवार्ड 2013" से माननीय राष्ट्रपति जी द्वारा सम्मानित किया गया।

ब्यूरो के वैज्ञानिकों को राष्ट्रीय डेरी संस्थान के संकाय सदस्यों में शामिल किया गया है। संकाय सदस्यों द्वारा स्नातकोत्तर विद्यार्थियों के अध्यापन व शोध कार्यो में मार्गनिर्देशन हेतु कार्य किया जा रहा है।

वर्तमान में ब्यूरो कार्य बल के रूप में 30 वैज्ञानिक, 18 तकनीकों, 19 प्रशासनिक एवं 5 कुशल सहायता कर्मचारी हैं। इस दौरान निदेशक सहित दो कर्मचारियों ने ब्यूरो कार्यभार सम्भाला तथा दो वैज्ञानिकों और चार तकनीकी अधिकारियों की पदोन्नति हुई।

ब्यूरो की नई अनुसंधान लेबोरेटरी विंग का उदघाटन डा. एस अय्यपन ने किया।

# राजभाषा प्रकोष्ठ की गतिविधियाँ

## राजभाषा सम्बंधी बैठकें

संस्थान राजभाषा कार्यान्वयन समिति की बैठकें प्रत्येक त्रैमासिक अंतराल पर नियमित रूप से निदेशक की अध्यक्षता में आयोजित की गई। इन बैठकों में राजभाषा प्रकोष्ठ द्वारा किये गए कार्यों की समीक्षा की गई तथा आगामी तिमाही हेतु राजभाषा हिन्दी की प्रगति हेतु विभिन्न निर्णय लिए गये। प्रत्येक बैठक में विभिन्न अनुभागों एवम् इकाईयों के प्रभारियों ने सक्रियता से भाग लिया।

## हिन्दी चेतना माह

प्रत्येक वर्ष की भांति इस बार भी सितंबर माह को हिन्दी चेतना माह के रूप में मनाया गया। स्टाफ सदस्यों में राजभाषा हिन्दी के प्रति रोचकता व जागरूकता बढ़ाने के लिये संस्थान में विभिन्न प्रतियोगिताएं आयोजित करवाई गई।

दिनांक 26–9–2013 को समापन समारोह व पुरस्कार वितरण समारोह आयोजित किया गया। इस अवसर पर मुख्य अतिथि डा. जी.आर. पाटिल, संयुक्त निदेशक, राष्ट्रीय डेयरी अनुसंधान संस्थान करनाल रहे। समारोह की अध्यक्षता संस्थान निदेशक डा. बी.के. जोशी ने की। इस अवसर पर सभी प्रतियोगिता विजेताओं को पुरस्कार वितरित किये गये। इसके साथ–साथ **पशुधन प्रकाश** के तृतीय अंक वर्ष 2012 के **तीन श्रेष्ठ शोध** लेखों को पुरस्कृत भी किया गया।

## पशुधन प्रकाश का विमोचन

दिनांक 21–9–2013 को संस्थान की वार्षिक हिन्दी पत्रिका **पशुधन प्रकाश** के चतुर्थ अंक (वर्ष 2013) का विमोचन डा. गुरबचन सिंह, चेयरमैन, कृषि वैज्ञानिक चयन मंडल की अध्यक्षता में हुआ।

## हिन्दी व्याख्यान का आयोजन

दिनांक 26.09.2013 को एक हिन्दी व्याख्यान का आयोजन किया जिसमें डा. जमीला ने **तनाव मुक्ति प्रबंधन** विषय पर हिन्दी में व्याख्यान देकर स्टाफ सदस्यों का ज्ञानवर्धन किया।

राजभाषा के प्रचार–प्रसार व प्रयोग की प्रगति हेतु दिनांक 23–01–2014 को संस्थान में **सकारात्मक चिंतन–स्वस्थ मानसिकता** विषय पर एक प्रेरक व्याख्यान करवाया गया। मुख्य व्याख्याता के रूप में इंदिरा गांधी मुक्त विश्वविद्यालय के करनाल स्थित क्षेत्रीय केन्द्र के निदेशक **डा. अशोक शर्मा जी** ने अपने औजपूर्ण व्याख्यान से ब्यूरो स्टाफ को प्रेरित किया।

डा. अशोक शर्मा जी द्वारा व्याख्यान की प्रस्तुति

## हिन्दी चेतना मास के दौरान आयोजित प्रतियोगिताओं में पुरस्कृत कर्मचारी

| प्रतियोगिता | पुरस्कृत कर्मचारी |
|---|---|
| उत्कृष्ट हिन्दी कार्मिक पुरस्कार<br>(अप्रैल 2012 – मार्च 2013) | प्रथम: श्री कर्मबीर मलिक, श्री बाबु राम<br>द्वितीय: श्री सोपाल (द्वितीय पुरस्कार),<br>तृतीय: श्रीमती अनीता चंदा, श्री महावीर सिंह |
| टिप्पणी मसौदा लेखन प्रतियोगिता | प्रथम: श्री कर्मबीर मलिक<br>द्वितीय: श्रीमती अनीता चंदा<br>तृतीय: डा. आर.एस. कटारिया |
| शब्दार्थ व अनुवाद प्रतियोगिता | प्रथम: श्रीमती अनीता चंदा<br>द्वितीय: श्री कर्मबीर मलिक<br>तृतीय: डा. साकेत निरंजन |
| आशु भाषण प्रतियोगिता | प्रथम: डा. मोनिका सोढी<br>द्वितीय: श्रीमती अनीता चंदा<br>तृतीय: डा. साकेत निरंजन |
| निबंध लेखन प्रतियोगिता | प्रथम: श्री कर्मबीर मलिक<br>द्वितीय: श्रीमती करूणा असीजा<br>तृतीय: डा. मोनिका सोढी |
| पत्र लेखन प्रतियोगिता | प्रथम: डा. साकेत निरंजन<br>द्वितीय: डा. आर. एस. कटारिया<br>तृतीय: श्रीमती अनीता चंदा |
| ब्यूरो वैज्ञानिको द्वारा शोध लेख प्रस्तुतिकरण प्रतियोगिता | प्रथम: डा. आर. के. पुंडीर<br>द्वितीय: डा. आर. एस. कटारिया<br>तृतीय: डा. साकेत निरंजन, डा. ए. के. मिश्र |

British
Certifications Inc.

JAS-ANZ

M4340909ID

*This is to Certify that the Management System of:*

**NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES**

*(Indian Council of Agricultural Research)*

G.T. Road By-Pass, Near Basant Vihar, PB.No. 129,
Karnal-132 001, Haryana, India

*has been assessed and found to comply with the requirement of*

*ISO 9001:2008*

*The Quality Management System is Applicable to*

Research and Trainings in Characterization, Conservation and Sustainable Utilization of Farm Animal Genetic Resources.

*Certificate No :* **BCI/Q/I/2839**

*Date of Certification Audit :* 04.05.2013

*Date of Issue :* 09.05.2013

*Date of Expiry :* 03.05.2016

1st Surveillance Audit : April - 2014
2nd Surveillance Audit : April - 2015

*MD*

IAF

British Certifications Inc.

Office No. 4, 1st Floor, C - 4/7, Shiva Arcade Acharya Niketan, Mayur Vihar, Phase- 1, Delhi-110091 (INDIA)
Tel.: +91-11-43601911, 43601987 Fax : +91-11-43601911, E-mail: bcicertification@gmail.com Web : www.bci.co.in
Visit for verification : www.jas-anz.org/register

भाकृअनुप
ICAR

हर कदम, हर डगर
किसानों का हमसफर
भारतीय कृषि अनुसंधान परिषद

Agrisearch with a human touch


NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES

*(An ISO 9001:2008 Certified Institute)*

G.T. Road By-Pass, Near Basant Vihar, Karnal - 132 001 (Haryana) India

Phones: 0184-2267918 (O), Fax: 0184-2267654

E-mail: dirnbagr@icar.org.in; directornbagr@gmail.com

Website: www.nbagr.res.in