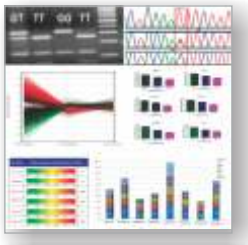


वार्षिक प्रतिवेदन
ANNUAL REPORT
2012-13

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

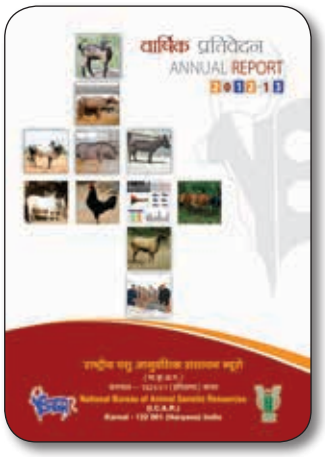
United Nations Decade on Biodiversity

वार्षिक प्रतिवेदन
ANNUAL REPORT

2012-2013

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. BK Joshi, 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. AK Mishra, Principal Scientist
Dr. Avnish Kumar, Senior Scientist
Dr. Rekha Sharma, Senior Scientist
Dr. Saket Kumar Niranjan, Senior Scientist
Sh. Satpal, T-5

Photographs

Sh. Moti Ram, T-5

Assistance

Dr. PS Dangi (Technical Officer, T-7/8)
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

2012-13

FOREWORD

I feel immensely pleased to present the Annual Report 2012-13 of National Bureau of Animal Genetic Resources. The trajectory of the following pages is aimed at shedding light on glimpses of our rich livestock biodiversity so far characterized, evaluated, conserved and documented by the Bureau during last one year. Twenty nine years ago, on 21st September, 1984 the Bureau got officially off the ground and is now marching ahead with renewed vigour to overcome the complex challenges and threats particularly in checking the loss of livestock biodiversity and enhancing their sustainable utilization. Within this short period, the Bureau has become an internationally renowned center of excellence for research on characterization, conservation and sustainable development of AnGR. Nature has bestowed upon our country with vast and varied forms of resources and ecological conditions which have enriched our country with immense biodiversity including domestic animal diversity. Farm livestock species are one of the major constituent of this biodiversity which comprised of large spectra of farm animal breeds. National Bureau of Animal Genetic Resources under its mandate of Identification, Evaluation, Characterization, Conservation and Utilization of livestock and poultry genetic resources has characterized and documented most of the well known breeds of different farm animal species. So far 37 breeds of cattle, 13 of buffalo, 39 of sheep, 23 of goat, 2 of pig, 6 of Horse & Ponies, 8 of camel, 1 of donkey and 15 of poultry have been registered. These characterized and classified descript breeds constitute about 25- 30% of total population of our farm animal resources whereas rest forms the non-descript animals which so far are inadequately studied. Now the efforts are to characterize, evaluate and document lesser known and unexplored animal populations and ultimately transform the nondescripts into well descript and registered breeds.

During the year scientists of the Bureau concentrated their efforts on conducting breed surveys, characterizing and establishing the physical attributes of Sanchori cattle of Rajasthan, local cattle of Mizoram, native cattle of Andhra Pradesh, Koraput sheep of Odisha, Raigari, Malkangiri and Narayanpatna goats of Odisha, Harringhata Black chicken of West Bengal and Sindhi donkey of Rajasthan. Conservation is another important activity which the Bureau is looking into by undertaking *ex-situ* and *in-situ* conservation programmes on the genetically eroded breeds and critically declining population. Under *ex-situ* conservation programme, the Gene Bank has added collection of around 15 thousands semen doses and now its inventory has more than 1 lakh cryo-preserved semen doses produced from 276 breeding males of 38 breeds of seven farm animal species. In the field also superior germplasm of purebred cattle, sheep and goat have been disseminated for the genetic enhancement of local livestock of the native ecologies. Now our focus is on conducting groundbreaking genomic research for proper understanding the unique attributes of the native AnGR. De-novo assembly of goat and camel transcriptome has been generated. The researchers are engaged in emerging areas of science for analyzing molecular basis of important economical and environmentally adaptive traits viz. milk production, milk constituents, meat yield & quality, disease resistance, thermoregulation, prolificacy, draftability, down to the smallest details under various institutional and externally funded projects.

Various research projects culminated with results have laid the foundation for development of new technologies, filing patents, protocols, models and database packages for storage, retrieval and analysis of data. Efforts initiated for developing technologies, filing the patents and their commercialization has shown good results. Three technologies i.e. DNA marker based kits for parentage verification in zebu cattle, camels and buffaloes were commercialized. Based on the research findings 62 scientific papers have been published in the national and international peer viewed journals of high impact factors. Sixteen popular/technical articles and seven monographs were also published during the year. Scientists have been rewarded for their research achievements presented at various fora. To encourage the researchers, Dr. P. G. Nair Award for the Institute's scientist excelling in the field of characterization and conservation of native livestock breeds has been instituted and is being conferred every year. Similarly promoting competitive spirit for excellence in working, best workers in technical, administrative and supporting staff have also been recognized with awards. I congratulate all my fellow colleagues, who received the awards for the year 2012. Apart from the research, the staff of Bureau has excelled in many other social and sports events.

I sincerely thank Dr S Ayyappan, Secretary, Department of Agricultural Research and Education & Director General, ICAR, for his guidance, help and support. I also acknowledge the cooperation and encouragement from Dr KML Pathak, Deputy Director General (Animal Sciences) and Dr S C Gupta, ADG (AP&B). Special thanks are due to my dynamic team of scientists, administrative, technical and supporting staff for their hard work and cooperation.

(B. K. Joshi)
Director

EXECUTIVE SUMMARY

National Bureau of Animal Genetic Resources and National Institute of Animal Genetics were set up on 21st September, 1984 and started at Regional Station of National Dairy Research Institute Bangalore. Bureau and 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. The Institute of Animal Genetics and Bureau were merged in 1995 to function as a single unit as National Bureau of Animal Genetic Resources. National Bureau of Animal Genetic Resources, Karnal has been the nodal organization in India with the mandate - 'Identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country' and is working to achieve the following objectives:

- 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.

During the period under report scientists of Bureau strived hard to achieve the objectives by working under various institute and externally funded research projects. The salient achievements emerged from different projects are summarized below:

The database on Livestock Genes and Proteins was enriched with gene-ontology data collected from ftp site (http://www.geneontology.org/GO.downloads.html). Presently 35,113 gene-ontology records have been stored in the database. User-interface using ASP.NET was created to search proteins through gene-ontology terms. Coding for classifying livestock proteins on the basis of cellular component, biological function and molecular function was also completed.

Nine new breeds of livestock species were registered and assigned accession numbers. This included three breeds of cattle (Pulikulam, Kosali, Malnad Gidda), one buffalo (Kalahandi), two each of goat (Konkan Kanyal, Berari) and pig (Ghoongroo, Niang Megha) and one of donkey (Spiti).

Exploratory visits were conducted in the breeding tracts of different livestock breeds/populations and data were collected on phenotypic and biometric traits. Information on management practices, socioeconomic parameters were collected through interactions with farmers. Following this systematic approach, characterization of Sanchori cattle of Rajasthan, indigenous cattle of Mizoram, local cattle of

Adilabad district (A.P), Koraput sheep of Odisha and Raigari, Narayanpatna and Malkangiri goats of Odisha were accomplished. Survey was also conducted to document migratory routes/ breeding tract and management practices of Gojri buffalo of Himachal Pradesh and Punjab state.

Information was collected to characterize Harringhata Black chicken of West Bengal.

Five ecotypes of Deccani sheep i.e. Kolhapuri, Lonand, Madgyal, Sangamneri and Solapuri were characterized by collecting data on seven morphometric traits of 224 adult sheep reared under extensive management system from their distribution area.

Sindhi donkey of Rajasthan was characterized by conducting systematic surveys in the native tract.

Under *ex-situ* conservation programme 14,150 frozen semen doses of 10 cattle breeds and 1 buffalo breed has been procured and added to repository in Gene Bank . The National Gene Bank at NBAGR now stores about 1,09,223 frozen semen doses belonging to thirty eight breeds of seven species (Cattle, Buffalo, Goat, Sheep, Camel, Equine and Yak).

As an attempt to develop the breed signature for Sahiwal, Gir and Hariana cattle, the allelic patterns across the three populations using 84 microsatellite loci was analyzed. Observed heterozygosity was less than the expected heterozygosity except for Gir.

Cattle admixture in domestic yak populations was assessed through analysing cattle mtDNA sequences in domestic yak populations. A total of 37 mitochondrial DNA sequences were characterized in Arunachali yak, which revealed total 15 haplotypes.

Fatty acid profiling of 500 goat milk samples was accomplished through gas chromatography. The value of different fatty acids varied from 0.002 to 41.70 gram per 100 gram of Fatty acid methyl ester (FAME). The unsaturated fatty acid was 28.89 in which monounsaturated fatty acids (MUFA) contributed 24.13% and Polyunsaturated fatty acids (PUFA) contributed 5.12%.

An attempt was made for development of human tissue plasminogen activator gene construct for mammalian cell culture expression system. Promoter and regulatory elements of ovine beta-lactoglobulin (oBLG) gene was taken to drive the expression of human tissue plasminogen activator in a mammary gland. Fragments of oBLG corresponding to UTRs were amplified.

For studying genetic variability in bovine cytokines, IFN-γ gene and lymphotoxin part (TNF β) of the TNF gene were characterized in 5 Zebu cattle breeds. Total 20 SNPs and polymorphic microsatellite repeats (GTTT)n were observed in IFN-γ gene. Total 6 SNPs were observed in TNF β promoter region and Fis values at all the SNP loci were negative which indicated a heterozygosity excess at these loci.

Comparative physiological and transcriptional adaptation of circulating polymorpho nuclear (PMN) cells in Murrah buffaloes, Sahiwal and Karan Fries cows was analysed during peri-

parturient period. Transcriptome analysis of buffalo PMN cells identified several hundred differentially expressed genes throughout the peripartum period. The microarray based analysis revealed several pathways that were significantly affected. Results revealed Sahiwal to be more resistant to physiological stress during the peripartum period.

In order to unravel genetic structure of Indian cattle, seven native cattle breeds-Amritmahal, Gir, Ongole, Red Kandhari, Sahiwal, Tharparkar, Leh cattle and two exotic breeds-Holstein and Jersey cattle were genotyped using 770K high density bovine SNP chip. The native cattle from Leh and laddakh region were genetically distinct from rest of the Indian cattle.

Differential heat shock response was assessed in mammary epithelial cells of Holstein Friesian, Sahiwal cows and Murrah buffaloes. The higher abundance of HSP mRNA after heat stress showed initial evidence of transcriptional differences in cattle as well as buffaloes, further suggesting their differential cellular tolerance to withstand heat stress. Heat shock proteins were found to be upregulated.

Transcriptome profile of buffalo mammary gland across different physiological stages was compared in heifer and involution stages from lactating stage to identify stage specific genes. Several genes related to apoptosis, immune and oxidative stress were found to be up-regulated during involution.

The transcriptome data was subjected for comprehensive analysis to reveal key differences in expression profile of buffalo and Sahiwal cow mammary epithelial cells during early lactation. A total 65 genes were found to be upregulated while only 5 genes were down regulated in buffalo during early lactation period.

De-novo assembly of goat transcriptome was developed using Illumina 2X75 bp paired end reads. The mean contig length was 1815.79 with GC contents of 50.75%. The gene ontology analysis revealed 21718, 22805 and 21901 entries from biological processes, cellular component and molecular functions.

Transcriptome data of 76 bp, paired end reads on 38 various tissues was generated for the comparison in the five biological groups, represented by five breeds (Kanniadu, Black Bengal, Sirohi, Osmanabadi and Changthangi) from different geographical locations. The expression profile revealed 1348 expressed protein coding genes to be compared among all the breeds.

De-novo assembly of dromedarian camel transcriptome was genrated using Illumina 2X75 bp paired end reads. The mean contig length was 1311.03 with GC contents of 51.24%. The transcriptome assembly had 32940 hits in NCBI nr-database. The gene ontology analysis revealed 24676, 26027 and 24949 entries from biological processes, cellular components and molecular functions. A total of 581614 accessions were obtained for dromedarian camel.

For identification of QTL for milk yield, fat and protein percentage in buffaloes, a total of 30 microsatellite loci from the cattle

NBAGR

genome database were amplified in 8400 buffalo daughters. Total 8 buffalo chromosomes have been genotyped using microsatellite markers with a genetic distance of 10-15 cM on each chromosome. Heifers with different age were analysed for the identification of markers associated with the QTL for body weights.

5'-upstream TLR8 gene was characterized in buffalo, cattle and goat. Buffalo breeds revealed varied allelic distribution. Ecto-domain regions of TLR2 and TLR4 genes were genotyped in Murrah, Toda and Swamp buffaloes, which showed seven haplotypes. Mastitis affected Murrah animals showed higher expression of pro-inflammatory cytokines in milk and blood compared with non-affected animals.

Genes associated with incidences of mastitis were characterized in buffalo. Buffalo haptoglobin showed internal duplication of large coding region. SNPs at PGLYRP1 and haptoglobin genes had significantly ($p<0.05$) different allelic frequencies between mastitis and healthy cattle. SAA3, Hp, PGLYRP1 and CCL2 genes had higher expression in acute mastitis in cattle.

Total 156 SNPs in TLRs (TLR 1, 2, 4, 5, 6, 8, 9 and10) coding region were found in Indian cattle breeds.TLR6 was most diverse while TLR9 showed minimum number of SNPs. Kankrej, Hariana and Gir cattle were found to have the highest number of SNPs and the Kangyam was least polymorphic. Sufficient diversity was observed within Indian cattle.

Genetic polymorphism at the growth differentiation factor 8 (GDF8), β3 adrenergic receptor (ADRB3) and calpain (CAPN) genes having effect on meat quality parameters has been documented in different Indian sheep breeds.

Spiti donkey population was evaluated for within breed genetic diversity and genetic bottlenecks using microsatellite markers. Results indicated presence of reasonably high levels of genetic variability.

Under the service project total 423 breeding bulls were screened for their cytogenetic parameters. Some of the bulls were identified to have chromosomal abnormalities.

Indian goat breeds having different prolificacy were screened for mutations in GDF9 and BMPR1B gene. Sequence analysis revealed absence of any polymorphism including the FecB mutation in BMPRIB exonic regions in Indian goats. Three novel SNPs were identified in KiSS1 gene of Indian goats.

Myostatin, Monocarboxylate transporters and CD147 genes were screened for SNPs in three equine breeds of India viz., Kathiawari, Marwari and Sindhi. Total 19 SNPs genes specific to indigenous breeds were identified.

Microsatellite loci were studied in three Kathiawari, Marwari and Sindhi horses population. Results showed Marwari and Sindhi horses forming two separate clusters, whereas Kathiawari did not form distinct cluster but overlapped with Marwari and Sindhi.

Molecular characterization was done for Kachchhi and Kharai camel from Gujarat,

Results indicated that Kharai breed is genetically different from Kachchhi breed.

Three indigenous pig populations viz., Votho pig from Nagaland, indigenous pig from Arunachal Pradesh and Mali pig from Tripura of Northeast India were characterized using 21 polymorphic microsatellite loci.

A total of six SNPs were identified in IGF-1 gene among three draft cattle breeds. Promoter microsatellite locus at the gene suggested to be a potential marker for draughtability in Kangayam, Bargur and Hallikar breeds of cattle.

For conservation of Krishna Valley Cattle, total 10,228 inseminations were performed since inception. So far 725 males and 627 females were born in the breeding tract. For conservation of Kilakarsal sheep, a total of 488 Kilakarsal progenies were produced.

In the Bureau library to keep track of the current scientific/technical developments 48 journals (Fourteen foreign and thirty four Indian Journals) were subscribed. In the current year, books and journals worth Rs. 8, 30, 846/- were procured for the benefit of NBAGR staff.

The Institute Research Committee meetings were held in time. The progress of research projects was reviewed during mid term Institute Research Committee (IRC), Research Advisory Committee (RAC) meetings. The final reports of four completed projects were deliberated and five new project proposals were approved during the annual IRC meeting. At present, 27 research projects including 1 DBT, 6 NAIP and 1 National Fellow project are ongoing in addition to the newly approved projects.

National Advisory Board on Management of Genetic Resources meeting was held at NBAGR on 5th March, 2013. The meeting was chaired by Dr. R.S. Paroda, Ex Director-General, ICAR and co-chaired by Dr. S. Ayyappan, Secretary DARE & DG, ICAR.

Three patents as parentage testing kits for goat and Indian ruminant livestock and DNA test for differentiation of cattle & buffalo meat and milk were filed to the Indian Patent Office, Delhi.

Three technologies on parentage verification in Zebu cattle, camels and buffaloes were commercialized, generating a revenue of total Rs. 6.00 Lakhs.

Scientific findings were published by the scientists through 62 research papers in national and international research journals of high impact factor. Apart from this seven monographs/ leaflets were also brought out.

One scientist was deputed for overseas participations in seminars/trainings.

NBAGR staff participated in different sports events held in North Zone and bagged medals in volleyball smashing & shooting and race competitions.

29th Foundation Day of the Bureau, National Science Day, Republic Day and Independence Day were celebrated at NBAGR campus. Biodiversity Day was celebrated with Gujjar migratory pastoralists at Shazadpur, Ambala (Haryana). Breed Saviour Award function was held on 8th March 2013 at NBAGR. Twenty farmers belonging to different states were

honoured for their contributions in breed conservation of indigenous germplasm.

One day Workshop on "Awareness of IPR issues" was held on 11.1.2013.

Bureau participated in various animal/dairy fairs and installed exhibitions on its various activities.

NBAGR scientists have been included in the faculty of NDRI, Karnal and IVRI, Izatnagar, Teaching and guiding of students for their thesis work is being undertaken by various faculty members. The consultancies/services were provided by Bureau through imparting trainings, cytogenetic evaluation of breeding bulls and acted as resource persons for conducting the training programmes.

Many distinguished personalities including the foreign dignitaries visited the laboratories of Bureau and interacted with scientists.

The Bureau work force is comprising of 32 scientific, 18 technical, 19 administrative, and 5 skilled supporting staff personnel. The staff strength fluctuated by new joining, superannuation and transfers. The eligible staff workers were promoted in time.

NBAGR

History and Profile

- About Bureau
- Organogram
- Financial Outlay

2012-13

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 the Institute. Therefore, 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 (NBAGR), Karnal has been the nodal organization in India with the mandate and objectives as given below:

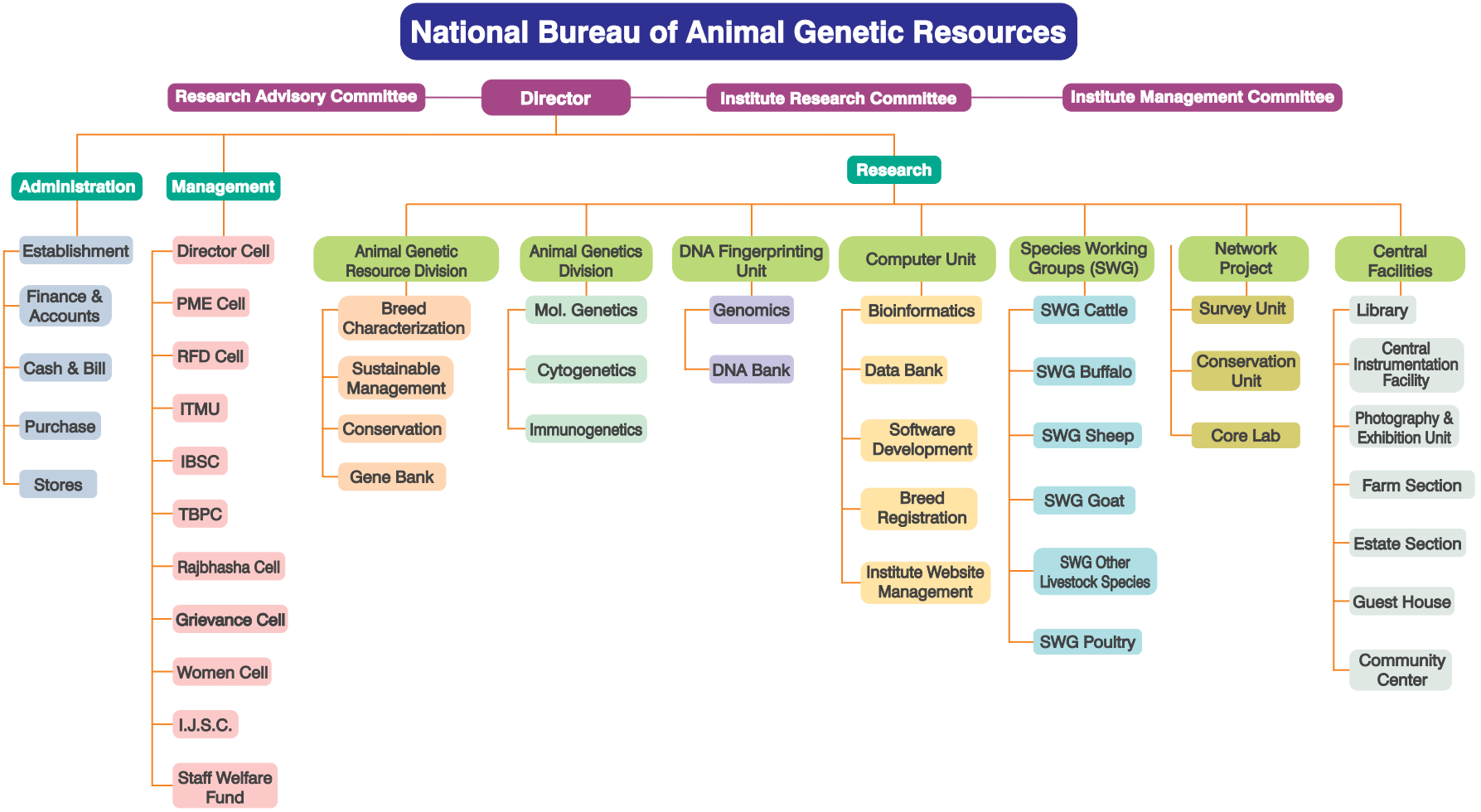
MANDATE

'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
Establishment
Finance & Accounts
Cash & Bill
Purchase
Stores
Management
Director Cell
PME Cell
RFD Cell
ITMU
IBSC
TBPC
Rajbhasha Cell
Grievance Cell
Women Cell
I.J.S.C.
Staff Welfare Fund
Research
Animal Genetic Resource Division
Breed Characterization
Sustainable Management
Conservation
Gene Bank
Animal Genetics Division
Mol. Genetics
Cytogenetics
Immunogenetics
DNA Fingerprinting Unit
Genomics
DNA Bank
Computer Unit
Bioinformatics
Data Bank
Software Development
Breed Registration
Institute Website Management
Species Working Groups (SWG)
SWG Cattle
SWG Buffalo
SWG Sheep
SWG Goat
SWG Other Livestock Species
SWG Poultry
Network Project
Survey Unit
Conservation Unit
Core Lab
Central Facilities
Library
Central Instrumentation Facility
Photography & Exhibition Unit
Farm Section
Estate Section
Guest House
Community Center

Financial Outlay

Financial outlay under Plan and Non-Plan & Network Project of NBAGR for the financial year 2012-13 alongwith expenditure.

(Rs. In Lakhs)

Sr. No.	HEAD	NON-PLAN		PLAN		Network Project	
		Receipt	Expenditure	Receipt	Expenditure	Receipt	Expenditure
01.	Capital						
	i) Works	5.00	4.70	103.70	103.70	0.00	0.00
	ii) Other capital expenditure	5.00	4.72	42.00	38.07	0.00	0.00
	Total Capital	10.00	9.42	145.70	141.77	0.00	0.00
02.	Revenue					67.00	64.47
	i) Establishment expenses	591.97	564.91	0.00	0.00	0.00	0.00
	ii) Traveling Allowance	2.89	2.41	12.00	11.89	0.00	0.00
	iii) Research & Operational expenses	20.00	19.66	74.90	74.89	0.00	0.00
	iv) Administrative Expenses	64.99	64.75	89.60	89.59	0.00	0.00
	v) Miscellaneous expenses	4.63	3.46	1.50	1.46	0.00	0.00
	Total Revenue	684.48	655.19	178.00	177.83	67.00	64.47
03.	Pension & Retirement benefits	20.00	11.47	0.00	0.00	0.00	0.00
	Grant Total	**714.48**	**676.08**	**323.70**	**319.60**	**67.00**	**64.47**

Revenue generated during the year 2012-2013

(Rs. in lakhs)

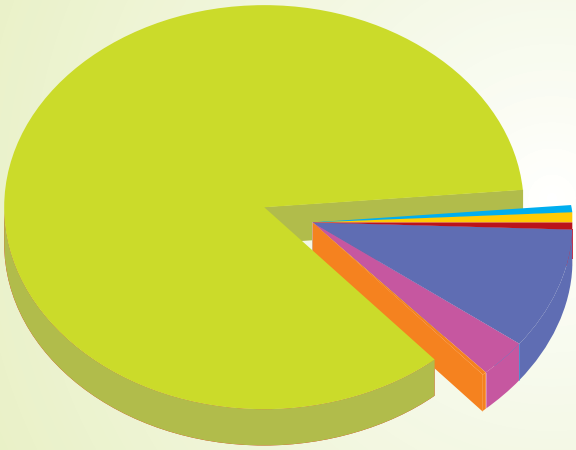
Sr. No.	Head of Account	Amount
1.	Sale of Publication & Advertisement	1.30
2.	Licence fee	2.70
3.	Training Programs - Income	0.40
4.	Hostel and Guest house rent	3.40
5.	Sale of Technology	5.02
6.	Sale of farm Produce	9.46
7.	Others Misc. Revenue Receipts	4.07
	Total	26.35

Revenue Target Fixed : 30.00 Lakhs

Target Achieved : 26.35 Lakhs

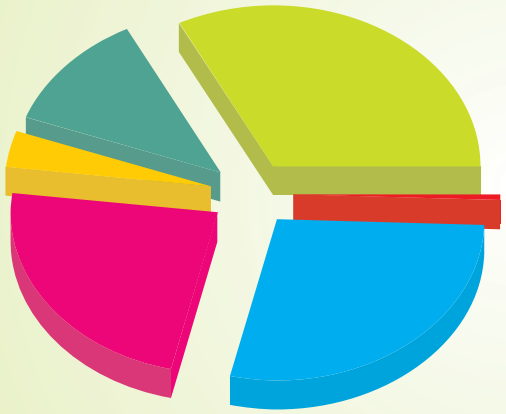
FINANCIAL OUTLAY

Funds Utilization under Non-Plan



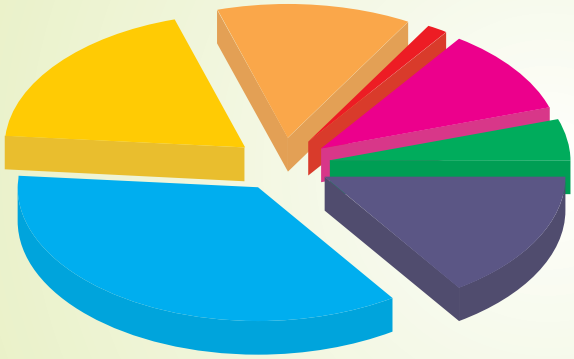
- Works
- Other Capital expenditure
- Establishment Expenses
- Traveling Allowance
- Research & Operational Expenses
- Administrative Expenses
- Miscellaneous Expenses

Funds Utilization under Plan



- Works
- Other Capital expenditure
- Establishment expenses
- Traveling Allowance
- Research & Operational Expenses
- Administrative Expenses
- Miscellaneous Expenses

Revenue Generated

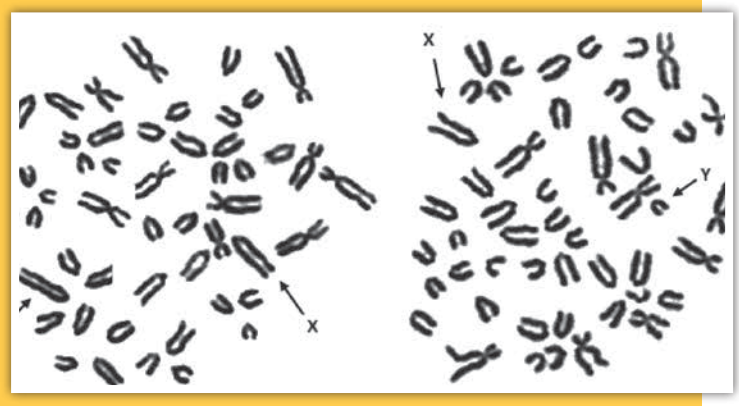


- Sale of Publication & Advertisement
- Licence fee
- Training Programs - Income
- Hostel and Guest house rent
- Sale of Technology
- Sale of farm Produce
- Others Misc. Revenue Receipts

NBAGR

Research Accomplishments

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



2012-13

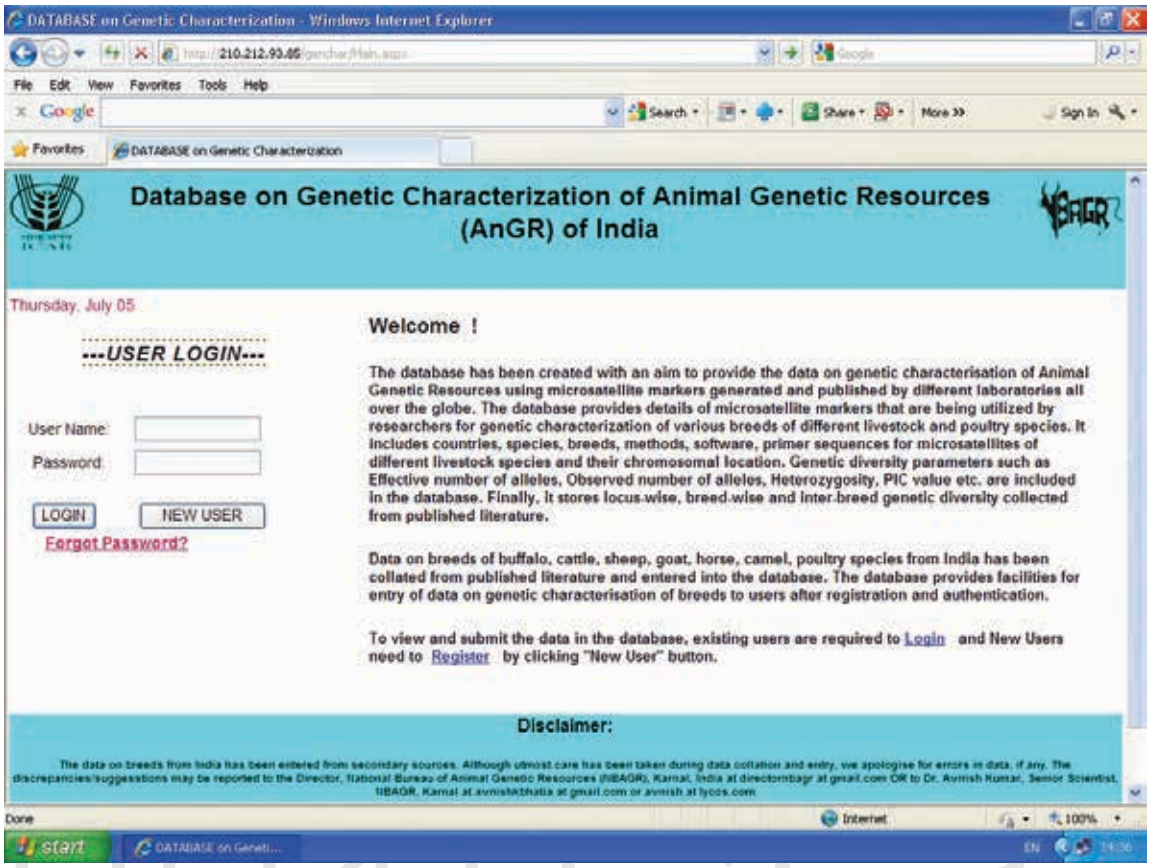
Livestock Information Management

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

A database on genetic characterization of Animal Genetic Resources (AnGR) of India has been developed at the institute. User-Login system for the database was developed using ASP.NET with C#. Two types of access have been provided to the user- View level and Data-submission level. After online registration of a user, its credentials are verified before granting permission for data entry.

The database on Livestock-EST was enriched with additional data. User interface of the database was also enhanced. EST data was downloaded from internet resources and Perl scripts were written to parse the files with different formats and fill the data into the database. EST's on various tissues for livestock species *viz.*taurus cattle (*Bos taurus),* Pig *(Sus scrofa),* chicken *(Gallus gallus),* yak *(Bos grunniens),* zebu cattle *(Bos indicus),* goat *(Capra hircus),* duck *(Anas platyrhynchos),* horse *(Equus caballus)* and sheep (*Ovis aries)* were inserted into the database. It contains more than 270,000 EST records on livestock and poultry species. Bioinformatics tool such as CAP3 for formation of contigs from selected EST's was incorporated into the database.

The database on Livestock Genes and Proteins was enriched with gene-ontology data collected from ftp site (http://www.geneontology.org/GO.downloads.html). Perl scripts were written and executed to store gene-ontology records into the database. Presently 35,113 gene-ontology records have been stored in the database. User-interface using ASP.NET was created to search proteins through gene-ontology terms. Coding for searching livestock proteins on the basis of gene ontology terms like cellular component, biological function and molecular function was also completed. Perl scripts for tools such as conversion of protein sequence to DNA sequence and counting amino acids for a particular protein were implemented in the database.



Registration of livestock and poultry breeds

Breed registration Committee in its meeting on 14th May, 2012 at New Delhi approved registration of nine new breeds of livestock species, which include three breeds of cattle, one of buffalo, two each of goat and pig and one of donkey. The institute has registered first time indigenous pig and donkey breeds. After including these newly registered breeds, total number of indigenous breeds in the country is 144, which include 37 for cattle, 13 for buffalo, 23 for goat, 39 for sheep, 6 for horses& ponies, 8 for camel, 2 for pig, 1 for donkey and 15 for chicken.

S.N.	Breed	Home Tract	Accession number
BUFFALO			
01	Kalahandi	Odisha	INDIA_BUFFALO_1500_KALAHANDI_01013
CATTLE			
01	Pulikulam	Tamilnadu	INDIA_CATTLE_1800_PULIKULAM_03035
02	Kosali	Chhattisgarh	INDIA_CATTLE_2600_KOSALI _03036
03	Malnad Gidda	Karnataka	INDIA_CATTLE_0800_MALNADGIDDA_03037
GOAT			
01	Konkan Kanyal	Maharashtra	INDIA_GOAT_1100_ KONKANKANYAL _06022
02	Berari	Maharashtra	INDIA_GOAT_1100_ BERARI _06023
PIG			
01	Ghoongroo	West Bengal	INDIA_PIG_2100_GHOONGROO_09001
02	Niang Megha	Meghalaya	INDIA_PIG_1300_NIANGMEGHA_09002
Donkey			
01	Spiti	Himachal Pradesh	INDIA_DONKEY__0600_SPITI_05001

Kalahandi buffalo: These buffaloes are dual type; used for milk and draught purpose in Kalahandi and Rayagada districts of Odisha. Animals are medium sized; having long, strong, half circled horns with broad base; and are excellent in heat and drought tolerance.


Pulikulam cattle: These cattle are maintained in large migratory herds in Madurai and nearby region of Tamilnadu. Used for draught and manure purposes. These cattle are also used in games like bull riding (Jallikattu) in local area. Breed is more resistance to communicable and parasitic diseases as compared to crossbreds of native area.


Kosali cattle: Small sized, draft purpose cattle breed of Chhattisgarh. Farmers prefer bullocks of this breed for cleaning of weeds from paddy field. Animals are known for efficient working ability and high disease resistance.

Malnad Gidda cattle: Short statured cattle breed from Western Ghat of Karnataka, reared for milk and manure purpose. Animal have excellent endurance power and resistance to diseases.

Konkan Kanyal goat: Meat type goat breed adapted to high rainfall and hot and humid climate of Konkan region of Maharasthra. Animals have typical white bands on black face and black ear with white margin.

Berari goat: Reared mainly for meat purpose in Vidarbh region of Maharashtra. As a unique feature, animals have light to dark strips on lateral sides from horn base to nostrils of face.

Ghoongroo pig: Reared for pork and manure purpose in Darjeeling and nearby Tarai area of West Bengal. Animals are black in colour and have upwardly curved snout and large heart shaped ears.

Niang Megha pig: Niann Megha pig are distributed in Garo, Khasi and Jaintia hills of Meghalaya and is reared for pork and bristle purpose. The animals have typical wild look with erect bristles on dorsal midline and small erect ears extended vertically.

Spiti donkey: This breed is native to Lahaul and Spiti region of Himachal Pradesh. These donkeys are used for transportation at high altitude (around 3500m above MSL) area with low level of environmental oxygen. These animals can survive well in scarcity of feed and fodder during harsh winter months when the area is completely snow bound.

Phenotypic Characterization and Conservation

Sanchori cattle

Breeding tract of Sanchori cattle includes Sanchor and adjoining tehsils of Jalore district of Rajasthan state. The animals derive the name Sanchori from the place of their habitat. Sanchor/ Desi cattle are kept in the herd size varying from 2 to 20 animals in the open houses adjacent to the farmer's house in their agricultural fields called *dhanis*. The animals are stall fed and grazing is practiced in nearby agricultural fields during the day time for a duration of 4-6 hours. The animals are hardy and well survived in all the seasons in the open housing system.

Sanchori cow

Standard eight body measurements and physical traits were recorded for 312 animals belonging to different age groups and sex. Coat colour of animals is generally white and horns are smaller in size and diameter as compared to Kankrej cattle. Bulls are white, grey or black in coat colour. Body is bigger than the Kankrej cattle. Hairs are short and straight. The muzzle colour is black in majority of animals; however, pinkish muzzle is also seen. Hoof colour is invariably black. Tail switch is black, greyish or mixed. Due to adequate mechanization of agriculture in the area, the male calves are either sent to the nearby *gaushalas* or sold to the farmers of other places for draft use. The age at first calving and inter-calving period is reported to be 3.0-3.5 years and 12-15 months, respectively. Average peak milk yield is

Sanchori bull

reported from 6 to 18 litres. The lactation length varies from 8 to12 months. The milk contains 4.5 to 5.0% fat and 8.5 to 8.8% SNF. The milk is sold either to the milk co-operatives or to the *gaushalas*. Since, the milk marketing is based on the fat percent, some farmers are shifting to have the buffaloes instead of Sanchori cattle. The breeding of cows is natural. In some cases, the semen of Kankrej is used, which might be the cause of dilution in the breed.

Indigenous cattle of Mizoram

Indigenous cattle of Mizoram were characterized in 11 villeges of Champhai and Kolasib districts of the state. A total of 33 farmers were interviewed. Majority of the farmers (66%) are 30 to 40 years of age. Total 88% farmers are literate. Land holding ranges from 0.20 to 12 ha. The land holdings are larger in Kolasib district than the Champhai. The annual income of farmers ranged from ₹ Rs. 0.75 lacs to 3.2 lacs however half of the farmers have less than 1.0 lacs, annual income. The contribution from livestock sector in the annual income is around 30%. The herd size ranges from 5 to 25 indigenous cattle per farmer. Herd size was larger in Kolasib district.

Mizoram cattle are reared mainly for drought power and manure; very few farmers rear them for milk and meat. Animal houses are mostly open and kachha. Breeding is natural. Breeding bulls are available in the herds. Vaccination against diseases like H.S., FMD and BQ is generally practiced.

Mizoram cattle

Animals are reared mainly on extensive system of management i.e. grazing from morning to evening.

Animals are wellbuilt, small in size with cylindrical type of body with strong legs. The body colour varies in different colours viz. brown (85%), black (11%) and gray (44%). Dewlap and hump is small. Ears are small to moderate in length and horizontal in orientation. Horns are small and black (72%) or gray (28%) in colour. Orientation is mostly outward, upward and then curved towards face. Udder is small and developed. Milk veins are not prominent. Teats are small (5-12 cm) in size, and funnel (78%) type. Tail switch is brown (54%), black (39%) and gray (7%). Temperament is docile.

The birth weight ranges from 10 to 20 kg. The cow and bullock weigh about 169 kg and 200 kg, respectively. The daily milk production ranges from 1.0 to 3.5 kg. The average milk yield is 1.54±0.11 kg. A pair of bullock may plough about 0.5 acre of land in 5-6 hours. The age at first calving, lactation length, dry period, service period and calving interval ranges from 28 to 42 months, 150 to 210 days, 4 to 6 months, 3 to 4 months and 12 to 24 months, respectively.

The average body length, height at wither, heart girth, paunch girth, horn length, ear length, face length and tail length without switch in cows (71) are 103.70±1.01, 103.60±0.62, 132.22±1.05, 131.90±1.15, 11.01±0.42, 18.02±0.33, 36.15±0.37 and 67.26±0.76 cms respectively. The corresponding averages in bullocks (84) are 109.03±1.39, 106.92±0.84, 139.52±1.59 cm, 146.64±1.80, 15.55±0.55, 18.20±0.18 cm, 38.73±0.39 and 68.54±1.07 cm, respectively.

Indigenous cattle of Adilabad (Jhari cattle)

Phenotypic characterization of local cattle from Adilabad district was done under NAIP Harmonizing biodiversity sub project. The utility of these cattle is primarily draft and agricultural operations & transport, followed by dairy and dung purpose. Phenotypic measurements and breed characteristics on 300 local cattle were recorded. Average body length, height at withers, chest girth, paunch girth, ear length, tail length and body weight (kg) of cow are 96.24±2.09, 102.52±1.66, 133.83±3.5, 136.60± 3.89, 19.40±0.34, 78.03±2.46 cm and 181.12±13.01kgs, respectively. In adult male the body length, height at withers, chest girth, paunch girth, ear length, tail length and body weight (kg) are 116.02±1.68, 120.33±1.17, 154.70±1.85, 153.01±1.78, 20.76±0.21, 87.93±0.54 cm and 263.98±9.55kgs, respectively. About 60% of the animals have white coat colour and rest are brown coat colours. Animals are medium in size with well developed dewlap. Horns are small to medium sized, curved forward, cylindrical and sickle shaped. The milk production in females ranges from 1.5 to 2.0 kg per day. Natural service is preferred by the farmers for breeding their animals.

Gojri buffalo

Gojri buffalo is reared by the Gujjar communities from Mohali, Roopnagar, Nawashehar, Hossiarpur, Sundernagar, Pathankot districts in Punjab and Nurpur, Jassur, Chawari, Jyot, Sahu, Rakh, Bharmaur and Tissa areas in Kangra and

Chamba divisions of Himachal Pradesh. Gujjars from these areas are engaged in buffalo rearing only. Migration by Gujjar pastoralists starts from plains / foot hills during mid-May to June and continue till last of September to early November (4-5 months) every year to reach Chamba division of Himachal Pradesh. The one way of migration takes around 10 to15 days.

Gojri buffalo

Average herd size ranges from 3 to 12 buffaloes. The Animals have black coat colour with brown hairs; 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*'. Gojri buffaloes are reared for milk and are found to be unique and possess distinct phenotypic appearance from extant buffalo breeds in the region. Adult animals are mostly housed in open, but young ones are housed in closed enclosures.

Belahi cattle

Milk samples (n=68) from Belahi cattle under different lactations were collected from three different villages of Raipurrani block and Khudakalan of Ambala region and analyzed for the milk constituent traits. Fat, protein, lactose, SNF and total Solids in percentages are 5.04, 3.33, 5.02, 9.073, 14.11, respectively for first lactation (30) and 5.25, 3.45, 5.20, 9.39, 14.64 for pooled lactation (38) other than first lactation.

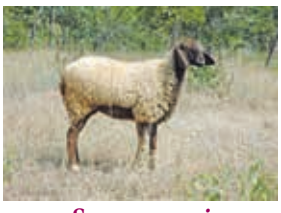
Deccani sheep ecotypes

Deccani sheep is widely distributed over eight districts viz. Pune, Ahmadnagar, Satara, Solapur, Sangli, Kolhapur, Nasik and Beed of Maharashtra. These districts host five ecotypes of Deccani sheep known as Kolhapuri, Lonand, Madgyal, Sangamneri and Solapuri. The aim of the present study is to characterize and classify them. An exploratory visit corroborated the distribution area of the five ecotypes with Department of the Animal Husbandry, Maharashtra. Data on seven morphometric traits (body weight, body length, height at withers, chest girth, paunch girth, ear length and tail length) of 224 adult sheep reared under extensive management system were recorded from their distribution area. It was observed that all five ecotypes have different coat colours. Almost similar types of managemental practices were observed. Shepherds remain on migration during December to June. Preliminary findings based on morphometric traits indicated differences between the ecotypes. The body measures of Madgyal sheep were higher than the others followed by Sangamneri sheep.

Kolhapuri

Lonand

Madgyal



Sangamneri

Solapuri

Adult body weight of Madgyal, Sangamneri, Solapuri, Kolhapuri and Lonand ewes were 38.7, 33.4, 30.4, 28.8 and 27.8 kg respectively. In view of preliminary findings, detailed survey of Lonand and Sangamneri sheep were conducted. Data on body biometry of 64 adult sheep and body weight of 24 lambs of Lonand sheep were recorded. Similar data on 145 adult sheep and 45 lambs of Sangamneri sheep were recorded. One hundred blood samples of Sangamneri sheep and fifty samples of Lonand sheep were collected to examine the differences at molecular level. DNA of the blood samples was extracted using standard protocol. It was observed that most of the Lonand sheep rearers have introduced Madgyal rams in their sheep flocks for having better growth of the offspring.

Koraput sheep

Koraput sheep is a lesser known sheep breed of Odisha state. Phenotypic data on about 250 adult animals, body weight on 160 lambs of different age groups and information on management practices, socio economic utility of this sheep from 36 sheep farmers were recorded. Data analysis based on body biometry revealed that Koraput sheep is quite distinct from the Ganjam sheep found in the same breeding tract.

The genotyping of 27 Samples of Koraput sheep population was carried out using 21

Koraput ram

Koraput ewe

Microsatellite markers. The observed number of alleles in different loci ranged from 3 to 12 with a mean value of 6.47±2.92 per locus. The observed heterozygosity was 0.57±0.20 and expected heterozygosity was 0.69±0.17. The average heterozygosity value was 0.6848±0.1671. The F_{is} value was found to be 0.1552 which indicate 15.52% inbreeding.

Table: Body biometry (Mean± SE) of Koraput sheep

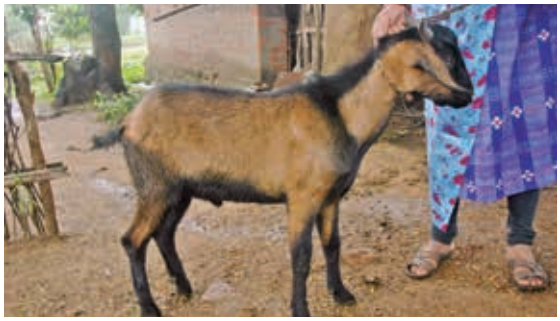
Trait	Koraput Ewes (N=113)	Koraput Rams (N=14)
Body Length(cm)	51.08±0.34	48.64±0.89
Height wither(cm)	55.58±0.42	56.50±0.99
Chest girth(cm)	66.34±0.45	67.43±0.77
Paunch girth(cm)	69.69±0.56	70.00±1.72
Ear length(cm)	4.61±0.23	4.86±0.52
Horn length (cm)	-	8.82±1.18
Tail length(cm)	9.77±0.15	9.29±0.22
Face length(cm)	14.44±0.10	15.36±0.23
Body Weight (kg)	18.89±0.35	18.32±0.82

Table: Average body weight (kg.)of Koraput lambs.

Age Group	Male (N=82)	Female (N=78)
0-3 months	8.01±0.62 (24)	7.76±0.48 (22)
3-6 months	10.94±0.38 42)	9.74±0.40 (28)
6-12 months	14.13±0.64 (16)	13.24±0.67 (28)

Malkangiri goat

A total of 147 animals of different age and sex group were recorded for eight body parameters of local goat population of Malkangiri district of Odisha state. Malkangiri goats are medium in size and weight and are reared for meat only. The goats are mostly light brown or black brown; however, white and black colour goats are also seen. The face is having strips of white of light brown colour extending from base of the ear to nose in case of brown colour goats. The top line is black. In males black ring is present around the neck. Muzzle and hooves are generally black. The flock size varied from 5 to 35.



Malkangiri buck

Raigari goat

Data were recorded on phenotypic attributes and body biometry (body length, height at withers, chest girth, paunch girth, face length, horn length, ear length and tail length) of Raigari goats of Odisha.

Data on biometry and management practices from 126 lesser known /local goats belonging to 40 farmers of 10 villages were recorded. Goats are reared mainly by marginal small farmers and landless tribes of the area for meat purpose only. Goats are medium in size. Coat colour is light brown to dark brown and some mixed coloured animal also seen in the flocks. White or light brown colour strips extending from base of the ear to muzzle are present on either side of the nose line. Muzzle colour is black or brown and hooves are black or grey. These goats are reared under extensive management system with 6-10 hours grazing during the day throughout the year. The overall averages body length, height at withers, chest/heart girth, face length, horn length, ear length, paunch girth and tail length are 57.79 ±0.67, 58.58±0.58, 62.01± 0.75, 14.76 ±0.16, 7.87 ±0.36, 12.79 ±0.18, 65.88 ±0.89, 11.95 ±0.16 cm., respectively in female and 53.75±1.60, 55.46±1.43, 55.92±1.72, 13.42±0.51, 6.42±0.78, 12.33±0.39, 58.96±1.68 and 15.17±1.25 cm, respectively in males. The overall average body weight at 3, 6, 9, 12 months and adult age are 9.06±0.33, 11.40±0.37, 15.0±0.45, 16.38±0.40 and 22.69±0.61 kg, respectively. The average age at sexual maturity and age at first kidding are 10-12 months and 15-18 months, respectively. Thatched houses with raised floor (2-4 ft) made up of wooden planks/ bamboos are used as goat shelter. No extra concentrate or supplementations are given to the goats. Flock size varies from 2 to 25 animals. Natural service is practiced. These goats should be multiplied and improved for better economic return for lift the economic status of the goat keepers through goat keeping.

Raigari goat

Table: Average body measurements of Raigari goats

Age Group	Sex (No.)	Height at Wither (cm)	Body length (cm)	Chest Girth (cm)	Paunch Girth (cm)	Face Length (cm)	Horn length (cm)	Ear length (cm)	Tail length (cm)	Weight (kg)
3 months	Female (9)	47.67 ±0.99	44.44 ±0.58	47.44 ±1.23	51.89 ±1.24	11.78 ±0.46	2.33 ±0.41	10.33 ±0.37	10.11 ±0.31	9.00 ±0.37
	Male (8)	47.88 ±1.09	46.00 ±2.12	47.63 ±1.27	50.75 ±1.16	10.63 ±0.32	2.50 ±0.38	11.00 ±0.38	10.75 ±0.37	9.13 ±0.58
	Overall	47.76 ±0.71	45.18 ±1.03	47.53 ±0.85	51.35 ±0.84	11.24 ±0.32	2.41 ±0.27	10.65 ±0.27	10.41 ±0.24	9.06 ±0.33
6 months	Female (7)	50.43 ±1.59	48.43 ±0.84	52.14 ±0.94	54.57 ±2.21	13.86 ±0.26	4.43 ±0.57	10.57 ±0.37	10.29 ±0.29	11.29 ±0.42
	Male (3)	55.33 ±1.33	50.00 ±1.53	50.33 ±0.33	55.00 ±1.73	13.00 ±0.58	5.00 ±0.58	11.00 ±0.58	11.33 ±0.33	11.67 ±0.88
	Overall	51.90 ±1.36	48.90 ±0.74	51.60 ±0.70	54.70 ±1.58	13.60 ±0.27	4.60 ±0.43	10.70 ±0.30	10.60 ±0.27	11.40 ±0.37
9 months	Female (7)	53.86 ±1.70	55.00 ±1.96	56.71 ±1.21	59.43 ±1.66	14.00 ±0.31	5.29 ±0.68	11.71 ±0.42	10.43 ±0.37	14.86 ±0.70
	Male (4)	55.25 ±1.49	55.50 ±1.44	58.25 ±2.02	61.00 ±2.55	14.75 ±0.48	7.50 ±0.50	11.75 ±0.25	11.25 ±0.63	15.25 ±0.25
	Overall	54.36 ±1.18	55.18 ±1.31	57.27 ±1.03	60.00 ±1.35	14.27 ±0.27	6.09 ±0.56	11.73 ±0.27	10.73 ±0.33	15.00 ±0.45
12 months	Female (11)	58.55 ±0.88	57.45 ±1.19	59.82 ±0.70	62.82 ±1.04	14.73 ±0.19	6.91 ±0.62	11.82 ±0.23	11.09 ±0.28	16.09 ±0.39
	Male (2)	58.50 ±2.50	59.00 ±2.00	60.50 ±0.50	65.00 ±0.00	15.50 ±0.50	7.50 ±0.50	12.50 ±1.50	12.00 ±1.00	18.00 ±1.00
	Overall	58.54 ±0.79	57.69 ±1.04	59.92 ±0.59	63.15 ±0.90	14.85 ±0.19	7.00 ±0.53	11.92 ±0.26	11.23 ±0.28	16.38 ±0.40
Adult	Female (68)	61.35 ±0.44	60.87 ±0.53	65.85 ±0.62	70.06 ±0.85	15.34 ±0.17	9.38 ±0.39	13.62 ±0.18	12.66 ±0.18	22.69 ±0.65
	Male (7)	63.43 ±1.49	61.71 ±1.43	65.14 ±2.10	67.14 ±2.43	15.43 ±0.78	10.57 ±1.29	14.71 ±0.42	13.57 ±0.69	22.71 ±1.54
	Overall	61.55 ±0.42	60.95 ±0.50	65.79 ±0.59	69.79 ±0.81	15.35 ±0.16	9.49 ±0.37	13.72 ±0.17	12.75 ±0.17	22.69 ±0.61

Figure in parentheses indicate number of observations.

Table: Average body measurements (cm) of Malkangiri goats

Age group	Sex (No.)	Height at Wither (cm)	Body length (cm)	Chest Girth (cm)	Paunch Girth (cm)	Face Length (cm)	Horn length (cm)	Ear length (cm)	Tail length (cm)
3 months	Female (7)	47.29 ±0.57	44.00 ±1.07	46.14 ±0.83	47.57 ±1.76	11.57 ±0.20	1.43 ±0.20	11.43 ±0.43	10.43 ±0.43
	Male (3)	51.33 ±1.67	46.33 ±1.33	48.67 ±0.33	51.00 ±1.53	12.67 ±0.67	2.33 ±0.33	11.67 ±0.33	11.33 ±0.33
	Ovearll	48.50 ±0.85	44.70 ±0.88	46.90 ±0.69	48.60 ±1.37	11.90 ±0.28	1.70 ±0.21	11.50 ±0.31	10.70 ±0.33
6 months	Female (8)	50.88 ±1.16	47.75 ±0.70	50.25 ±1.11	53.50 ±1.48	12.63 ±0.26	2.63 ±0.53	12.88 ±0.58	11.38 ±0.38
	Male (4)	58.25 ±1.31	50.75 ±1.49	56.50 ±1.32	58.50 ±0.87	13.25 ±0.48	4.25 ±1.31	12.50 ±0.65	11.50 ±0.29
	Overall	53.33 ±1.35	48.75 ±0.77	52.33 ±1.21	55.17 ±1.22	12.83 ±0.24	3.17 ±0.58	12.67 ±0.40	11.42 ±0.26
9 months	Female (10)	54.80 ±0.79	53.00 ±0.77	55.90 ±0.50	58.70 ±1.51	13.40 ±0.16	4.40 ±0.48	12.90 ±0.57	11.70 ±0.56
	Male (6)	55.50 ±1.52	53.17 ±1.05	56.83 ±0.65	57.00 ±1.10	13.67 ±0.33	4.83 ±0.70	13.00 ±0.58	12.67 ±0.67
	Overall	55.06 ±0.73	53.06 ±0.60	56.25 ±0.40	58.06 ±1.03	13.50 ±0.16	4.56 ±0.39	12.94 ±0.40	12.06 ±0.43
12 months	Female	58.00 ±1.04	54.60 ±0.90	59.70 ±0.76	60.90 ±1.19	14.10 ±0.23	6.00 ±0.47	13.70 ±0.47	12.40 ±0.62
	Male	56.00 ±0.58	56.00 ±1.15	57.67 ±1.76	61.00 ±1.00	14.33 ±0.67	5.67 ±0.67	13.67 ±0.33	13.33 ±0.33
	Overall	57.54 ±0.84	54.92 ±0.74	59.23 ±0.72	60.92 ±0.92	14.15 ±0.22	5.92 ±0.38	13.69 ±0.36	12.62 ±0.49
Adult	Female	63.20 ±0.39	61.79 ±0.37	67.37 ±0.51	70.69 ±0.61	15.62 ±0.10	9.64 ±0.33	13.94 ±0.24	13.80 ±0.18
	Male	65.53 ±1.02	62.67 ±0.99	67.53 ±0.86	69.47 ±1.21	15.80 ±0.22	11.00 ±0.76	15.13 ±0.52	15.27 ±0.44
	Overall	63.56 ±0.37	61.93 ±0.35	67.40 ±0.45	70.50 ±0.55	15.65 ±0.09	9.85 ±0.30	14.13 ±0.22	14.03 ±0.18

Figure in parentheses indicate number of observations.

These goats are reared on semi- extensive management system. The average body length (BL), height at withers (BH), chest girth (CG), paunch girth (PG), face length (FL), horn length (HL), ear length (EL) and tail length (TL) in adult male and female are 62.67±0.99, 65.53±1.02, 67.53±0.86, 69.47±1.21, 15.80±0.22, 11.00±0.76, 15.13 ±0.52, 15.27±0.44 cm and 61.79±0.37, 63.20±0.39, 67.37±0.51, 70.69±0.61, 15.62±0.10, 9.64±0.33, 13.94±0.24, and 13.80±0.18 cm, respectively. The average body weight of males at 3, 6, 9 and 12 months of age were 9.00±0.00 ,12.25±0.48, 14.50±0.85, 16.67±0.33 kg, respectively, whereas, for female the corresponding values were 8.14±0.34, 11.13±0.52, 13.20±0.63, 16.30±0.68 kg, respectively. The body weights of adult female and male animal are 23.93±0.55 and 26.73±0.90 kg, respectively. Female animals show sexual maturity at about 12-18 months of age. Natural service is practiced in area.

Narayanpatna goat

Narayanpatna goats are medium in size. These are mostly brown black in colour. However, brown, off white and even mixed coloured animal were also seen. These goats are reared by poor tribal (Kondhs) people for meat purpose under extensive management without any supplementation of feed and fodder. The flock size varied from 2 to 34. Breeding is through natural service. Female animals show sexual maturity at about 12-15 months of age. The average body length (BL), height at withers (BH), chest girth (CG), paunch girth(PG), face length (FL), horn length (HL), ear length (EL) and tail length (TL) in adult male are 74.40 ± 2.77, 69.60 ± 3.71 , 70.60 ± 4.39, 71.40 ± 4.07, 16.00 ± 1.05, 9.60 ± 2.38, 15.20 ±0.86, 16.20 ± 0.37 cm, respectively and in female 68.47 ±0.56, 65.63 ± 0.57, 70.86 ± 0.60, 73.14 ± 0.73, 16.34 ± 0.12, 11.49 ± 0.46, 13.96 ± 0.24, and 13.96 ± 0.22 cm, respectively. The average body weights of adult female and male animal were 27.33 ± 0.61 and 32.80 ± 6.82 kg respectively.

Narayanpatna goat

Table: Average body measurements (cm) and body weights (kg) of Raigari goats

Age Group	Sex (No.)	Height at Wither (cm)	Body length (cm)	Chest Girth (cm)	Paunch Girth (cm)	Face Length (cm)	Horn length (cm)	Ear length (cm)	Tail length (cm)	Body wt.
3 months	Female (5)	54.00 ±1.26	52.00 ±1.48	51.40 ±1.60	51.40 ±1.50	12.20 ±0.37	2.00 ±0.55	13.00 ±0.55	12.40 ±0.60	11.40 ±0.40
	Male (6)	54.17 ±1.68	50.33 ±1.99	51.50 ±1.20	54.33 ±1.98	12.00 ±0.37	4.33 ±0.56	13.00 ±0.52	12.17 ±0.70	11.50 ±0.67
	Overall	54.09 ±1.03	51.09 ±1.25	51.45 ±0.93	53.00 ±1.30	12.09 ±0.25	3.27 ±0.52	13.00 ±0.36	12.27 ±0.45	11.45 ±0.39
6 months	Female (5)	57.60 ±1.91	54.60 ±1.99	57.60 ±2.25	59.00 ±1.67	13.40 ±0.60	4.80 ±0.58	13.00 ±0.32	12.60 ±0.51	15.00 ±0.45
	Male (5)	58.60 ±0.81	55.00 ±1.30	58.80 ±0.92	60.80 ±1.53	14.20 ±0.58	6.00 ±0.63	13.40 ±0.51	12.60 ±0.68	16.20 ±0.49
	Overall	58.10 ±0.99	54.80 ±1.12	58.20 ±1.16	59.90 ±1.11	13.80 ±0.42	5.40 ±0.45	13.20 ±0.29	12.60 ±0.40	15.60 ±0.37
9 months	Female (5)	62.00 ±2.17	60.20 ±1.91	60.60 ±2.04	60.20 ±1.20	13.80 ±0.37	5.20 ±0.49	13.80 ±0.58	13.40 ±1.12	17.60 ±1.08
	Male (5)	65.20 ±1.07	61.00 ±0.63	63.00 ±1.38	61.80 ±2.08	14.40 ±0.40	6.20 ±0.73	14.20 ±0.37	14.80 ±0.20	19.60 ±0.81
	Overall	63.60 ±1.26	60.60 ±0.96	61.80 ±1.23	61.00 ±1.16	14.10 ±0.28	5.70 ±0.45	14.00 ±0.33	14.10 ±0.59	18.60 ±0.72
Adult	Female (73)	68.47 ±0.56	65.63 ±0.57	70.86 ±0.60	73.14 ±0.73	16.34 ±0.12	11.49 ±0.46	13.96 ±0.24	13.96 ±0.22	27.33 ±0.61
	Male (5)	74.40 ±2.77	69.60 ±3.71	70.60 ±4.39	71.40 ±4.07	16.00 ±1.05	9.60 ±2.38	15.20 ±0.86	16.20 ±0.37	32.80 ±6.82
	Overall	68.85 ±0.57	65.88 ±0.58	70.85 ±0.62	73.03 ±0.72	16.32 ±0.13	11.37 ±0.45	14.04 ±0.24	14.10 ±0.22	27.68 ±0.71

Figure in parentheses indicate number of observations

Harringhata Black chicken

Local chicken population was cheractrised from Harringhata Block of Nadia district and adjoining areas of North 24 Parganas district in West Bengal. About 15-20% of birds in each flock are of Harringhata Black type. Plumage colour is black. Pure black cocks are few in numbers. Majority have brown feathers on neck and wings. Comb is red; mainly single, some birds have rose type. Earlobe is generally white, sometimes red. Body weight is about 1kg in hens and 1.5 kg in cocks. Annual egg production is about 40-50. Eggs are small in size, mostly light brown in colour. Average egg weight is 36.5g. Albumen index, yolk index and haugh units are 0.07±0.00, 0.47±0.04, 76.97±1.70 respectively.

Sindhi donkey

Sindhi donkeys are reared by Kumhar, Sansi and Bhil Communities in Barmer and Jaisalmer districts of Rajasthan. They are well adapted to feed, fodder and water scarcity, endemic to this region. About 1-6 donkeys are kept per household. The Sindhi donkeys are able to carry about 100 kg of load as back pack even on sandy tracts. They are also used extensively in carting and ploughing.

The donkeys of Sindhi breeds are of smaller size with leaner built. The predominant coat colour is light brown with small percentage of brown and grey animals. The belly, inner surfaces of legs, ventral side of neck and inner sides of ears are generally of lighter shade or white in most animals. The small manes are present which are usually of darker shade than the rest of the body colour. The face is longer and thinner with an average length of 46.5 ± 3.22 and 45.77 ± 3.1 cm, in male and female , respectively. The forehead is slightly convex. The nasal bone is straight to slightly concave. The height at withers of male and female animals are 98.8 ± 3.9 and 97.93 ± 4.9 cm, respectively. The body length varies from 82 to 105 cm. The chest girths are 104.3 ± 5.35 in males and 106.52±5.97 cm in females. The estimated weights of adult (above 3 years) male and female animals are 84.95 ± 10.12 and 89.54 ± 14.57 kg, respectively. The canon lengths of fore and hind limbs in male animals are 19.7±1.42 and 28.39±1.51 cm, respectively. Whereas, in females the corresponding values are 19.0±1.38 and 27.33±1.62 cm, respectively. The tail extends slightly beyond hocks having lengths of 52.1 ± 4.42 and 51.14 ± 4.56 cm in male and female animals, respectively. The tail switch is distinguishable and of darker colour in most of the animals. Although, significant differences were not found in most of the morphometric parameters between male and female animals, however some of the limb parameters especially canon length, canon circumference, pastern circumference and hoof circumference showed significant differences in male and female animals. With better road development and increased mechanization, their population is showing declining trend.

Male Sindhi donkey

Utilization of caprine cauda -epididymal spermatozoa for cryopreservation

Goat testis were collected from slaughter house and sperms extracted at room temperature within 2-3 hours from epididymis, cutting caudal region of epididymis. The motility of extracted sperms

was around 75% and live sperm proportion was 90%. The sperms so obtained were diluted in five different extenders having varying proportion of glycerol (4%, 7%, 10% and 14%) to see the effect on post thaw motility parameters and finalize the optimum level of glycerol to be used in further experiments. It was observed that 7% glycerol was most optimum in maintaining the motility, viability, acrosomal and membrane integrity of sperm and hence subsequently this level was used in all extenders. An extender containing trehalose, 20% egg yolk and 7% glycerol could retain the maximum motility (65%) after 60 minutes at room temperature out of seven different extenders tried. The sperms diluted in different extenders were frozen through gradient cooling in a programmable freezer and after 28 days of storage in liquid nitrogen sperms extended in trehalose, 20% egg yolk and 7% glycerol showed maximum post thaw motility (55%). The viability, acrosomal integrity and membrane integrity was 72, 71 and 60% respectively.

Breeding intervention for harmonizing biodiversity (NAIP Project)

To upgrade the local germplasm with the intervention of selective breeding in goats, poultry and cattle, the superior selected breeding males were distributed in the region. A total of 20 elite breeding bucks and 3 elite breeding bulls were procured and distributed to the beneficiaries in Indervally, Kerameri and Beemini mandal. The bulls were distributed to the beneficiaries through Biodiversity Management Committee and bull register is maintained to access the impact. A total of 170 chicks (Aseel type chicken) of 1-2 weeks old were distributed to 17 beneficiaries of Keramerimandal (Jhari and Modi villages). Eighty two kids born were recorded in farmer's flocks where bucks were supplied in Bheemini mandal. The average body weight of kids at 5-6 months of age is 14.16±0.17kg.

Ex situ conservation

A total of **14,150** frozen semen doses of 10 cattle breeds and 1 buffalo breed were procured and added to repository in Gene Bank during the year (table). The National Gene Bank at NBAGR now stores about 1,09,223 frozen semen doses belonging to thirty eight breeds of seven species (Cattle, Buffalo, Goat, Sheep, Camel, Equine and Yak).

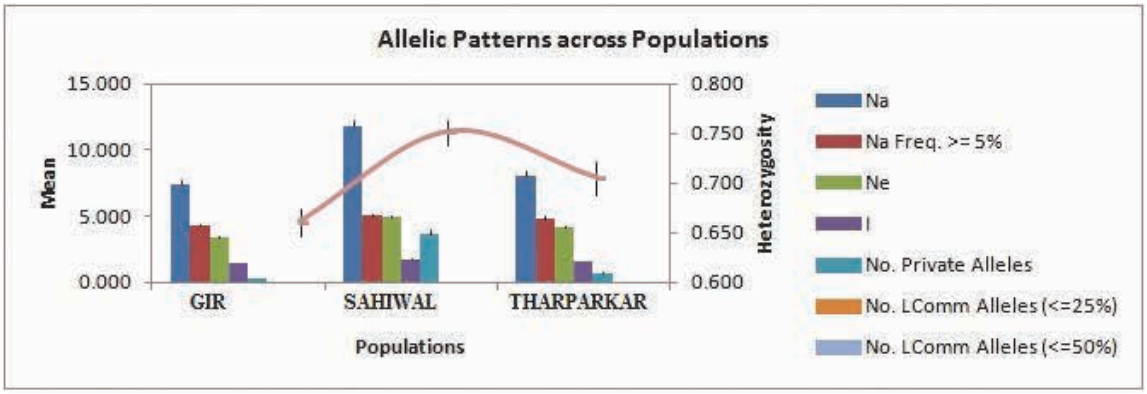
Table : Semen doses added in Gene Bank during the year 2012-13

Species	Breeds	Number of bulls	Semen doses
Cattle	Red Sindhi	2	2000
	Tharparkar	2	2250
	Sahiwal	1	1000
	Amritmahal	1	500
	Dangi	1	500
	Hallikar	1	500
	Red Kandhari	2	1000
	Gangatiri	2	1000
	Frieswal	5	2450
	Khillar	3	1450
Buffalo	Banni	3	1500
Total		23	14150

Genetic Characterization and functional genomics

Development of breed signature for Sahiwal, Gir and Hariana cattle

The data for allelic patterns across the three populations using 84 microsatellite loci distributed on all the chromosomes was analyzed. Mean number of alleles, effective number of alleles, private alleles, and expected heterozygosity are presented graphically in figure below. The mean number of alleles was highest in Sahiwal (11.845) while, lowest in Gir (7.464). The effective number of alleles was maximum in Sahiwal (4.898) and minimum in Gir (3.347).



Graphic representation of Allelic Patterns across three cattle populations (Pop1-Gir; Pop2-Sahiwal; Pop3-Tharparkar Na=Observed number of alleles, Ne=Effective number of alleles, He=Expected heterozygosity, I=Shannon's information index)

The number of private alleles was also highest in Sahiwal (3.655) and least in Gir (0.661).

The observed heterozygosity was 0.675, 0.574 and 0.664; expected heterozygosity was 0.669, 0.755 and 0.714 for Gir, Sahiwal and Tharparkar breeds, respectively. Among three populations, the observed heterozygosity was less than the expected heterozygosity except Gir.

Assessment of cattle genetic introgression in the domestic yak populations

Hybridization between yak and indicine cattle is highly common and widely practiced throughout the geographical region rearing yak populations. Gene flow between yak and cattle affects genetic make-up of domestic yak. The cattle admixture in domestic yak populations was assessed through analysing cattle mtDNA sequences and cattle-specific microsatellite alleles. PCR amplification of mitochondrial DNA was carried out for Arunachali yak and a total of 37 mitochondrial DNA sequences were obtained. The mitochondrial DNA sequence analysis revealed 15 haplotypes in Arunachali yak with haplotypic frequency ranging from 0.056 to 0.167. Total 14 cattle specific microsatellite primers viz. MGTG7, TGLA126, AGLA293, CSSM066, MGTG4B, BM2113, ILSTS028, TGLA122, TGLA53, ILSTS008, ETH225, TGLA57, ETH152 and TGLA73 were also amplified in Himachali Yak and all markers were found polymorphic. Observed number of alliles were higher than 4.0 for all the microsatellite primers in Himachali Yak.

Identification of SNPs in QTL region in Indian goats and their association with milk quality traits for healthfulness (DBT Project)

Fatty acid profiling of milk samples from 500 goats was done through gas chromatography (GC). The value of different fatty acids varied from 0.002 to 41.70 gram per 100 gram of Fatty acid methyl ester (FAME). The percentage of saturated fatty acids in the goat milk samples was found to be 70.79 and that of unsaturated

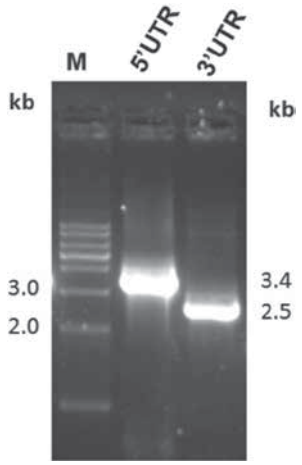
fatty acid was 28.89 in which monounsaturated fatty acids (MUFA) contribute 24.13% and polyunsaturated fatty acids (PUFA) contribute 5.12%. GC estimates of both the isomers (cis9t11 and t10c12) were generally lower than that of total conjugated linoleic acid (CLA) estimated through spectrophotometer. The values of CLA isomers cis9 trans11 and trans 10 cis 12 varied from 0.006 to 7.88 and from 0.002 to 3.72 mg per gram of milk fat, with an average value of 2.41 and 1.02, respectively. GC estimates of both the isomers (cis9t11 and t10c12) were generally lower than that of total CLA estimated through spectrophotometer.

Table: Composition of goat milk

Milk constituents (percent)	Average (%)	Range (%)
Fat	4.5	2.06-7.97
Protein	4.18	1.84-5.66
Lactose	6.02	2.62-8.20
SNF	11.06	4.86-15.07

Development of human tissue plasminogen activator gene construct

Promoter and regulatory elements of ovine beta-lactoglobulin (oBLG) gene was taken to drive the expression of human tissue plasminogen activator (tPA) in a mammary gland specific manner. A 2.5 kb fragment of oBLG, corresponding to 3'-UTR, containing part of transcription unit and polyA tail was amplified using Expand Long Template PCR System. The amplified fragment was subsequently sequenced to check mutation error. Similarly, a fragment of 3.4 kb 5'UTR including part of transcription unit of oBLG was also amplified.



Amplification of 5' and 3' UTR of ovine BLG gene. M-1Kbp DNA ladder.

Study of the genetic variability in the bovine cytokines

The exon-1, exon-2 and exon-3, 5'UTR and their flanking regions comprising approximately 3.4 Kb of the IFN-γ gene was amplified and sequenced in 40 Zebu cattle representing 5 breeds viz. Tharparkar, Rathi, Sahiwal, Hariana and Kankrej. A total of 20 SNPs (10 transitions, 8 transversions and 2 indels) were observed, spread across the 3.4 Kb region of the bovine IFN-γ gene. The SNP (T>G) at position +176 pposition in exon-1 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 paratuberculosis infection in the *Bos taurus* populations. The exon-2 and exon-3 of the IFN-γ were fond to be conserved. The microsatellite repeat (GTTT)n in the intron-1 of the gene exhibited a very high degree of polymorphism. The promoter region of the IFN gamma was found to contain transcription factor binding sites for the FOXJ2 and Evi-1 transcription factors at positions c.1672 and c.1697.

Using gene specific primers, the 3.5Kb region of the lymphotoxin part of the TNF β gene, which is closely linked to TNF-alpha gene and the promoter region and exon-1 of the TNF-alpha gene were amplified in 40 Zebu cattle of Sahiwal, Hariana, Tharparkar, Rathi and Kankrej breeds.

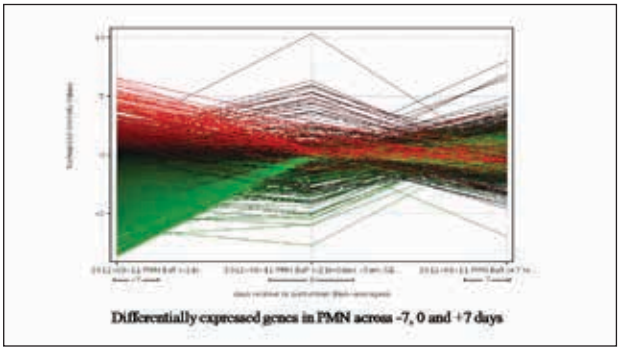
Overall 6 SNPs at positions 156(T>G), 343(G>C), 360(G>C), 750(A>G), 794(A>C) and 851(C>T) were observed across the promoter region of the lymphotoxin gene. The region studied had two transcription factor binding sites viz. for Cre-1 at position 185 and Pax-4 at position 531of the TNF-beta gene in indicine cattle. Eight, most probable haplotypes of the gene corresponding to the 10 genotypes were observed. The SNPs were strongly linked to each other. The genotypes of all the SNPs except 156(T/G) were in Hardy Weinberg equilibrium. They belonged to a single haplotype block and no recombination was observed. The F*is* values at all the SNP loci in the promoter region of TNF-β gene were negative which indicated a heterozygosity excess at these loci and low or no inbreeding. All the loci were polymorphic. The observed heterozygosity for all the loci was greater than the expected heterozygosity. These were all *Bos indicus* specific SNPs that had not been previously reported in TNF-beta (lymphotoxin) promoter region of cattle. Therefore, these SNPs could be used for genotyping and characterizing the indigenous cattle breeds with respect to their TNF gene promoter region, for their effect on gene expression.

Transcriptome analysis of circulating PMN cells to characterize parturition-induced immune suppression in buffalo and cattle

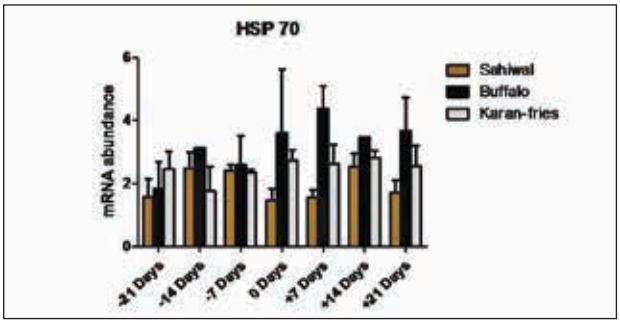
Comparative physiological and transcriptional adaptation of Murrah buffaloes, Sahiwal and Karan Fries (KF) cows was analysed during peri-parturient period. Several biochemical parameters (complete blood counts, AST, ALT, GGT, BHBA FFA/ NEFA, ROS levels) indicated the presence of physiological stress during the peri-partum period in all types of dairy animals. However, higher physiological stress was observed in KF in comparison to Sahiwal cattle and buffaloes.

Transcriptome analysis of buffalo polymorpho nuclear (PMN) cells identified several hundred differentially expressed genes (DEG) throughout the peripartum period. However substantial changes were observed across 1 week prior to calving, day of calving and 1 week post calving.

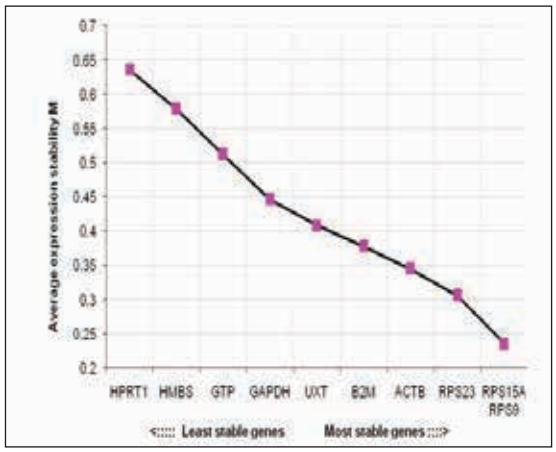
The microarray based analysis revealed several pathways viz; inflammatory response, cytokines, MPAK signaling, TNF-β, NF-κb pathways that



Differental gene expereries in PMN cells across -7, 0 and +7 days during peripartum period



HSP70 expression in PMN cells

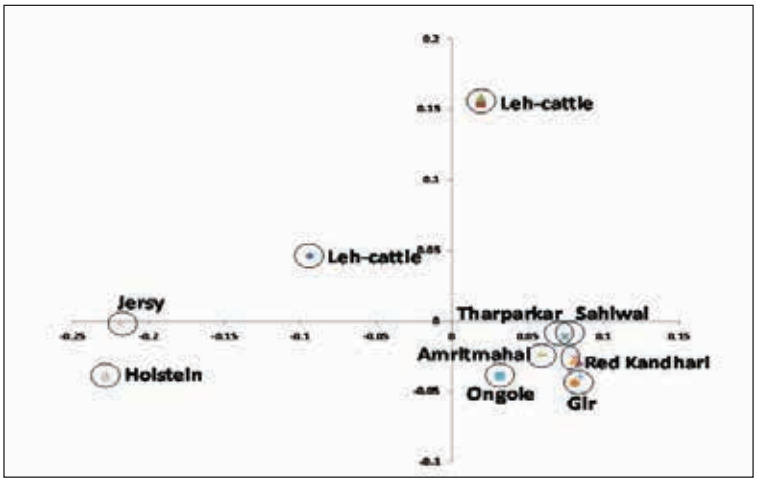


Identification of suitable ICG in PMN cells

being significantly affected. A panel of three internal control genes (ICG) viz., *RSP9*, *RPS15A* and *RPS23* were identified as most appropriate for normalization of PMN transcriptional data during the peripartum period. Comparative expression analysis of immune related, oxidative stress and HSPs revealed Sahiwal to be more resistant to physiological stress during the peripartum period.

Genome wide SNP based assessment of genetic relationship of Indian native cattle adapted to different agroclimatic condition

In order to discover the genome wide SNPs and unravel whole genome based genetic structure of Indian cattle, a total of 23 individuals representing 7 native cattle breeds adapted to different agro-climatic regions viz; Amritmahal, Gir, Ongole, Red Kandhari, Sahiwal, Tharparkar, Leh cattle and two exotic breeds viz; Holstein and Jersey cattle were genotyped using 770K high density bovine SNP chip. The native cattle from Leh and Laddakh region were genetically distinct from the rest of the Indian cattle. This study represents a first approach to assess population structure of Indian native cattle breeds using the high density SNP chip and re-establishes the genetic distinctness of indicine cattle from taurine cattle.



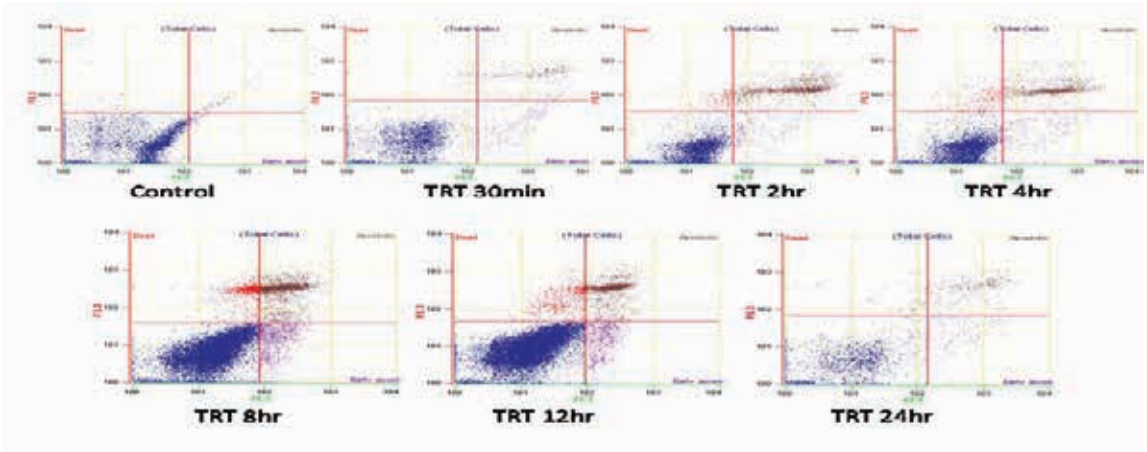
Multi-dimensional scaling plot revealing genetic relationship between Indian native and Taurine cattle

Differential heat shock response in cattle and buffaloes

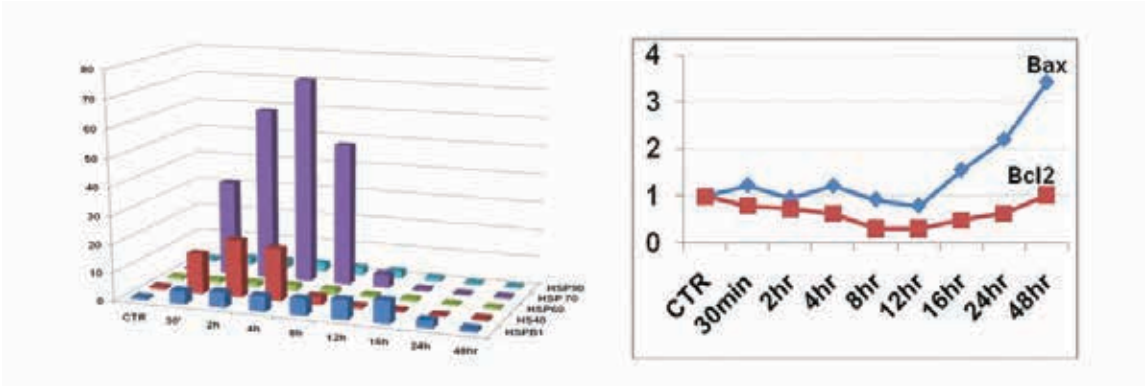
Peripheral blood mononuclear cells (PBMCs) were utilized to unravel comparative heat shock response of different cattle types; *Bos taurus* (Holstein Friesian cows), *Bos indicus* (Sahiwal cows); and *Bubalus bubalis* (Murrah buffaloes). The quantification of different members of heat shock protein family viz; *HSP27*, *HSP60*, and *HSP70* was carried out to understand the magnitude of transcriptional response of heat stressed PBMCs in cattle and buffaloes. Comparatively at 2h time point, *HSP70* peaked to the highest level in buffaloes (~73.0 fold), followed by Holstein (~65.0 fold) and Sahiwal (~54.0 fold). Similarly, *HSP60* and *HSP27* transcripts were maximally induced in buffalo at this time point. The higher abundance of *HSP* mRNA after heat stress showed initial evidence of transcriptional differences in PBMCs of cattle as well as buffaloes suggesting their differential cellular tolerance to withstand heat stress.

Impact of heat stress on cellular and transcriptional response of mammary epithelial cells in buffalo (National Fellow Project)

Riverine buffaloes have less physiological adaptation and exhibit signs of greater distress when exposed to direct heat stress. The buffalo mammary epithelial cells (MECs) were taken as *in-vitro* model to evaluate heat stress response both at cellular and transcriptional level. Several cellular and transcriptional parameters viz. lactate dehydrogenase activity (LDH), cell proliferation (MTT) assay, cellular viability, cell death, cellular apoptosis were assessed by flow cytometry. At transcriptional level, expression of heat shock proteins (*HSP27, HSP40, HSP60, HSP70* and *HSP90*) and apoptotic/ pro-apoptotic genes (*Bax*, BCl_2) were examined under heat stress conditions. All the *HSPs* showed immediate induction in their expression after heat shock and remained upregulated at the later stages, as well. For transcriptome analysis, the unstressed samples were compared with 8h, 12h and 24h post stress samples using Agilent bovine microarray expression chip. A total of 3756 probe sets displayed 2-fold or more changes in expression at different time points of heat treatment in comparison to control. Most of the heat shock proteins like HSPA1A, HSP90B1, HSP90AA1, HSP90AB1, HSPA2, HSPA5, HSPD1, HSPD8, DNAJA2, DNAJB11 etc. were upregulated.



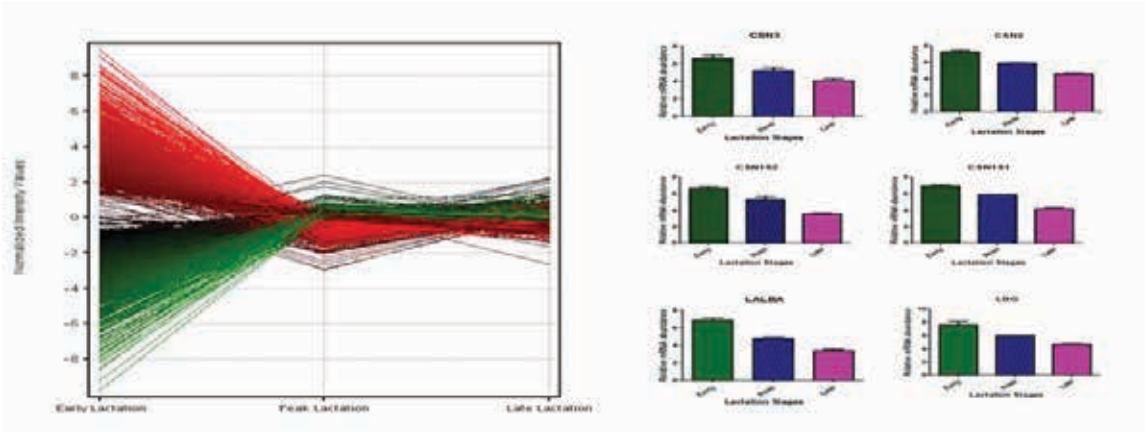
Flow cytometric analysis of heat stressed buffalo mammary epithelial cells



Transcriptional variation of heat shock and apoptotic genes in heat stressed buffalo mammary epithelial cells

Complete transcriptome signature of milk derived mammary epithelial cells (MEC) of Sahiwal cows (NAIP Project)

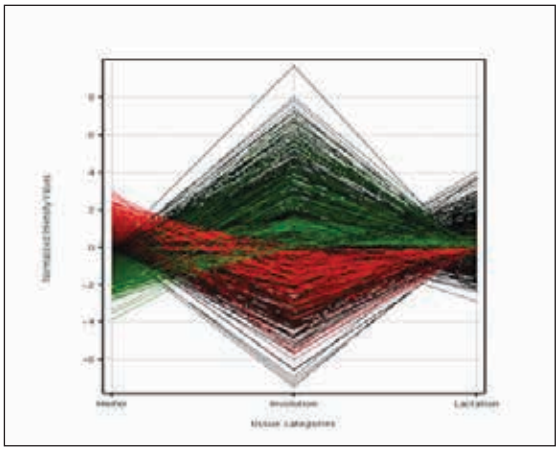
Transcriptional profiling of mammary epithelial cells (MEC) in Sahiwal cows at 15 (early), 120 (mid) and 240 (late) days of lactation was compared using Agilent 44K microarray chip. Genes associated with caseins and milk fat synthesis pathways were expressed more during early lactation stages.



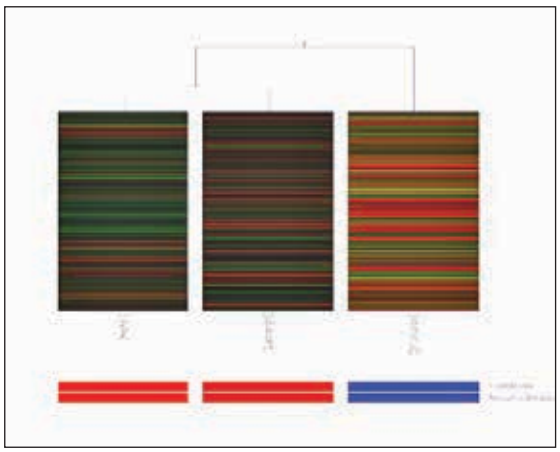
Transcriptome profile of Sahiwal mammary epithelial cells during different lactation stages

Identification of genes expressed in buffalo mammary gland during involution stage (NAIP Project)

Transcriptome profile of buffalo mammary gland across different physiological stages was compared in a total of 10 mammary tissues, three each from heifer and involution stages and four from lactating stage to identify stage specific genes. During involution, several genes related to apoptosis, immune and oxidative stress were found to be up-regulated while genes associated with milk fat synthesis, milk protein synthesis were down regulated in involution comparison to lactation and heifer stages of buffalo mammary gland.



Differential gene expressions in buffalo mammary gland across different physiological stages.



Transcriptome profile of buffalo mammary gland across different physiological stages (lactation, involution, and heifer)

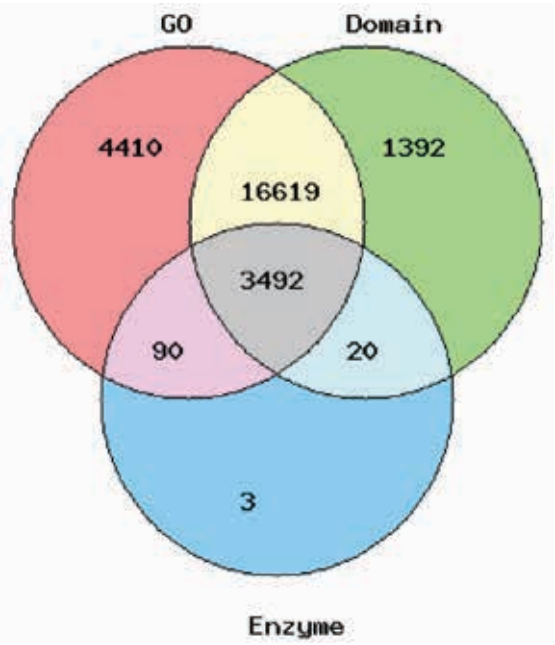
Pathway analysis of early lactation stage transcriptome data in cattle and buffalo (NAIP Project)

The transcriptome data was subjected to comprehensive analysis to reveal key differences in expression profile of buffalo and Sahiwal cow mammary epithelial cells during early lactation. A total 65 genes were found to be upregulated while only 5 genes were down regulated in buffalo MEC during early lactation period. Additionally, a number of pathways involved in the milk production were found to be significantly involved during early lactation period in buffalo MEC.

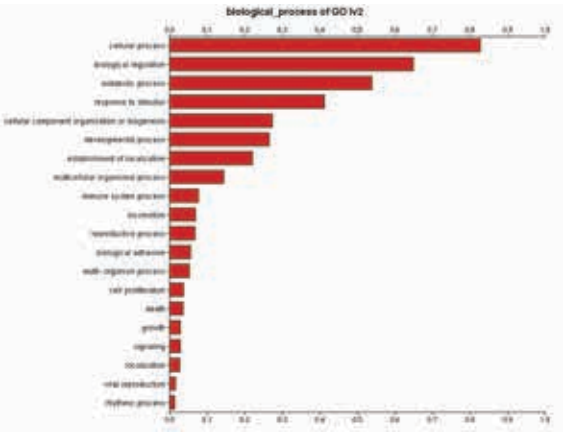
De-novo assembly of goat transcriptome (NAIP Project)

De-novo assembly of goat transcriptome was developed using Illumina 2X75 bp paired end reads. The de-novo assembly was generated first for 10 tissues separately using Trinity De-novo Assembler. The contigs obtained from the ten tissues were then merged with one another to form a goat de-novo transcriptome using CAP3 software. The mean contig length was 1815.79 with GC contents of 50.75%. The transcriptome assembly had 30053 hits in NCBI -nr database. The gene ontology analysis revealed 21718, 22805 and 21901 entries from biological processes, cellular component and molecular functions.

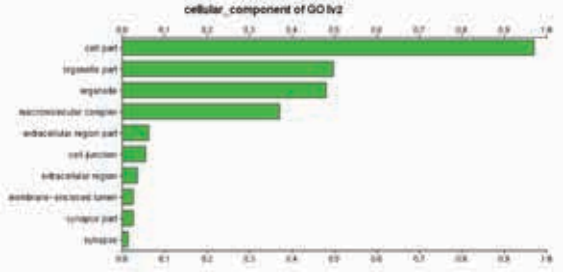
The assembly analysis revealed 3605 entries to



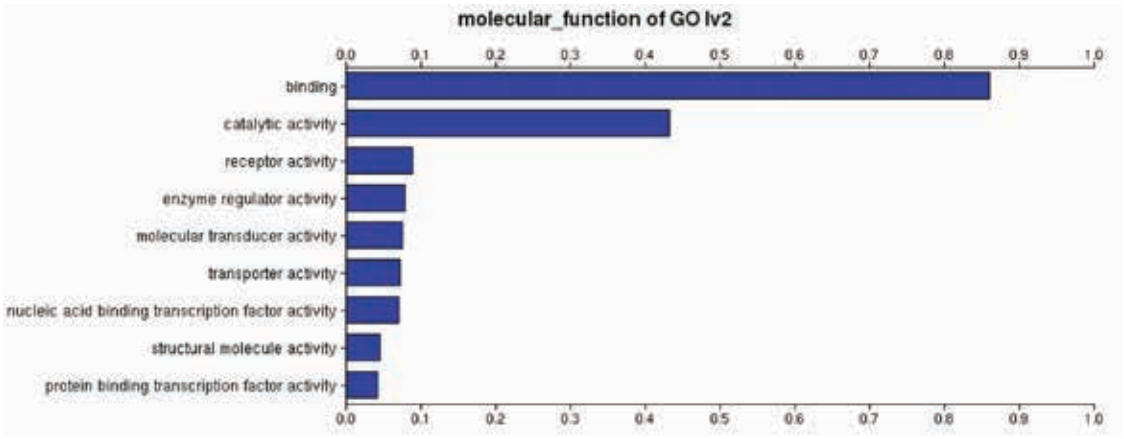
Venn diagram of annotation of goat de-novo transcriptome



Gene ontology (Biological Process) for goat de-novo contigs



Gene ontology (Cellular component) for de-novo contigs in goats



Gene ontology (molecular function) for de-novo contigs in goats

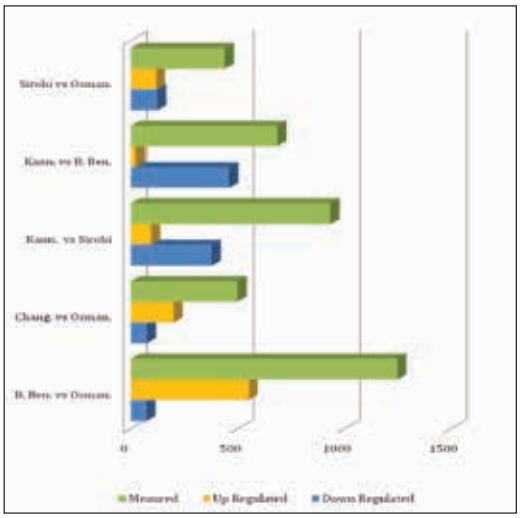
have at least one enzyme hit, with 21523 entries identified to have at least one domain.

Differential expression of genes across goats of different geographical locations (NAIP Project)

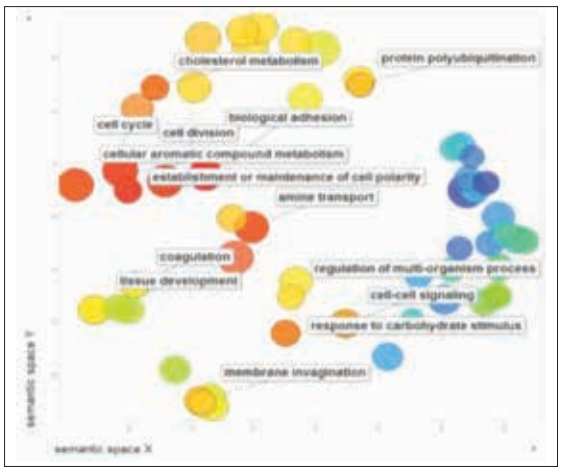
Transcriptome data of 76 bp, paired end reads on 38 various tissues was generated for the comparison in the five biological groups, represented by five breeds (Kanniadu, Black Bengal, Sirohi, Osmanabadi and Changthangi) belonging to different geographical locations. The reads were mapped to the cattle annotated genome using TopHat software utilizing standard annotations of the cattle genome. Within each tissue the comparison was made between different geographical regions so as to find out which of the protein coding genes, non-coding mRNAs and micro-RNAs were being up-regulated.

Since the mapping of the raw reads was carried out on the genome, in addition to protein coding mRNA sequences, 184 non-coding RNAs (ncRNAs) as well as micro-RNAs were also mapped. The comparison of expression level for each of the mapped gene and the expression occurring in exon or alternative splice junction was also carried out. For each tissue ten comparisons were made involving two different breeds each time.

The expression profile using the *junction.bed* files revealed 1348 expressed protein coding genes to be compared among all the breeds. In addition, a number of micro-RNAs found to be up-regulated and down-regulated were discerned. The pair-wise comparison of different breeds of goat revealed a large number of genes to be up-regulated in Sirohi Vs Black Bengal while the largest number of genes down-regulated were for Kanniadu Vs Sirohi (911 genes). The maximum down regulation of ncRNA genes was 185 for Kanniadu Vs Sirohi breeds of goats. The number of micro-RNAs being down regulated was also the highest in this set of comparison. The number of genes measured, up and down regulated are graphically depicted below for skin tissue.



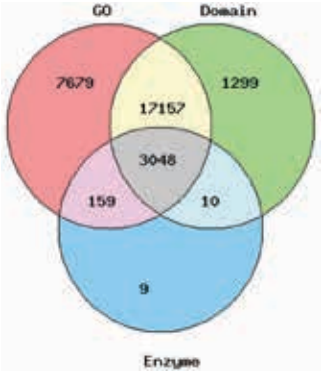
Differential expression of genes in pair-wise comparisons in goats



Gene ontology of the differentially expressed genes

De-novo assembly of camel transcriptome (NAIP Project)

De-novo assembly of dromedarian camel transcriptome was genrated using Illumina 2x75 bp paired end reads. The de-novo assembly was generated first for 10 tissues separately using Trinity De-novo assembler. The contigs obtained from the ten tissues were then merged with one another to form a camel de-novo transcriptome using CAP3 software. The mean contig length was 1311.03 with GC contents of 51.24%. The transcriptome assembly had 32940 hits in NCBI nr-database. The gene ontology analysis revealed 24676, 26027 and 24949 entries from biological processes, cellular components and molecular functions. The assembly analysis revealed 3226 entries to have at least one enzyme hit with 21514 entries identified to have at least one domain. A total of 5.81614 lakh accessions were obtained for the 9 tissues of dromedarian camel.



Venn diagram of annotation of dromedarian camel de-novo transcriptome

Identification of QTL for in buffaloes (NAIP Project)

Total 30 microsatellite loci from the cattle genome database were selected and amplified in 8400 buffalo daughters of the 12 sires with correct paternity. This genotyping was done in addition to the genotyping carried out in five chromosomes. Thus in all eight buffalo chromosomes have been genotyped using microsatellite markers with a genetic distance of 10-15 cM on each chromosome. Data on body weights was collected in different age groups for QTL mapping.

A total of 509 records of body weight of heifers were received from the field which belonged to twelve sires. The mean body weight was found to be 112.2063 Kg The data was analysed for the identification of markers associated with the QTL for this trait. The analysis was carried out for eight chromosomes. The QTLs associated with the markers were marker 10 on chromosome 1, marker 2 on chromosome 8, marker 9 on chromosome 3, marker 12 on chromosome 4, marker 11 on chromosome 5, marker 10 on chromosome 6, marker 9 on chromosome 7 and marker 10 on chromosome 8.

A total of 1946 records A body weights were received for 12 months of age. The data was analysed collectively. The mean body weight was found to be 132.9414 Kg with a standard deviation of 57.29. Major QTL with very highly significant effect were associated with marker 8 of chromosome 1, marker 7 of chromosome 2, marker 5 of chromosome 3, marker 9 of chromosome 4 and marker 11 of chromosome 5. Minor QTLs were also found to be associated with chromosome 1 (marker1), chromosome 3 (marker 5), and chromosome 5 (marker 2 and 3).

A total of 2789 records were received for 18 months of age. The data was analysed collectively. The mean body weight was found to be 152.754 Kg. Major QTL with very highly significant effect were associated with marker 2 of chromosome 2, marker 6,7,9 of chromosome 3, marker 8 of chromosome 4, marker 3 of chromosome 6 and marker 6 of chromosome 7 and marker 8 of chromosome 8.

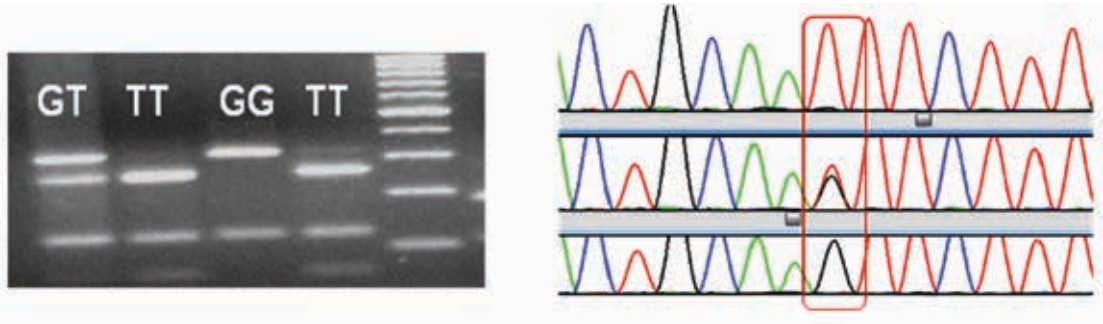
A total of 2936 records were received for 24 months of age. The data was analysed collectively for all the daughters. The mean body weight was found to be 196.5954 Kg. Major QTL with very highly significant effect were associated with marker 1 and 9 of chromosome 3, marker 1,7,9,12 of chromosome 4. Minor QTLs were also detected for marker 8 each of chromosome no. 2 and chromosome no. 3.

A total of 2650 records were received for 30 months of age. The data was analysed collectively for all the daughters. The mean body weight was found to be 218.9249 Kg. Major QTL with very highly significant effect were associated with marker 8 of chromosome 4. Minor QTLs were also detected for marker 8 each of chromosome no. 2 and chromosome no. 3.

A total of 1394 records were received for 36 months of age. The data was analysed collectively for all the daughters. The mean body weight was found to be 243.8293 Kg. Major QTL with very highly significant effect were associated with marker 3 of chromosome 7. Minor QTLs were also detected for marker 8 each of chromosome no. 2, marker 1 of chromosome no. 4 and marker 5 of chromosome no. 7.

Characterization of Toll-like receptor (TLR) genes in farm animals (NAIP Project)

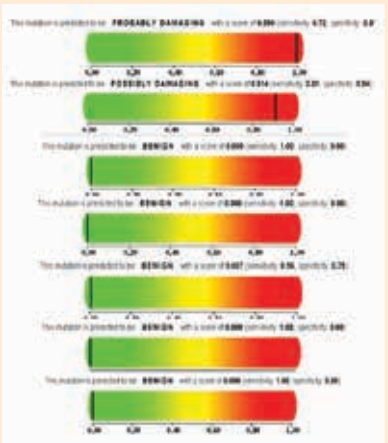
More than 1 kb nucleotides long 5'-upstream region of TLR8 gene of buffalo, cattle and goat was amplified, sequenced and compared. Buffalo and goat had highly variable region from 724 nucleotides upwards to first exon in comparison to cattle. To detect polymorphism in 5'-upstream of TLR8 gene, eight samples of swamp and riverine buffaloes were sequenced, which revealed two polymorphic sites, at 139 nucleotides and 128 nucleotides upstream to the ORF. A PCR-RFLP genotyping assay was developed for the g-139G>T SNP using Tsp509I restriction enzyme to screen 710 samples of Indian buffalo breeds including both swamp and riverine types from different agro-climatic zones and allelic distribution varied across swamp and riverine buffaloes. Besides this, most variable ectodomain regions of TLR2 and TLR4 genes were genotyped by sequencing in 112 animals representing Murrah, Toda and Swamp types, which showed seven haplotypes in TLR4, one haplotype with a frequency of 25.9% being specific to Murrah and another major haplotype having 69.6% frequency was shared by Toda and swamp buffaloes. Two animals each representing one of the four haplotypes observed in TLR4 were screened for expression variation after lipopolysaccharides (LPS) ligand stimulation of neutrophils purified from blood. There was higher expression of TLR4 at four hours post stimulation, whereas cytokines expression increased 8 hours post stimulation. Somatic cells purified from milk and neutrophils from blood samples of mastitis affected and non-affected Murrah animals showed higher expression of pro-inflammatory cytokines in mastitis animals. In another study, polymorphism detected in goat TLR7 gene was further investigated for impact on gene structure and function using Polyphen 2 programme and one of the possibly damaging amino acid substitutions, 127 Thr>Met has been identified. Overall, these results helped in identification of genetic diversity among indigenous livestock populations, which could be further utilized for association with disease resistance traits.



Polymorphism detection in buffalo TLR8 promoter at -139G>T by Tsp509I PCR-RFLP

Haplotype	Time interval post stimulation	Fold change in expression				
		TLR4	CXCR2	PGLY	TNF	IL6
B479	4hr .	24.59	4.98	8.22	2.08	5.45
	8hr .	105.79	1.87	1.74	3.47	6.75
B478	4hr .	7.59	41.50	7.46	47.18	7.89
	8hr .	1.27	91.46	14.72	103.61	14.47
B5724	4hr .	1.64	11.27	5.08	62.03	54.95
	8hr .	2.25	2.22	37.66	66.26	93.70

Expression analysis of TLR4 and cytokines in LPS ligand stimulated neutrophils of Murrah buffalo representing three haplotypes

Nucleotide	Amino acid	Transition/ Transversion	Domain	Effect of amino acid change
130 G>A	44 Ala>Thr*	Transition	LRRNT	
377 C>T	127 Thr>Met*	Transition	LRR	
845T>C	282 Leu>Pro	Transition		
1177 T>C	393 Cys>Arg	Transition	LRR	
1340 T>G	448 Met>Arg	Transversion		
2548 A>G	850 Ile>Val	Transition	Low Complexity Region	
2802 T>C	935Leu>Ser	Transition	TIR Domain	

*Polyphen analysis of goat TLR7 polymorphism showing impact of non-synonymous SNPs on its structure and function. (*indicates amino acid having possibly damaging effect)*

Candidate gene analysis and identification of allelic variants associated with incidence of mastitis in dairy cattle and buffaloes

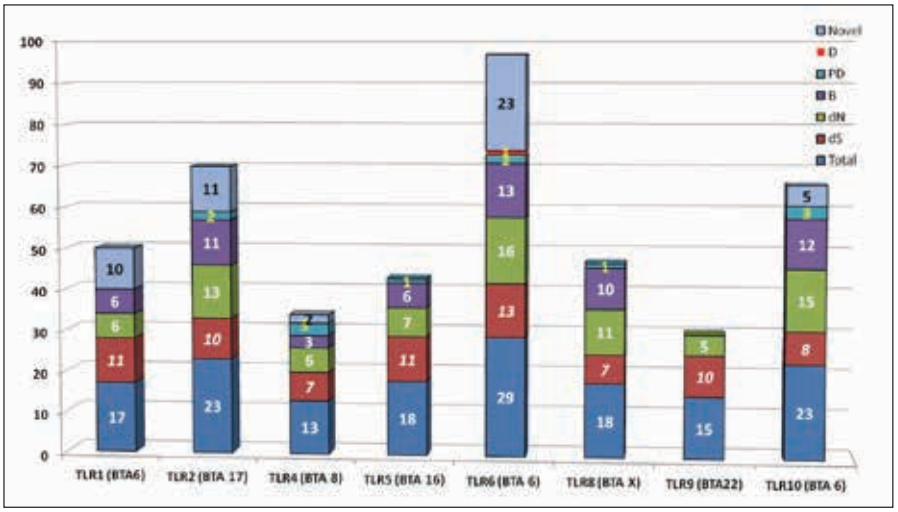
Haptoglobin (Hp) gene associated with mastitis was characterized in buffalo, cattle and yak through sequencing of genomic region. Sequence analysis of various regions including 5' upstream, exonic and intronic regions of the gene showed a large number of nucleotide variations including indels. Buffalo haptoglobin gene revealed 35 nucleotide changes in CDS, 5 in 5'UTR compared to cattle. Further, a 1329 bp long Haptoglobin cDNA was amplified and sequenced from riverine buffalo mammary gland tissue. Buffalo haptoglobin molecule showed unique

characteristics as internal duplication of large coding region compared to other non ruminant species. Phylogenetic tree of haptoglobin showed clustering of all bovine species along with human, revealing convergent evolution having taken place between ruminants and human. About 330 bp and 400 bp long buffalo S100A8 and SAA3 cDNA molecules, respectively were amplified, covering complete CDS. Buffalo S100A8 cDNA had 96, 94 and 86% identities with that of cattle, sheep and pig sequences, respectively. The buffalo SAA3 showed 96, 95 and 94% nucleotide identities with that of cattle, goat and sheep sequences. Phylogenetic analysis of CDS and predicted amino acid sequences of SAA3 and S100A8 revealed clustering of cattle, yak and buffalo species in same node, overall. Other non ruminant species clustered separately away from these three species.

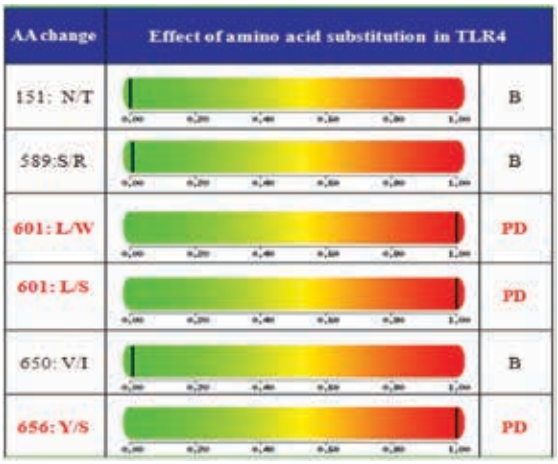
SNPs identified in TNFα, haptoglobin and PGLYRP1 were studied in a panel of mastitis (24) and healthy (24) buffaloes and cattle for association with incidence of mastitis in Murrah buffalo and Sahiwal cow. SNPs at position 136C>A, 153G>T of PGLYRP1 and at 340A>G, 418T>C of Hp were found to have significantly ($p<0.05$) different allelic frequencies between mastitis and healthy cattle. SNPs at TNF, Hp, PGLYRP1 were not found to have significant difference of allele frequencies between mastitis affected and healthy buffalo. Variable numbers (12/13) of glycine residues in cattle FEZL gene responsible for resistance/susceptibility to mastitis was also found in buffaloes, however, without any significant association with mastitis in buffalo. Expression of SAA3, Hp, PGLYRP1 and CCL2 molecules was also assessed in healthy and mastitis affected cattle through real time-PCR. Higher expression of all the four proteins was observed in acutephase mastitis compared to healthy cattle.

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

Sequence characterization and genotyping of eight Toll like receptor (TLR 1, 2,4,5,6,8,9 and10) genes was undertaken in Indian native cattle breeds (*Bos indicus*) to identify novel single nucleotide polymorphisms (SNPs). Comparative sequence analysis of coding region revealed 156 SNPs in the TLRs studied. TLR6 was most diverse with 29 SNPs while TLR9 showed minimum number (15) of SNPs. Out of 156 SNPs, 79 were non-synonymous and 51were novel to the Indian cattle breeds.



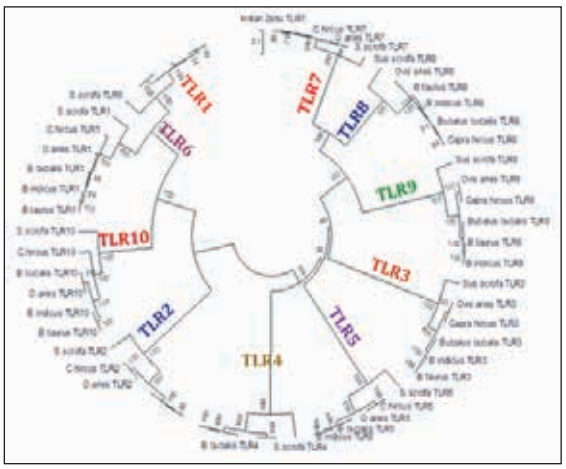
Details for the SNPs across studied Toll like receptor genes (TLRs) in cattle



PolyPhen-2 Analysis of amino acid substitution effects in TLR 4; B: Benign; PD: possibly damaging

Analysis of 79 non-synonymous SNPs (nsSNPs) predicted 12 SNPs having possibly damaging effect while only one of the nsSNPs observed in the coding region of TLR6 was found to be damaging, all other SNPs were benign.

Amongst the analyzed breeds, Kankrej, Hariana and Gir cattle were found to have the highest number of SNPs and the Kangyam was least polymorphic. Overall, all the observed polymorphic nucleotide sites were biallelic, unbiased and distributed across all the domains. Except few, polarities of most of amino acids were found to be conserved. Comparison of protein domain architecture for different TLR gene clusters of Indian native cattle with other mammalian species revealed regions of conservation in the TLR variable LLR patterning. Several predicted amino acid replacements in bovine TLR2, 4, 6, 7, 9 and 10 resulted in the confident prediction of protein domain alterations whereas, TLR1 and TLR8 molecules seem unaffected. Preliminary analysis for evidence of selection in the studied TLRs revealed positive selection in TLR4 and 1. Overall, the study suggests the existence of sufficient diversity within Indian cattle and divergence from the taurine counterpart. The analysis revealed close grouping of *Bos taurus* and *Bos indicus* (Indian native cattle breeds) at all the analyzed genes, when compared with other species.



Phylogenetic relationship among TLRs (1-10) from different mammalian species.

TLR 1, 6 and 10 were grouped in one cluster followed by TLR2. Similarly, TLR7 and 8 showed close grouping followed by TLR9. Additionally, protein modeling and structure visualization was performed for the non-synonymous SNPs observed across different TLRs.

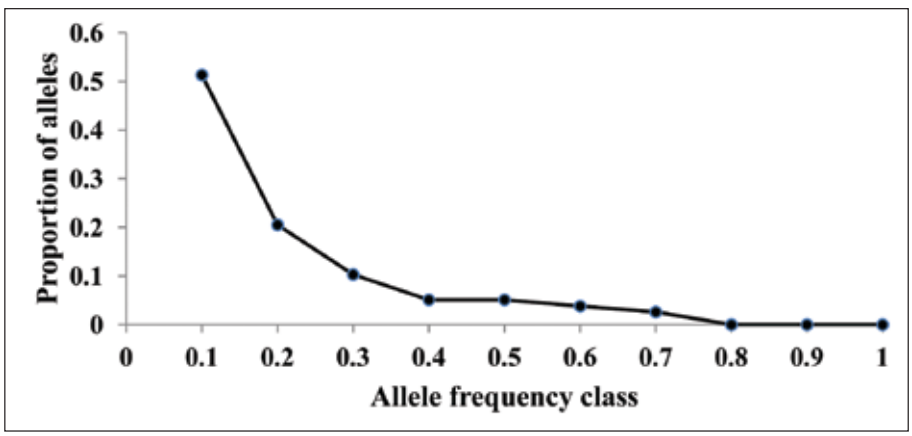
Nucleotide diversity in candidate genes for mutton quality traits in Indian sheep

A total of 50 samples from ten Indian sheep breeds namely Bandur, Chokla, Deccani, Ganjam, Garole, Madgyal, Magra, Malpura, Muzzafarnagri and Nali were analyzed for genetic polymorphism at the growth differentiation factor 8 (*GDF8*), β3 adrenergic receptor (*ADRB3)* and calpain (*CAPN)* gene. Specific primers were used to amplify the target gene loci. The amplified products were purified and sequenced in an automated DNA sequencer. The sequences, after trimming were aligned and analysed. The analysis of the edited sequences of *GDF8* gene loci revealed an absence of SNPs in the exon 3 region with 100% homology with the reference sequence (GenBank DQ530260). It was observed that the g.6723G>A SNP in the

3'UTR, reported to affect muscularity in exotic sheep, appeared to be fixed for g.6723G allele in the Indian sheep investigated. A total of three SNPs (-41C>A; g.3995G>T) were identified in the non coding regions of *GDF8* gene in Indian sheep, out of which -16C>T has not been reported previously. Two SNPs identified in the Indian sheep are known to be associated with mutton quality and carcass traits in exotic sheep. These initial results showing genetic variability and presence of favourable alleles/ SNPs in the *GDF8* gene may lead to exhaustive analysis of genetic polymorphism in *GDF8* gene in Indian sheep breeds. The results also suggest potential prospects for genetic improvement of Indian sheep through selective breeding. A 900 bp region spanning the 5'UTR and partial exon 1 as well as 245bp of 3'UTR of ovine *ADRB3* gene was screened for possible SNPs in these sheep breeds. The sequence analysis revealed two SNPs in the exonic region (g.333C>T and g.497G>C), both of which were synonymous. No SNPs were detected in the 5'UTR. One SNP was also detected in the 3'UTR (g.2621T>C). The identified SNPs were present in the heterozygous state. Further, a 190 bp polymorphic region of ovine *CAPN* gene covering partial exon 5, intron 5 and exon 6 was also sequenced across the panel of ten sheep breeds. A single C>T transversion in the heterozygous state was detected in the intron 5. The frequency of the C and T alleles was 0.564 and 0.436 respectively.

Genetic characterization of Spiti donkey

The Spiti donkeys distributed in Spiti and Yangthang regions of Himachal Pradesh were evaluated for within breed genetic diversity and genetic bottlenecks using twelve heterologous microsatellite markers. The genomic DNA was amplified by PCR using FAM and HEX labeled primers and resolved for alleles on automated DNA sequencer. The PCR product size range varied from 78-87 bp at locus VHL20 to 253-271 bp at locus COR18. The observed number of alleles ranged from 4 (VHL20, HTG6) to 10 (HTG7), with a mean of 6.33 ± 1.72 alleles per locus. The effective number of alleles (Ne) ranged from 2.03 (VHL209) to 4.84 (HTG7), with a mean value of 3.35 ± 0.94. The observed heterozygosity (Ho) values across the twelve loci ranged from 0.48 (NVHEQ54) to 0.89 (HTG7), with a mean value of 0.72±0.13. The expected heterozygosity (He) varied from 0.51 (VHL209) to 0.80 (HTG7 and AHT4), with a mean of 0.69 ±0.09. The allele number and heterozygosity values observed across the studied loci indicated presence of reasonably high levels of genetic variability in Spiti donkeys. The mean PIC for all loci assessed from allele frequency data was 0.68±0.09, ranging from 0.51 (VHL209) to 0.79 (HTG7 and AHT4). These PIC values suggested that these loci were sufficiently polymorphic reflecting their suitability for genetic variability



Normal 'L'-shaped curve for allelic distribution in spit donkeys.

studies of indigenous donkey breeds. The mean genetic diversity estimate (F_{IS}) was 0.048 indicating moderate levels of inbreeding. The normal 'L' shaped distribution of allelic frequency strongly indicated absence of any recent genetic bottlenecks in the Spiti donkeys.

Cytogenetic screening of livestock species

As per Department of Animal Husbandry, Dairying and Fisheries, Ministry of Agriculture guidelines under the National Programme for Cattle and Buffalo Breeding, cytogenetic screening of all cattle and buffalo bulls to be used for breeding has been made mandatory. A total of 423 breeding bulls were screened for their cytogenetic parameters during the year and the screening results communicated to the concerned stakeholders. A total revenue of more than Rs. 2 lakhs was also generated by karyotyping of these animals from various agencies. The detail of bulls screened is provided in table below.

Number of buffalo screened cytogenetically

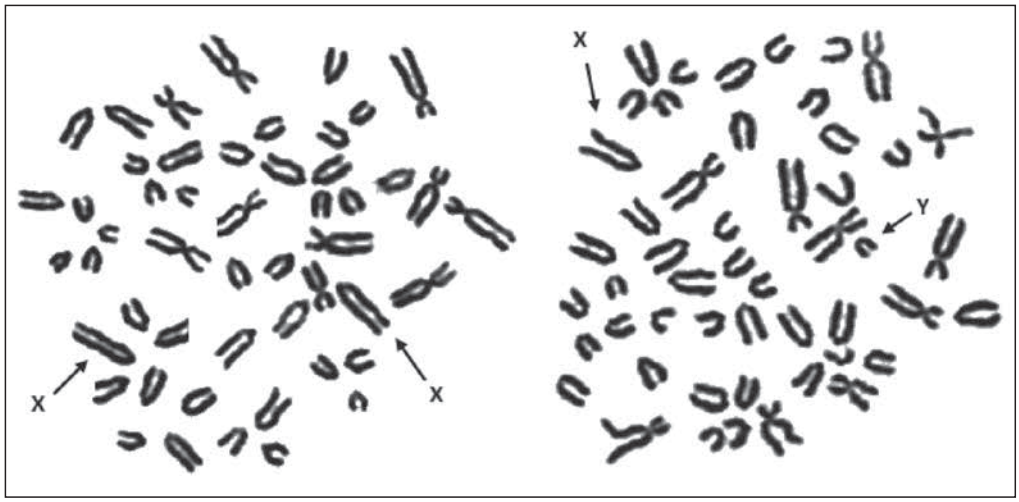
S. No.	Agency	Bulls		
		Buffalo	Cattle	Total
1	Haryana Livestock Development Board, Hisar	16	4	20
2	Haryana Livestock Development Board, Jagadhari	0	3	12
3	Haryana Livestock Development Board, Gurgaon	4	1	5
4	Himachal Pradesh Livestock Development Board, Palmapur	0	5	5
5	Central Institute for Research on Buffaloes, Hisar	4	1	5
6	Project Directorate on Cattle, Meerut	0	91	91
7	Uttar Pradesh Livestock Development Board, Chak Ganjaria	1	30	31
8	Punjab Livestock Development Board, Nabha	83	63	146
9	Kerala Livestock Development Board, Mattupatty	0	86	86
10	Uttar Pradesh Livestock Development Board, Dalpatpur, Moradabad	8	3	11
11	Milkfed Khanna, Punjab	10	10	20
Total		126	297	423

Five bulls were identified to have chromosomal abnormalities, thus constituting 1.18% of the total bulls investigated. One buffalo bull calf was a sex chromosome chimeric (50, XX/50, XY). Though no record was available with the concerned agency whether it was born single or twin. Sex chromosome chimerism (50,XY/ 50, XX) is depicted in figure below.

One bull had a major translocation such that the translocated chromosome was much larger than any of other chromosomes in the complement. Moreover, there appeared a constriction at the point of translocation. All crossbred bulls derived by mating exotic Holstein Frisian bulls with indigenous females should have a *Bos taurus* type of Y chromosome (a metacentric). Of the 91 such crossbred bulls (Frieswal) investigated two bulls had acrocentric type Y chromosome, characteristic of *Bos indicus* cattle. There could be breakage of small arms near the centromere, rotation of the broken part at 180^0 and reunion with the remaining part thus transforming the metacentric Y chromosome into acrocentric Y chromosome. This was considered as a

chromosomal abnormality and the bulls were culled from the breeding programme.

Another cattle bull had a high frequency of chromatid gaps and breaks (more than 16%). While in the normal bulls frequent occurrence of chromatid gaps and breaks is observed but the frequency never exceeds 5% of the cells examined. Counselling was accordingly provided to the concerned agencies regarding use of bulls for breeding.



Karyotypes showing sex chromosome chimerism (Female-50, XX (left) and Male- 50, XY (right))

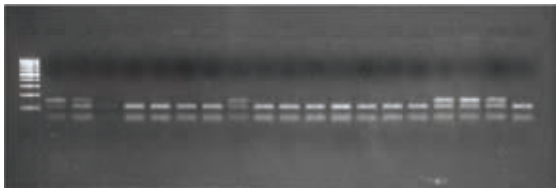
Network Project on AnGR

PCR-RFLP genotyping of SNPs in goat GDF9 (Core Laboratory, NBAGR)

Eight goat breeds differing in prolificacy viz. high prolific (Black Bengal, Beetal, Barbari, Jhakrana), medium prolific (Sangamneri, Osmanabadi) and low prolific (Sirohi, Ganjam) were screened for the A959C and G1189A mutations in GDF9 gene through PCR-RFLP genotyping. A959C SNP is known to be associated with high prolificacy in Chinese goats. Screening of A959C SNP showed all the three genotypes: AA, AC and CC only in prolific Black Bengal goat, whereas only two genotypes (AA and AC) were recorded in other Indian breeds. The proportion of animals with favorable C allele was also highest (0.27) for the Black Bengal goats.

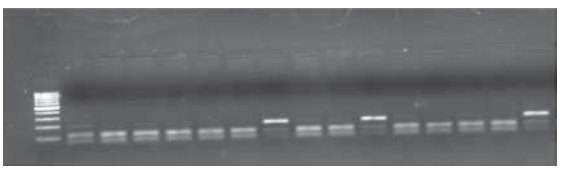
BstNI PCR-RFLP genotype frequencies of GDF9 SNP 959A>C in different goat breeds

Breed	Number of animals screened	Genotype (No. of animals)		
		AA	AC	CC
Black Bengal	52	25	26	1
Beetal	28	27	1	0
Barbari	50	46	4	0
Jhakrana	14	13	1	0
Sangamneri	50	42	7	0
Osmanabadi	41	39	2	0
Sirohi	50	36	13	0
Ganjam	50	36	4	0



PCR-RFLP genotype of A959C SNP in goat GDF gene

Three genotypes GG, GA and AA were observed for SNP 1189 G>A in Beetal goat only. Whereas, only two genotypes (GG and GA) were recorded in other Indian breeds. Indian goats with different prolificacy did not show differences in the allele distribution at G1189A polymorphic loci. Allele frequency was of similar range for both prolific Black Bengal (G=0.98, A=0.02) and non-prolific Ganjam (G=0.93, A=0.07). Results revealed that the genetic factor responsible for twinning or multiple kidding might not be related to G1189A mutation of GDF9 gene in indigenous goat.



Genotyping of G1189A SNP in goat GDF9 by PCR-RFLP

MspI PCR-RFLP genotype frequencies of GDF9 SNP 1189 G>A in different goat breeds

Breed	Number of animals	Genotypes (Number of animals)		
	screened	GG	GA	AA
Black Bengal	52	50	2	0
Beetal	28	72	19	2
Barbari	50	39	10	0
Jhakrana	14	1	13	0
Sangamneri	50	28	22	0
Osmanabadi	41	28	13	0
Sirohi	50	44	6	0
Ganjam	50	43	7	0

Detection of polymorphism in caprine BMPR1B gene (Core Laboratory, NBAGR)

Caprine BMPR1B gene was amplified and screened for polymorphism analysis in a panel of eight goat breeds-Beetal, Sirohi, Osmanabadi, Malabari, Jakhrana, Barbari, Black Bengal and Ganjam differing in prolificacy, geographical distribution and genetic diversity.

Geographical distribution of selected goat breeds

Sequence analysis revealed absence of any polymorphism including the *FecB* mutation in BMPRIB exonic regions of all the investigated breeds of Indian goats. Coding DNA sequences (CDS) of caprine BMPR1B gene revealed 97% homology with *Bos taurus* (BC134547) and 99% with *Ovis aries* (AF357007) and reported *Capra hircus* (DQ666418). BMPR1B promoter region was also amplified in two fragments and a 1032 nucletides length contig was generated and four putative binding sites for the transcription factors viz. COMP1, BR-C Z1, HNF-1 and FOXJ-2 were identified. Total almost one hundred variations were observed between cattle and goat promoter sequence. Two novel SNPs T(-242)C and G(-623)A have been identified in the promoter region of caprine BMPR1B gene, of which all the three genotypes (GG, GA and AA) were observed for -623G>A SNP whereas, two genotypes (TT and TC) were observed for -242T>C SNP.

Polymorphism in the promoter region of caprine BMPR1B gene did not change any transcription factors binding sites.

Characterization of candidate genes for sexual precocity in indigenous goats (Core Laboratory, NBAGR)

KiSS-1 (kisspeptin) gene (5′UTR, exon 1, intron 1 and exon 2 along with downstream region) was amplified and sequenced for the identification of SNPs in a panel of 9 Indian goat breeds differing in precocity and prolificacy. Ninety nine nucleotide changes were observed in caprine KiSS1 as compared to Bos taurus (NW_003104427.7). Insertions were observed at 3 positions, whereas deletions were recorded at four positions that included continuous 26 (1417-1442 of NW_003104427.7) and 47 (1806-1852 of NW_003104427.7) nucleotides deletions in caprine sequence as compared to cattle. However, no variation was observed between amplified KiSS1 sequence of Indian goats and exotic Jining grey goat (GU142847.1). Comparison of 45 amplified sequences of indigenous goats resulted in identification of three novel SNPs (T693C, T950C, T1125C) as well as three previously described SNPs (G296C, T454G and A505T), of which G296C has been associated with multiple kidding.

Allele frequencies of SNPs in caprine KISS-1 gene

S. No.	SNP	Region	Genotype frequency	Allele frequency
1	G296C	Intron 1	GG=0.675 GC=0.275 CC=0.050	G=0.81 C=0.19
2	T455G		TT=0.325 TG=0.550 GG=0.125	T=0.6 G=0.4
3	A505T		TT=0.425 TA=0.575	T=0.71 A=0.29
4	T693C		TT=0.75 TC=0.20 CC=0.05	T=0.85 C=0.15
5	T950C		TT=0.854 TC=0.125 CC=0.021	T=0.92 C=0.08
6	T1125C	Intron 2	TT=0.917 TC=0.083	T=0.96 C=0.04

Polymorphism in candidate genes for physical performance in horses (Core Laboratory, Anand)

Myostatin (MSTN), Monocarboxylate transporters (MCTs) and CD147 genes were targeted to explore SNPs in three saddle type equine breeds of India *viz.*, Kathiawari, Marwari and Sindhi. Four SNPs in MSTN, 12 SNPs in MCT and 3 SNPs in CD147 genes specific to indigenous breeds were identified.

Genetic characterization of Kathiawari, Marwari and Sindhi horses (Core Laboratory, Anand)

Total 263 alleles were observed at the 25 microsatellite loci studied in three horse population. AMOVA indicated 11% variation among breeds. FST differentiation between Kathiawari and Marwari (0.034), between Kathiawari and Sindhi (0.058) and between Sindhi and Marwari (0.084) was observed. Principal Component Analysis (PCA) showed the distribution of individual horses in four clusters in which Marwari and Sindhi

horses formed two separate clusters whereas Kathiawari did not form distinct cluster but overlapped with Marwari and Sindhi.

Molecular characterization of Kharai camel (Core Laboratory, Anand)

Total 224 samples (108 from Kachchhi and 118 from Kharai) with 25 microsatellite loci revealed F_{IS} for Kachchhi and Kharai breeds 0.197±0.033 and 0.397±0.053 respectively. Overall F_{IT} and F_{ST} values were 0.336±0.038 and 0.044±0.009 respectively. High and positive F_{IS} values indicating strong heterozygote deficiency within population. Mean F_{ST} indicated breed differentiation among these breeds which was supported by PCA and STRUCTURE analysis showing three distinct clusters indicating that Kharai breed is genetically different from Kachchhi breed.

Molecular characterization of pig populations (Core Laboratory AAU, Khanapara)

Three indigenous pig populations viz., Votho pig from Nagaland, indigenous pig from Arunachal Pradesh and Mali pig from Tripura of North East India has been studied using 21 polymorphic microsatellite loci. Mean numbers of observed alleles were 5.591±0.598, 4.909±0.562 and 5.636±0.663; and effective number of alleles were 3.021±0.284, 2.885±0.279 and 3.165±0.328, in Vatho, Arunachali and Mali pig populations, respectively. F_{IS} values were 0.273±0.079, 0.409±0.066 and 0.290±0.066 in Vatho, Arunachali and Mali pig populations, respectively.

Votho Pig

Arunachali Pig

Mali Pig

Analysis of genes associated with draught power in cattle (Core laboratory, TANUVAS, Chennai)

Analysis of genes associated with draught power in cattle: Biochemical parameters pertaining to draught power like creatine kinase and blood lactate levels were estimated in Hallikar and other southern breeds of cattle. ADRB2 gene was sequenced with 5 primer sets with the product sizes of 422, 472, 661, 700 and 694 bp. Tetra-ARMS PCR primers were designed for SNPs in ADBR2 gene at positions - 568, 1293, 1311, 1351 and were genotyped in Kangayam (n=130), Bargur (n = 100) and Hallikar (n=96) breeds of cattle.

Table: Polymorphism across ADRB2 gene in Indian cattle breeds.

SNPs	Genotype	Genotype frequencies		
		Bargur	Kangayam	Hallikar
568 G>A (SNP 1)	GG	0.76	0.53	0.02
	GA	0.24	0.47	0.89
	AA	0.0	0.0	0.09
1293C>T (SNP 2)	CC	0.0	0.0	0.02
	CT	0.44	0.43	0.27
	TT	0.56	0.57	0.71
1311T>C (SNP 3)	TT	0.74	0.17	0.21
	CT	0.05	0.57	0.25
	CC	0.21	0.26	0.54

Genotypic frequency of SNPs at ADRB2 gene in indigenous cattle breeds (Core laboratory, TANUVAS, Chennai)

A total of six SNPs were found in IGF-1 gene among 3 cattle breeds; SNP 1 (GG, GA and AA) of IGF-1 gene was found to be associated with stride length. High He values of promoter microsatellite locus suggest this is a potential marker for draughtability in Kangayam, Bargur and Hallikar breeds of cattle. Vascular endothelial growth factor (VEGF) affects peripheral circulation through endothelial cell proliferation and migration. Promoter and exonic regions were sequenced with 7 primer sets with the product sizes of 660 bp, 732 bp, 450 bp, 701 bp, 340 bp and 712 bp. Products were amplified and sequenced in cattle breeds. Six SNPs at positions 7877, 8283, 11270, 11272, 13285 and 13287 were found in the intronic regions. GA microsatellite repeats found between 11250 to 11290 exhibited polymorphisms and needs further evaluation.

Conservation of Kilakarsal sheep (Instructional Livestock Farm Complex, Ramayanpatti, Tirunelveli, TANUVAS)

A total of 451 (209 male + 242 female) Kilakarsal progenies were produced during 2012-13. Overall 1504 (707 male + 797 female) progenies of Kilakarsal have been recorded during the scheme period up to 31/03/2013. The tupping and lambing percentage at farm was 81.48 and 98.48, respectively.

Kilakarsal sheep being reared at Tirunelveli farm

Table: Average body weights (kg) in Kilakarsal sheep

Sex	Birth weight	3 months	6 months	9 months	12 months
Male	2.79 ± 0.05 (30)	10.21 ± 0.57 (14)	13.11 ± 0.49 (10)	15.20 ± 0.89 (03)	21.00 ± 1.05 (14)
Female	2.64 ± 0.08 (27)	9.27 ± 0.52 (15)	12.94 ± 0.35 (14)	14.15 ± 0.28 (07)	17.04 ± 0.45 (24)
Overall	2.72 ± 0.04 (57)	9.71 ± 0.39 (29)	13.00 ± 0.28 (24)	14.40 ± 0.31 (10)	18.57 ± 0.53 (38)

Table: Carcass characteristics in Kilakarsal sheep

	Age - 6 months			Age – 12 months		
	Male	Female	Overall	Male	Female	Overall
Weight at slaughter (kg)	14.47 ± 0.14	13.79 ± 0.07	14.13 ± 0.13	19.75 ± 0.59	17.27 ± 0.22	18.51 ± 0.48
Carcass weight (kg)	6.82 ± 0.16	6.29 ± 0.04	6.55 ± 0.11	8.80 ± 0.22	7.60 ± 0.16	8.20 ± 0.22
Dressing percentage	47.10 ± 0.70	45.50 ± 0.15	46.33 ± 0.41	44.60 ± 0.60	43.99 ± 0.45	44.33 ± 0.37

(Values are means of six observations)

Conservation of Krishna Valley cattle (BAIF Development Research Foundation Uruli-Kanchan)

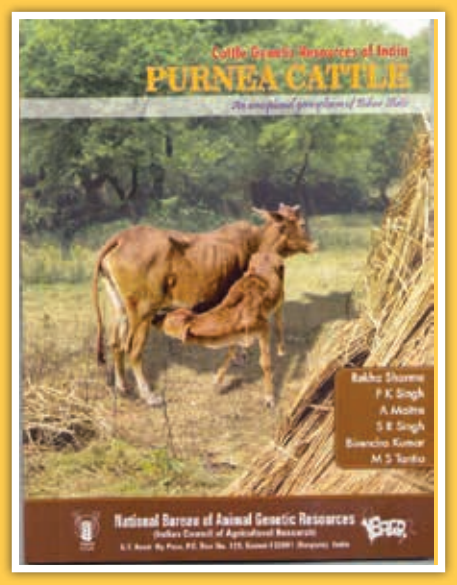
The project was operational in 25 cattle development centers and Govt. dispensaries of Department of Animal Husbandry Karnataka state. Since inception of the project on conservation of Krishna Valley cattle total 10,228 inseminations were performed. 2,777 pregnancies were followed and recorded average conception rate of 51.55 per cent. So far 725 males and 627 females were born in the breeding tract. Along with this 433 pregnant animals were sold by the owners.

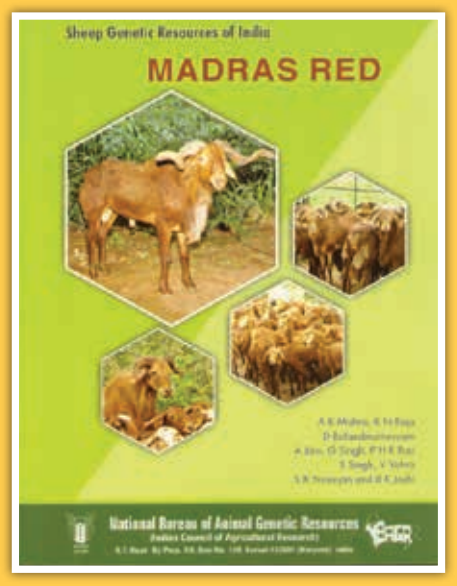
2012-13

NBAGR

Research Projects & Publications

- Research Projects
- Publications
- Awards/Recognition


Cattle Genetic Resources of India
PURNEA CATTLE
Rekha Sharma
P K Singh
A Mishra
S K Singh
Balaraju Kumar
M S Tantia
National Bureau of Animal Genetic Resources


Sheep Genetic Resources of India
MADRAS RED
National Bureau of Animal Genetic Resources


Goat Genetic Resources of India
BERARI
- An important goat germplasm of Vidarbha
NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES

2012-13

Research Projects

Completed Research Projects

1. Characterization of lesser known goat populations of Maharashtra and Odisha states of India- NK Verma, RAK Aggarwal, SP Dixit, PS Dangi, SK Das (OUAT), SV Kuralkar (PGI VAS, AKOLA) and VS Kawitkar (DBSKKV, DAPOLI).

2. Phenotypic and genetic characterization of Indigenous donkey population-Rahul Behl, Jyotsna Behl and DK Sadana. (SC Gupta up to 08.02.2010, Neelam Gupta up to 31.07.2010 and KN Raja & BK Joshi up to 30.06.2011)

3. Transcriptome analysis of circulating PMN to characterize parturition-induced immune suppression in buffalo and cattle-M Mukesh, M Sodhi, MS Tantia, AP Mohanty (NDRI) and Indrajit Ganguli w.e.f. 22.10.2011. (BP Mishra up to 24.02. 2011and RS Kataria up to 30.06, 2011)

4. Candidate gene analysis and identification of allelic variants associated with incidence of mastitis in dairy cattle and buffaloes-SK Niranjan (w.e.f. 26.08.2011), RS Kataria and AK Dang (NDRI) (BP Mishra up to 24.02.2011, BK Joshi up to 06.07.11 and P Kathiravan up to 09.09.11).

On-going Research Projects

1. Characterization and Evaluation of Sanchori and Nari Cattle of Rajasthan - PK Singh, RK Pundir, DK Sadana and HS Rathore (LPPS, Sadri) - April, 2011 to March, 2014.

2. Characterization and Evaluation of Indigenous Cattle Germplasm in Northern Eastern States of India- RK Pundir, PK Singh and DK Sadana - April, 2011 to March, 2014.

3. Phenotypic and genetic characterization of Koraput sheep. - Sanjeev Singh, KN Raja, Reena Arora, Indrajit Ganguli and Sanat Mishra, CEO, OLRDS, Bhubaneshwa - April, 2012 to March, 2014.

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

5. Characterization of non-descript goat genetic resources of R*ohilkhand* Region of Uttar Pradesh and Uttarakhand. SP Dixit, Triveni Dutt (IVRI), PS Dangi, RS Barwal, Neel Kant (GBPUAT) and Vikas Vohra (w.e.f. 14.07, 2011)- January 2010 – March 2014.

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

7. Phenotypic characterization of Harrighata Black breed of chicken - PK Vij**,** MS Tantia and S Pan (WB Univ. Calcutta) - April, 2012 to March, 2014.

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

9. 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) -October, 2011 to March, 2014.

10. Development of breed signature for Sahiwal, Gir and Tharparkar cattle- MS Tantia -April, 2012 to March, 2015.

11. Study of the genetic variability in the Bovine Cytokines (*Bos indicus*). - Jyotsna Behl, Rahul Behl and NK Verma.- January, 2009 to December, 2013.

12. Delineating polymorphism and evolution of Toll like receptors in Indian native *Bos indicus* cattle breeds - Monika Sodhi , M Mukesh and Indrajit Ganguly (w e f. October., 2011) -January, 2010 to December, 2013.

13. Nucleotide diversity in candidate genes for mutton quality traits in Indian sheep. - Reena Arora, DK Yadav and S Bhatia (up to Feb., 2012) - April, 2011 to March, 2014.

14. Development and validation of human Tissue Plasminogen Activator gene construct in mammalian cell culture system. - Indrajit Ganguly and Sanjeev Singh- April, 2012 to March, 2015 .

15. 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, 2014.

16. Application of Microorganisms in Agriculture and Applied Sectors (AMAAS) (ongoing, ICAR Funded 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) Dinesh Kumar (up to 18.05. 2012), Rameshwar Singh (up to 03.09.2012) and SK Tomar (NDRI) - 19th July, 2006 to 31st March, 2012, Extended up to March, 2014.

17. Network Project on Animal Genetic Resources- BK Joshi, Project coordinator and MS Tantia (I/c, Network Project) - 1992-Contd.

18. Candidate gene analysis and identification of allelic variants of fecundity in indigenous goat. (Core Lab-Network Project-) - Sonika Ahlawat and Rekha Sharma - April, 2011 to December 2013

19. Characterization of candidate genes for sexual precocity in indigenous goats. - Rekha Sharma, Sonika Ahlawat (on study leave w e f 1.08.12), Manoranjan Roy (AH & VS WB) and Sanjay Mandakmale (MPKV, Rahuri) - April, 2012 to March, 2014

External Funded Projects

20. Identification of SNP's in QTL region in Indian goats and their association with milk quality traits for healthfulness. (DBT) - SP Dixit, M Mukesh and Rajesh Kumar and AK Tyagi (NDRI) - 4th June, 2010 to 3rd June, 2013.

21. Identification of Quantitative Trait Loci for Milk yield, Fat and Protein Percent in Buffaloes. (NAIP)- RK Vijh, SB Gokhale, DN Shinde and RL Bhagat - January, 2008 to March, 2013. Extended upto Sept. 2013.

22. Toll-like receptors in farm animals- Evolutionary lineages and application in disease resistance (NAIP) -RS Kataria, SK Niranjan and Sanjeev Singh w.e.f. 24.09.2011 - July, 2008 to December, 2013

23. Analysis of mammary gland transcriptome and proteome during lactation and involution in indigenous cattle and buffalo for identification of probable mammary biomarkers(NAIP)- M Mukesh, (BP Mishra CCPI-up to 24.02.11), RS Kataria and Monika Sodhi (w.e.f. January, 2012) -July 2008 to March, 2014

24. Bio-prospecting of Genes and Allele Mining for Abiotie Stress Tolerance. (NAIP) - RK Vijh CCPI and Animal Sciences Group Leader -April, 2009 to March, 2013. Extended upto March, 2014.

25. Establishment of National Agricultural Bioinformatics Grid (NABG) in ICAR. (NAIP) -Avnish Kumar, DK Yadav, Dinesh Kumar (BT), B Prakash and PK Vij - April, 2010 to March, 2014.

26. Harmonizing Biodiversity conservation and Agricultural Intensification through Integration of plant Animal and fish genetic resources for livelihood security in fragile ecosystem (NAIP) - BK Joshi, Anand Jain, PK Vij, NK Verma, RAK Aggarwal KN Raja and Vikas Vohra (w.e.f 10th July 2012)- September, 2009 to June, 2013.

27. Genome data mining to unravel molecular basis of thermo tolerance and adaptation to diverse environment in native cattle and buffaloes. (National Fellow) - Manishi Mukesh - 17th Feb., 2011 to 2016.

Publications

Research Articles

1. Aggarwal J, Sharma A, Kishore A, Mishra BP, Yadav A, Mohanty A, Sodhi M, Kataria RS, Malakar D and Mukesh M (2012). Identification of suitable housekeeping genes for normalization of quantitative real-time PCR data during different physiological stages of mammary gland in riverine buffaloes (*Bubalus bubalis*). Journal of Animal Production and Nutrition, DOI: 10.1111/jpn.12027.

2. Ahlawat S and Sharma R (2013). Contribution of goat to rural poverty alleviation and food security. Livestock Line. 6 (11): 11-14

3. Ahlawat S, Sharma R and Maitra A (2012) Nucleotide diversity in promoter of bone morphogenetic protein receptor type 1B (BMPR1B) gene in Indian goats. Journal of Biotechnology and Biomaterials, 2(6): 44.

4. Ahlawat S, Sharma R and Maitra A (2013). Screening of indigenous goats for prolificacy associated DNA markers of sheep. Gene, 517:128–131.

5. Ahlawat S, Sharma R and Maitra A. (2011) (Published in 2013). Fec B mutation responsible for fecundity in sheep not detected in Indian goats- a short note. Journal of Livestock Biodiversity, 3(1):28-30.

6. Ahlawat S, Sharma R and Maitra A. (2012). Analysis of coding DNA sequence of GDF9 gene in Indian goats for prolificacy associated markers. Indian Journal of Animal Sciences, 82(7): 721–725.

7. Ahlawat S, Sharma R, Maitra A (2012) Prolificacy genotypes of Bone Morphogenetic Protein 15 (BMP15) gene in sheep were not detected in Indian goats. Indian Veterinary Practitioner, 13 (2): 234-240.

8. Arora R, Yadav DK and Yadav HS (2013). SNP analysis of Growth differentiation factor 8 (GDF8) gene in Indian sheep. Indian Journal of Animal Science, 83 (3): 304–306.

9. Arora R, Yadav HS and Mishra BP (2013). Mitochondrial DNA diversity in Indian sheep. Livestock Science, 153: 50–55.

10. Banerjee P, Gahlawat SK, Joshi J, Sharma U, Tantia MS, Vijh RK (2012). Sequencing, Characterization and Phylogenetic analysis of TLR genes of *Bubalusbubalis*. DHR International Journal of Biomedical and Life Sciences, 3(1): 137-159.

11. Banerjee P, Joshi J, Sharma U and Vijh RK (2012). Population Differentiation in

Dromedarian camel: A Comparative Study of Camel inhabiting Extremes of Geographical Distribution. International Journal of Animal and Veterinary Advances, 4(2): 84-92.

12. Banerjee P, Joshi J, Sharma U, Ganai N and Vijh RK. (2012). Genetic characterisation of two humped camel of India (*Camelusbactrianus*). Indian Journal of Animal Sciences, 82 (10): 1205–1212.

13. Barman NN, Bora DP, Tiwari AK, Kataria RS, Desai GS and DekaPJ (2012). Classical swine fever in the pygmy hogs. Revue scientifiqueet technique (International Office of Epizootics) 31: 919-930.

14. Dixit SP, Aggarwal RAK, Dangi PS, Verma NK, Vyas MK, Rana J, Sharma A, Kharadi VB, Sabapara GP and Deshpande SB. (2013). Phenotypic characteristics, management, performance and genetic variability in Surti breed of goat. Indian Journal of Animal Sciences, 83 (4): 423–427.

15. Dixit SP, Verma NK, Aggarwal RAK, Vyas MK, Rana J, Sharma A (2012). Genetic Diversity and relationship among Indian goat breeds based on microsatellite markers. Small Ruminant Research, 105: 38-45.

16. Dubey PK, Aggarwal J, Goyal S, Gahlawat SK, Kathiravan P, Mishra BP and Kataria RS (2012). Sequence and topological characterization of Toll-like receptor 8 gene of Indian riverine buffalo (*Bubalus bubalis*). Tropical Animal Health and Production, 45:91-99.

17. Dubey PK, Goyal S, Aggarwal J, Gahlawat SK, Kathiravan P, Mishra BP and Kataria RS (2012). Development of tetra primers ARMS-PCR assay for the detection of A1551G polymorphism in TLR8 gene of riverine buffalo. Journal of Applied Animal Research, 40: 17-19.

18. Dubey PK, Goyal S, Kathiravan P, Mishra BP, Gahlawat SK and Kataria RS (2013). Sequence characterization of river buffalo Toll-like receptor (TLR) genes 1-10 reveals distinct relationship with cattle and sheep. International Journal of Immunogenetics, 40: 140-148.

19. Goyal S, Kathiravan p, Kataria RS, Niranjan SK and Jayakumar S (2013). Yak TNFα gene: Sequence analysis reveals high amino acid identity with cattle but variations in potential binding sites for transcription factors. Indian Journal of Animal Sciences, 83 (1): 46–50.

20. Joshi BK, Sodhi M, Mukesh M and Mishra BP (2012). Genetic characterization of farm animal genetic resources of India: A review. Indian Journal of Animal Sciences, 82(11): 1259-1275.

21. Joshi J, Salar RK, Banerjee P, Gokhale SB, Sharma U, Gaur U, Tantia MS and Vijh RK (2012). Microsatellite analysis of buffaloes of Indo-Gangetic Plains. Indian Journal of Animal Sciences, 82(11):1434-1437.

22. Joshi J, Salar RK, Banerjee P, Sharma U, Tantia MS and Vijh RK (2012). Comparative evaluation of Murrah breeds with buffaloes of Indo-Gangetic Plains. DHR International Journal of Biomedical and Life Sciences, 3(1): 93-105.

23. Kapila N, Kishore A, Sodhi M, Sharma A, Kumar P, Mohanty AK, Jerath T and Mukesh M. Identification of appropriate reference genes for qRT-PCR analysis of heat-stressed mammary epithelial cells in riverine buffaloes (*Bubalus bubalis*). ISRN Biotechnology, http://dx.doi.org/10.1155/2013/ 735053

24. Kathiravan P, Kataria RS and Mishra BP (2012). Power of exclusion of 19 microsatellite markers for parentage testing

in river buffalo (*Bubalus bubalis*). Molecular Biology Reports, 39: 8217-8223.

25. Khatri I, Upasna S, Banerjee P, Joshi J and VijhRK. (2012). Genome wise identification of long terminal repeats in *Bubalus bubalis*. Indian Journal of Animal Sciences, 82(4): 392-396.

26. Kishore A, Sodhi M, Khate K, Kapila N, Kumari P, Mukesh M. (2013). Selection of stable reference genes in heat stressed peripheral blood mononuclear cells of tropically adapted Indian cattle and buffaloes. Molecular Cellular Probes (doi:pii: S0890-8508 (13) 00013-3. 0.1016/j.mcp.2013.02.003

27. Kishore A, Sodhi M, Sobti RC, Mukesh M, Mishra BP (2012). Variation analysis in the regulatory region of alpha S1-casein milk protein gene among tropically adapted Indian zebu cattle (*Bos indicus*). ISRN Biotechnology http://dx.doi.org/10.5402/2013/926025.

28. Mckenzie GW, Arora R and Hickford JG H (2012). Genetic variation in the 5 UTR of the KRT2.13 gene of sheep. Animal Science Journal, 83: 194–198.

29. Mishra P, Ali AS, Aggarwal RAK, Dixit SP, KawitkarVS, Dangi PS and Verma NK. (2012). Genetic diversity and bottleneck analysis of KonkanKanyal goats. Animal Genetic Resources, 50: 43-48.

30. Mishra P, Ali AS, Dixit SP, Aggarwal RAK, Dangi PS, Tyagi N, Dash SK and. Verma, NK.(2013). Microsatellite based genetic evaluation of Ghumusar goats of Orissa, India, Animal Genetic Resources, (doi:10.1017/S2078633612000811)

31. Mishra P, Ali AS, Verma NK (2012), Phenotypic, Biometric and Genetic Characterization of Bundelkhandi Goats. Indian Journal of Animal Sciences, 82(11):1442-1445.

32. Prakash B, Pundir RK, Singh PK, Sharma D, Neelkant and Singh CV (2012). Assessment of genetic variability in Hill cattle of Garhwal region of Uttarakhand by microsatellite markers. Indian Journal of Animal Sciences, 82 (11): 1353–1357.

33. Pundir RK, Singh PK, Neelkant, Sharma D, Singh CV and Prakash B (2013). Uttara- A new cattle germplasm from Uttarakhand hills. Indian Journal of Animal Sciences, 83 (1): 51-58.

34. Pundir RK, Singh PK, Sharma D, Saini A, Singh CV and Prakash B (2012). Hill cattle of Pithoragarh district of Uttarakhand. Indian Journal of Animal Sciences, 82(12): 135-137.

35. Raja KN, Jain A, Singh G, Kumar L,Yadav HK and Arora R (2012). Ramnad White Sheep-phenotypic and genetic characterization. Indian Journal of Animal Sciences, 82 (9): 1082–1086.

36. Saste SR, Ghalsasi PM, Kataria RS, Joshi BK, Mishra BP and Nimbkar C (2012). ARMS-PCR as an alternative, cost effective method for detection of FecB genotype in sheep. Indian Journal of Biotechnology, 11: 274-279.

37. Sharma A, Gautam B, Jayakumar S, Saroha V, Verma NK and Dixit SP (2013) Genetic structuring of nine Indian domestic goat breeds based on SNPs identified in IGF-I gene. Animal Biotechnology, 24: 148-157.

38. Sharma R, Maitra A and Ahlawat S (2012). New genetic polymorphism of goat KiSS-1 gene. Journal of Biotechnology and Biomaterials, 2 (6): 41

39. Sharma R, Maitra A, Pandey AK and Mishra BP (2012). Differentiation of four Indian

aboriginal cattle populations revealed by STR markers. Russian Journal of Genetics (Genetika), 48 (6): 611–617.

40. Sharma U, Banerjee P, Joshi J and Vijh RK (2012). Identification of SNPs in Goats (*Capra hircus*) using RNA-Seq Analysis. 2012. International Journal of Animal and Veterinary Advances. 4(4): 272-283.

41. Sharma U, Banerjee P, Joshi J and Vijh RK (2012). Genetic Discontinuities and Sub structuring in buffaloes of Indo Gangetic Plains. International Journal of Animal and Veterinary Advances, 4(4): 284-291.

42. Sharma U, Banerjee P, Joshi J and Vijh RK (2012). Ubiquitous Expression of Genes in tissues of Goat (Capra hircus) Using RNA-seq. International Journal of Animal and Veterianary Advances. 4(4): 292-302.

43. Sharma U, Banerjee P, Joshi J, Khatri I and VijhRK (2012). Distribution of satellite markers in water buffalo genome. Indian Journal of Animal Sciences, 82 (5): 491–494.

44. Singh LV, Jayakumar S, Kaur N, Kumari N, Sharma A, Chopra M, GuptaV, Kumar K, Shukla S, Shukla SK, Kumar S, Gupta SC and Gupta N (2012). Sequence Analysis of keratin associated protein (KAP7) gene in indigenous breed of yak. Cibtech Journal of Biotechnology, 1:38-41.

45. Singh LV, Sharma R, Pandey AK, Tripathi V, Maitra A and Mishra BP (2012). Genetic variation in CAPN1 gene in Sirohi goat breed. Indian Journal of Veterinary Research 21 (2): 1-4.

46. Singh LV, Tripathi V, Sharma R, Pandey AK, Maitra A and Mishra BP (2012). Genetic polymorphism of CAPN1 gene in Sirohi goat. International Journal of Meat Science, DOI: 10.3923.

47. Singh PK, Pundir RK, Kumarasamy P and Vivekanandan P (2012). Management and physical features of migratory Pulikulam cattle of Tamil Nadu. Indian Journal of Animal Sciences 82(12):131-134.

48. Sodhi M, Kishore A, Khate K, Kapila N, Mishra BP, Kataria RS, Mohanty AK, Varshney N and Mukesh M (2012). Evaluating suitable internal control genes for transcriptional studies in heat stressed mammary explants of buffaloes. Journal of Animal Breeding and Genetics, DOI: 10.1111/j.1439-0388.2012.01004

49. Sodhi M, Mukesh M, Mishra BP, Kishore A, Prakash B, Kapil R, Khate K, Kataria RS and Joshi BK (2012). Screening of taurine and crossbred breeding bulls for A1/A2 variants of β-casein gene. Indian Journal of Animal Sciences, 82: 183-186.

50. Sodhi M, Mukesh M,.Kataria RS, Mishra BP, Joshi BK (2012). Milk proteins and human health: A1/A2 milk hypothesis. Indian Journal of Endocrinology and Metabolism, 16(5): 856

51. Tanpure T, Dubey PK, Kathiravan P, Mishra BP, Niranjan SK, Singh KP and Kataria RS (2012). PCR-SSCP analysis of leptin gene and its association with milk production traits in river buffalo (*Bubalus bubalis*). Tropical Animal Health and Production, 44:1587–1592.

52. Tantia MS, Mishra B, Banerjee P, Joshi J, Sharma U and Vijh RK (2012). Phylogeny and Sequencing of Toll Like Receptor genes (TLR-2 and TLR-4) in buffaloes. Indian Journal of Animal Sciences, 82 (8): 875–878.

53. Dureja V, Singh S, Rana S, Banerjee P, Joshi J, Tantia MS, VijhRK (2013). Characterization of GPX1 and DIO1 Genes in *Bubalus bubalis*. Journal of Biology and life Sciences, 4(1): 153-163.

54. Varshney N, Mohanty AK, Kumar S, Kaushik JK, Dang AK, Mukesh M, Mishra BP, Kataria RS, Kimothi SP, Mukhopadhyay TK, Malakar D, Prakash BS, Grover S and Batish, VK (2012). Selection of suitable reference genes in milk somatic cells of lactating cows (*Bos indicus*) for quantitative gene expression studies. Journal of Dairy Science, 95(6):2935-45

55. VermaNK, Aggarwa1RAK, Dixit SP, KawitkarVS, Dangi PS, Kaur N, Mishra P and Joshi BK (2012). Konkan Kanyal – Characters and performance of a newly discovered goat germplasm of Maharashtra state. Indian Journal of Animal Sciences, 82(9):1079-1081.

56. Vohra V, Niranjan SK and Joshi BK (2012). Belahi Cattle: Uniform but distinct germplasm of Haryana. Journal of Animal Research, 2(1): 47-51

57. Vohra V, Niranjan SK and Joshi BK (2012). Gojri: A novel migratory buffalo germplasm in Punjab and Himachal Pradesh. Journal of Animal Research, 2(3):317-321.

58. Yadav DK, Jain A, Kulkarni VS, Govindaiah MG, Aswathnarayan T, Sadana DK (2013). Classification of four ovine breeds of southern peninsular zone of India: Morphometric study using classical discriminant function analysis. SpringerPlus 2:29. doi:10.1186/2193-1801-2-29

59. Yadav DK, Vij PK. Cattle herd structure and herd dynamics in Gaushalas of Haryana. Journal of Livestock Biodiversity 3 (1): 35-38.

60. Yadav HS, Gupta R, Mishra BP and Arora R (2012). Assessment of genetic relationships between Kheri sheep and its founder breeds using molecular coancestry information. Indian Journal of Dairy Science. 65(6):484-489.

61. Yadav P, Mukesh M, Kataria RS, Yadav A, Mohanty AK, Mishra BP (2012). Semi-quantitative RT-PCR analysis of fat metabolism genes in mammary tissue of lactating and non-lactating water buffalo (*Bubalus bubalis*). Tropical Animal Health Production, 44(4):693-696.

62. Yadav P, Singh DD, Mukesh M, Kataria RS, Yadav A, Mohanty AK, Mishra BP (2012). Identification of suitable housekeeping genes for expression analysis in mammary epithelial cells of buffalo (*Bubalus bubalis*) during lactation cycle. Livestock Science, 147 (1):72-76.

Popular/Technical Articles

1. आर एस कटारिया, बी पी मिश्रा, बी प्रकाश एवं डी के सदाना (2012) पूर्वोत्तर भारत की विलक्षण भैंस नस्लें। पशुधन प्रकाश 3: 11–14.

2. प्रताप सिंह पँवार एवं विकास वोहरा (2012) भारतीय भैंस। पशुधन प्रकाश 3: 74–75.

3. विकास वोहरा एवं प्रताप सिंह पँवार (2012) पशु आनुवंशिक संसाधन का सतत उपयोग। पशुधन प्रकाश 3: 71–73.

4. इन्द्रजीत गाँगुली एवं संजीव सिंह (2012) ऊंट दूध का पोषण और चिकित्सीय पहलू। पशुधन प्रकाश 3: 84–88.

5. विज पी.के., अग्रवाल आर. ए.के., टांटिया मधुसूदन, शर्मा पंकज एवं जोशी बी.के., (2012) हिमाचल प्रदेश के चंबा ज़िले में पशुधन विविधता, पशुधन प्रकाश 3: 5–10.

6. मनीषी मुकेश, अमित किशोर, प्रवेश मुंजाल, मोनिका सोढ़ी (2012) बदलते वैश्विक परिवेश में भारतीय पशुधन सम्पदा – एक अवलोकन। पशुधन प्रकाश 3: 64–70.

7. रेखा शर्मा एवं सोनिका अहलावत (2012). गायों में गर्भ परीक्षण की विधियाँ वर्तमान स्थिति और भविष्य की संभावनाएं। पशुधन प्रकाश 3: 79–83.

8. सोनिका अहलावत एवं रेखा शर्मा (2012). लघु रुमंथी पशुओं में चयन प्रक्रिया: कल आज और कल। पशुधन प्रकाश 3: 34–36.

9. सोनिका अहलावत एवं रेखा शर्मा (2011). पशुओं में थिलेरियोसिस रोग के कारण और निवारण। कृषि किरण 4: 96–98. (2012 में प्रकाशित)

10. पुंडीर आर.के. और शर्मा डी. (2012), उत्तराखंड की गाय का मूल्यांकन, खेती (अगस्त) 19–21.

11. पी.के. सिंह और करुणा असिजा (2012) भारतीय प्रमुख गो नस्लें: पहचान एवं उपयोगिता। (2012) पी.डी.सी. मेरठ की हिन्दी पत्रिका "सुरभि" के रजत जयंती वर्ष में प्रकाशित। पृष्ठ 13–19.

12. बी.के. जोशी और पी.के. सिंह (2012) उन्नत प्रजनन तकनीकों द्वारा पालतू पशुओं का आनुवंशिक विकास। केन्द्रीय एरिड जोन अनुसंधान संस्थान, जोधपुर द्वारा प्रकाशित "मरु कृषि चयनिका (पशु पालन विशेषांक)"। पृष्ठ 17–19.

13. Priyanka M and Verma NK (2012). Goat Genetic Resources of India. Indian Farming, July 2012, pp 30-33.

14. Sharma R and Ahlawat S. 2012. Selection in small ruminants: The journey so far. Livestock International,16(3): 19-21.

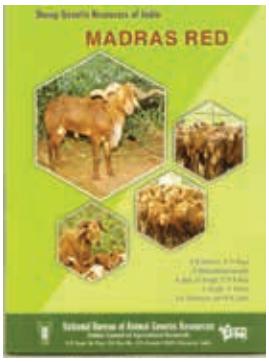
15. Sharma R, Ahlawat S and Maitra A. (2012). Molecular markers in Assessment of Meat Quality. Livestock International, 16(1): 14-15.

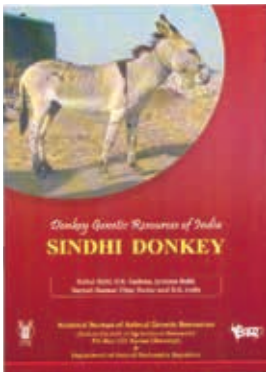
16. Sharma R, Singh PK and Ahlawat S (2012). Shahabadi: An important cattle germplasm of Bihar. Livestock International. 16(4):2-4

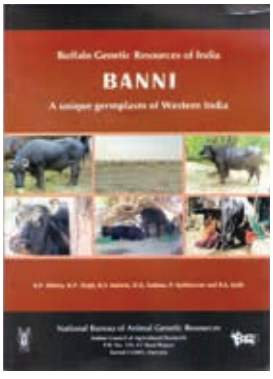
Breed Monographs/Bulletin/Leaflet

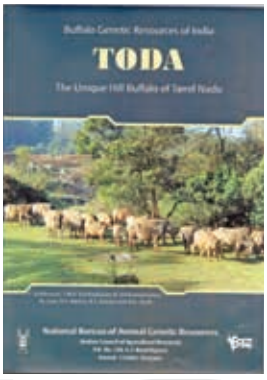
1. Banni- A Unique Germplasm of Western India by BP Mishra, KP Singh, RS Kataria, DK Sadana P Kathiravan and BK Joshi. Monograph # 68, 2012.

2. Toda- The Unique Hill Buffalo of Tamil Nadu by P Kathiravan, SMK Karthickeyan, R Venkataramanan, M Iyue, BP Mishra, RS Kataria and BK Joshi. Monograph # 72, 2012.









3. Buffalo Genetic Resources of India-Marathwadi by RS Kataria, P Kathiravan, BP Mishra, DK Sadana, BV Gujar, V Vohra and BK Joshi. Monograph # 73, 2012.

4. Berari-An important goat germplasm of Vidarbha by NK Verma, SV Kuralkar, RAK Aggarwal, SP Dixit, Priyanka Mishra, Prajakta Kuralkar, PS Dangi, and BK Joshi. Monograph# 76, 2012

5. Sheep Genetic Resources of India, Madras Red by A K Mishra, K N Raja, D. Balasubramanium A Jain, G Singh, P H R Rao, S Singh, V Vohra, S K Niranjan and B K Joshi. Monograph # 72, 2012

6. Protocol on "Isolation of mammary epithelial cells (MECs) from milk of cattle and buffalo" by AK Mohanty, Jagdeesh Janjanam, Manu Jamwal, Surender Singh, Vijay Anand J, Sudarshan Kumar, Neha Charavarty, Pradeep Behare, Ajay K. Dang, Jai K. Kaushik, D Malakar (NDRI, Karnal), Manishi Mukesh, Monika Sodhi

7. भारतीय गो–धन: ए2 दूध के लिए एक प्राकृतिक संसाधन इल एम सोढी, एम मुकेश, ए किशोर, बी पी मिश्रा, बी प्रकाश, आर एस कटारिया एवं बी के जोशी

Awards/Recognitions

- Dr. R.S. Kataria, Principal Scientist, received first Dr. P.G. Nair award (2012) instituted by NBAGR for his outstanding scientific contributions made during 2009 to 2011, in the field of identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country. The award consisting of a citation and cash of Rs. 5000/- was received during Foundation Day celebrations of the Bureau.

- Second best poster award for the poster entitled" Phenotypic characterization of Narayanpatna goats of Odisha" by PS Dangi, NK Verma, SP Dixit, RAK Aggarwal, SK Dash and Manoj Sarangi during National Seminar on "New paradigms in livestock production: from traditional to commercial farming and beyond" held at NDRI, Karnal on 28-30 January, 2013.

Dr. R.S. Kataria, Principal Scientist, receiving Dr. P.G. Nair award (2012) from Dr. B. Pisupati, Chairman, National Biodiversity Authority

- Best poster Award for the poster entitled "Bharat ke pashu aanuvanshik Sansadhan" by Karuna Asija and P K Singh at the occassion of Foundation day of NBAGR.

- Young Scientist Award for the paper entitled "Detection of polymorphism in the nucleotide-binding oligomerization domain like receptor-2 gene of Indian riverine and swamp buffalo (*Bubalus bubalis*)" by Asmita, P. K. Dubey, N. Kumari, S. Goyal, S.K. Niranjan, S. Singh and R.S. Kataria (2013) presented at Xth SOCDAB National Symposium held at Pantnagar during February 7-8, 2013.

- Second best poster for "Peripheral blood mononuclear cells: a potential cellular system to understand differential heat shock response in cattle and buffaloes" A. Kishore, M. Sodhi, K Khate, N. Kapila, RS Kataria, and M Mukesh at Xth SOCDAB National Symposium held at Pantnagar during February 7-8, 2013.

- Ist Prize awarded to Dr Rekha Sharma for Best Oral presentation entitled "Investigation of indigenous goat GDF9 gene for

AWARDS/RECOGNITIONS

polymorphism associated with twinning in exotic goat using PCR-RFLP method" at the National conference on "NexGen Biotechnology: Amalgamating Science & Technology" November 23-24, 2012 at UIET, Kurukshetra, Kurukshetra University.

- डॉ एन के .वर्मा द्वारा वार्षिक हिन्दी शोध–पत्रिका "पशुधन प्रकाश" के प्रथम अंक वर्ष 2010 में प्रकाशित लेख "भारतीय बकरी–प्रबंधन, सरंक्षण व भारतीय अर्थव्यवस्था में योगदान" को प्रथम पुरस्कार दिया गया।
- मोनिका सोढ़ी, बी पी मिश्रा, एम मुकेश, अमित किशोर, आर कपिल, पी कुमारी, के खाते एवं बी के जोशी द्वारा वार्षिक हिन्दी शोध–पत्रिका "पशुधन प्रकाश" के द्वितीय अंक वर्ष 2011 में प्रकाशित लेख "भारतीय गो नस्लों में बीटा–केसीन ए2 एलील की प्राकृतिक प्रचुरता" को द्वितीय पुरस्कार दिया गया ।
- मनीषी मुकेश, अमित किशोर, अंकिता शर्मा, प्रवेश मुंजाल एवं मोनिका सोढी को एन.बी.ए.जी.आर. के स्थापना दिवस पर आयोजित पोस्टर प्रतियोगिता में "बदलते जलवायु परिवेश में भारतीय पशुधन की महत्वता" के लिए द्वितीय पुरस्कार दिया गया।
- डॉ बी के जोशी द्वारा वार्षिक हिन्दी शोध–पत्रिका "पशुधन प्रकाश" के प्रथम अंक वर्ष 2010 में प्रकाशित लेख "भारतीय पशु आनुवंशिक संसाधन की स्थिति एवं चुनौतियाँ'' को द्वितीय पुरस्कार दिया गया।
- डॉ सोनिका अहलावत एवं डॉ रेखा शर्मा द्वारा वार्षिक हिन्दी शोध–पत्रिका "पशुधन प्रकाश" के द्वितीय अंक 2011 में प्रकाशित लेख ''सेक्सड वीर्य – प्रजनन प्रौद्योगिकी के क्षेत्र में एक क्रांति'' को तृतीय पुरस्कार दिया गया।
- Best worker awards for different categories were conferred on the occasion of foundation day of NBAGR. Sh Karambir (Administrative), Sh Moti Ram (Technical officer), Sh. Mahavir (Technicals) and Sh Satbir (Supporting Staff) received the best worker awards.

Best worker award being conferred during Foundation Day celebrations

Other Activities

- Library Services
- Important Meetings
- Institute Technology Management Unit
- Trainings / Workshops attended and organized
- Celebrations
- Sports Activities
- Fairs/Exhibitions
- Distinguished Visitors
- Teaching


अंतर्राष्ट्रीय जैव-विविधता दिवस
के शुभ अवसर पर

Library Services

The NBAGR library plays an important role in serving the needs of scientists and technical staff of the Bureau. There is always an intension to equip the library with most suitable books for the researchers. In this regard, library Advisory Committee (LAC) is a guiding force in the management of the library issues specially pertaining to purchase of scientific books/ journals etc. The Bureau LAC was reconstituted on 15.11.2012. During the year 2012-13, books and journals worth Rs. 8,30,846/- were procured in the library. Fourteen foreign journals and thirty four Indian Journals have been subscribed for the benefit of scientific readers.

Library Collections

1. Total collection	3865
2. No. of books added	52
3. No. of Indian Journals subscribed	34
4. No. of Foreign journals subscribed	14
5. No. of News papers subscribed	07

Important Meetings

Institute Research Committee (IRC)

Annual Institute Research Committee meeting for the year 2011-12 was held on 20th, 21st & 24th April, 2012 under the chairmanship of Dr. B.K. Joshi, Director, NBAGR. Final reports of nine projects completed by March 2012 and proposals of eight new research projects were discussed and approved. Mid-term IRC meeting was held on 25th & 26th September, 2012. Progress reports of all the on-going research projects were discussed. The annual IRC for the year 2012-13 was held on 28th March 2013. Where in the final reports of four completed projects and five new projects were approved.

Annual Review Meeting of Network Project

11th Annual Review Meeting of Network Project on AnGR was held on 25th August, 2012

Network Project review meeting

under the chairmanship of Dr. K.M.L. Pathak, DDG (AS), ICAR, Delhi. The meeting was also attended by Dr. S.C. Gupta, ADG (AP&B), Dr. Gaya Prasad, ADG (AH) and Dr. Vineet Bhasin, Pr. Scientist, Animal Science Division, ICAR, New Delhi. The In-charges of core labs under Network project and of buffalo genomics presented the reports of their respective units. Updated version of cattle and buffalo breed calenders; breed monographs on Toda buffalo and Berari goat were released on this occasion. All the scientists from the Bureau also attended the meeting.

Quinquennial Review Team

The Quinquennial Review Team (QRT), headed by Dr. P. Thangaraju, Former Vice-Chancellor, TANUVAS, Chennai visited the Bureau on 26th October, 2012 and 19-20th December, 2012 to review the work done by the NBAGR, Karnal, for the period 2007 to 2012. The In-charges of Divisions/Sections made a presentation of various activities before the QRT. The team visited the laboratories and had interactions with the scientists.

Chairman QRT showing interest in lab activities

Constitution of NBAGR QRT

1	Dr. P. Thangaraju, Chairman Ex- Vice Chancellor , TANUVAS, Chennai
2	Dr. N. Kandasamy, Member Ex- Professor, Veterinary College, Nammakkal
3	Dr. K. Thangaraj, Member Dy. Director, CCMB, Hyderabad
4	Dr. V. K. Singh, Member Ex-Director, CSWRI, Awikanagar
5	Dr. K.P. Agarwal, Member Ex- NC, NATP
6	Dr. Kamlesh Gupta, Member Ex-Professor & Head, AG&B Deptt. CSKHPKV, Palampur
7	Dr. R.K. Pundir, Member Secretary Principal Scientist, NBAGR

National Advisory Board on Management of Genetic Resources

A meeting of NABMGR was held on 5th March, 2013. The meeting was chaired by Dr. R.S. Paroda and co-chaired by Dr. S. Ayyappan, Secretary DARE & DG, ICAR. News Letter, Monographs on Sindhi donkey, Purnia cattle and Madras Red Sheep and NBAGR Web portal were released on this occasion.

NABMGR meeting in progress

Institutional Biosafety Committee (IBSC)

IBSC of NBAGR, constituted for monitoring the research projects of the Bureau engaged in cloning/recombinant DNA work/transgenics involving biosafety issues, held its six monthly meetings on 06.08.2012 and 24.01.2013. The research projects falling under the purview of IBSC were reviewed and necessary permissions granted. A lecture on biosafety guidelines was delivered by Dr. R.S. Kataria, Principal Scientist, NBAGR on 30-07-2012, as a measure to create awareness among laboratory staff of NBAGR, regarding biosafety issues.

Institute Technology Management Unit

Patents

Following three patents were filed to the Indian Patent Office, Delhi by the Bureau during last year;

S. No.	Application No.	Patent Title	Inventors	Date of filing patents
1	50/DEL/2013	A kit for parentage verification in goats	Dr. Ramesh Kumar Vijh, Priyanka Banerjee, Jyoti Joshi, Shivani Rana, Upasna Sharma	8-Jan-13
2	298/DEL/2013	A kit for parentage verification in Indian ruminant livestock	Dr. R.K. Vijh, Priyanka Banerjee, Jyoti Joshi and Upasna Sharma	4-Feb-13
3	607/DEL/2013	PCR based DNA test for the differentiation of cattle and buffalo meat and milk	Dr. R.S. Kataria, P.K. Dubey, Dr. S.K. Niranjan and Dr. Monika Sodhi	4-Mar-13

Commercialization of Technology

Three technologies viz., A kit for parentage verification in Zebu cattle (*Bos indicus*), A kit for parentage verification in Camels (*Camelus dromedarius* and *Camelus bactrianus*) and A kit for parentage verification in buffaloes (*Bubalus bubalis*), were commercialized on 5th February 2013. The amounts for which the technologies have been commercialized were Rs. 2.00 Lakhs, Rs. 1.00 Lakh and 3.00 Lakhs respectively with royalty of 1%. The 50% of the cost of technology has been received at the time of signing of MoA between M/s Sandor Proteomics Pvt. Ltd. Hyderabad and NBAGR, Karnal and balance 50% shall be paid after grant of patent or 5 years period whichever is earlier for which bank guarantee shall be obtained by the institute.

MoA being signed between M/s Sandor Proteomics Pvt. Ltd. Hyderabad and NBAGR, Karnal.

Trainings/Workshops attended and organized

- Dr. R.K. Vijh, Principal Scientist was deputed for three week training under the NAIP subproject "Bioprospecting of genes and allele mining for abiotic stress tolerance" . The training program entitled " Prediction of genetic merit from genotype data- the analytical system", was organized by Professor James Reecy, Department of Animal Science, IOWA State University of Science and Technology, Ames, IOWA, USA from April 27, 2012 to May 17, 2012.
- Dr. R.K. Vijh, Dr. M.S. Tantia and Dr. RAK Aggarwal attended a training program" Management Development Programme on Leadership Development- (A pre-RMP Programme)" organised at National Academy of Agricultural Research Management, Hyderabad from 8th October to 19th October, 2012.
- A summer short course was organised on Genomic and Phenomic tools for the analysis of livestock genome during June 14- 23, 2012. The course was sponsored by Education Division, Indian Council of Agricultural Research (ICAR).
- A training programme on "Conservation and sustainable utilization of farm animal genetic resources" commenced from 29th January, 2013 and concluded on 2nd February, 2013. The officers from State Animal Husbandry Department, Jammu & Kashmir participated in this training programme.

Dr. Gurubachan Singh, Chairman, ASRB, Delhi releasing the training manual

Participants and faculty of training programme

- Organized A Subject training on 'Bioinformatics for Conservation and Improvement of Animal Genetic Resources was organised under NAIP subproject "Establishment of National Agricultural Bioinformatics GRID (NABG) in ICAR" during February 18-28, 2013 at NBAGR, Karnal.

- One day Workshop on "***Awareness of IPR issues***" was held on 11.1.2013 at NBAGR, Karnal. In this workshop four lectures on different aspects of IPR were delivered by Scientists of ZTM-BPD Unit of IVRI, Izatnagar and *In-charge* ITMU, NDRI, Karnal. A total of 43 staff members including scientists, administrative staff and research scholars attended the workshop.

Celebrations

Foundation Day

The Bureau celebrated its 29th Foundation day on 21st September, 2012. The function was presided by Dr. B. Pisupati, Chairman, National Biodiversity Authority. Dr. D.K. Sharma, Director, CSSRI, Karnal graced the occasion as Guest of Honor. A poster exhibition was held to mark the occasion. Foundation Day address was delivered by Dr. Pisupati emphasizing the holistic and sustainable approach for conservation of AnGR. A Monograph on Banni buffalo, NBAGR Newsletter (Jan- June 2012) and CD on "Bhartiya Paltu Pashu Jaiv Vividhita" (in Hindi) and the latest issue of "Pashudhan Prakash" were released by honorable guests.

Dr. B. Pisupati, releasing the Hindi Magazine Pashudhan Prakash

International Biodiversity Day

To commemorate International Biodiversity Day, 2012 and to bring awareness amongst migratory pastoralist, the bureau organized "Pashu Mela cum Animal Genetic Resource Exhibition" on 22nd May 2012 in the village Ajeet Nagar, Shazadpur block, Ambala (Haryana). Milking cow competitions among the pastoral Gujjar communities rearing Belahi cattle in the villages of Ambala, Yamuna Nagar and Panchkula districts of Haryana were organized in collaboration with Haryana State Animal Husbandry Department. Highest milk production recorded in Belahi Cattle was 8.4 liters per day. The winners were given prizes on this occasion.

Vigilance Day

Director NBAGR, addressing the farmers on the occasion of Biodiversity Day

NBAGR staff members took the oath against corruption on 29th October, 2012 to commemorate the Vigilance Day.

Independence Day and Republic Day

The NBAGR staff and families celebrated 65th Independence Day on 15th August, 2012 and Republic Day on 26th January, 2013 in the campus. Dr. B. K. Joshi, Director, NBAGR hoisted the tricolor and addressed the staff and family members on these occasions. Children

Independence Day celebrations in the campus

presented cultural programmes and participated in athletic events.

Breed Saviour Award Ceremony

The function was held on 8th March 2013 at NBAGR. Twenty farmers belonging to different states were honoured for their contributions in breed conservation of indigenous germplasm.

Sports Activities

- The institute volleyball team has won volleyball smashing and finished runners up in volleyball shooting events during ICAR Inter-institutional sports meet (North Zone) held at National Dairy Research Institute, Karnal from April 25-28, 2012.
- In order to commemorate the Institute Foundation Day, Institute Sports Meet-2012 was organized for the Bureau staff and family members from 15-18 Sept., 2012. During the event, various sporting events like basketball, table tennis, badminton, carom, athletics etc. were conducted. The event has attracted an overwhelming response from the participants of all age groups.
- The institute volleyball smashing team being the winner during North Zone sports meet, represented NBAGR in the inter-zonal ICAR sports meet held at IARI, New Delhi from 18-21 January, 2013.
- A 32 member sports contingent represented NBAGR to participate in ICAR Inter-institutional sports meet (North Zone) held at IISR, Lucknow, from March 19-22, 2013. The institute team won volleyball smashing and finished runners up in volleyball shooting events. Sh. Yoginder, bagged third position in 400 meter race Assistant.

Participation in Zonal Sports Meet and Winning Contingent with trophies

Fairs/ Exhibitions

- NBAGR participated in Fish Festival on 22.09.2012 at Rohtak Centre (Lahli) of CIFE.
- NBAGR exhibited its activities in International Conference of the Parties (COP11) to Convention on Biological Diversity (CBD) held at HITEX City, Hyderabad during 2-19 Oct, 2012.

Sh. Bhupinder Singh Hooda, Hon'ble Chief Minister Haryana appreciating the NBAGR publications

- NBAGR participated in National Seminar on "Prosperity through diversification in agriculture" on 22.12.2012 and Kisan Divas on 23.12.2012 at NDRI, Karnal and showcased the activities in the exhibition.
- An exhibition was installed at Guru Gobind Singh Stadium at Muktsar, Punjab from 8th to 12th Jan 2013 on occasion of National Livestock Championship 2013.

Distinguished Visitors

- Dr. (Md.) Nure Alam Siddiky, Program Officer (Livestock), SAARC Agriculture Centre, Bangladesh visited NBAGR on 16.04.2012.
- A delegation comprising of 7 senior officers from Royal Govt. of Bhutan, Ministry of Agriculture and Forests, Bhutan visited on 14.05.2012 for institutional visit.
- A team of 12 farmers led by Sh. Balraj Singh from Branala visited Bureau on 29.05.2012.
- A delegation from FAO led by Dr.Venkateswarlu Dasyam visited NBAGR on 30.05.2012.
- Dr. R.K. Sethi, Director, CIRB visited on 07.07.2012.
- Dr. R.M. Acharya, Former DDG (AS) visited on 13.08.2012.
- Dr. K.M.L. Pathak, DDG (AS), Dr. S.C.Gupta, ADG (AP&B) and Dr. Gaya Prasad, ADG (AH) visited on 25.08.2012.
- Dr. Sabyasachi Das, Chief Executive Officer, Sahjeevan, Kutch visited the Bureau on 28.08.2012.
- Faculty and students from Zoology Department, Hansraj College, Delhi visited on 13.09.2012.
- Prof. U.B. Mohapatra, Director (Technology), Biotechnology and Dr. C.C. Rath, Deputy Director (Technical), Biotechnology, Science & Technology Department, Govt. of Odisha, Bhubaneswar visited on 05.11.2012.
- Prof. James M. Reecy from ISU, Ames, USA visited NBAGR on 21.12.2012.
- Dr. K.M.L. Pathak, DDG(AS), ICAR, Dr. R.K. Sethi, Director, CIRB, Hisar and Dr. R.K. Singh, Director, NRCE, Hisar visited looked NBAGR on 22.12.2012.
- Dr. Parag Vilas Naik, Lead Scientist (IAD&R-ITD) ITC Limited, Bangalore visited on 18.01.2013.
- A 12-member delegation from Bhutan visited NBAGR on 01.02.2013.
- Dr. R.S. Paroda, Former DG, ICAR, Dr. S.Ayyappan, DG, ICAR, Dr. K.M.L. Pathak, DDG (AS), ICAR, Dr. M. Mahadevappa, Former Chairman, ASRB Dr. P.L. Gautam, Former Chairperson, Protection of Plant Varieties and Farmers' Rights Authority, Ministry of Agriculture, GOI, New Delhi and other Members of the NABMGR visited the Bureau on 05.03.2013.
- The Technical Advisor and Veterinary Officer from Punjab Livestock Development Board visited on 06.03.2013.
- Dr. Tinni Sawhney, Programme Director, South Asia Pro Poor Livestock Policy Programme, New Delhi visited on 12.03.2013.

Teaching

The Scientists of NBAGR have been approved as Post Graduate faculity by the Academic Council of National Dairy Research Institute and Indian Veterinary Research Institute Deemed Universities, in the disciplines of Animal Biotechnology, Animal Genetics & Breeding and Biochemistry. They are actively involved in the teaching of regular courses of Master and Ph.D programmes. Besides, four M.Sc. students registered with NDRI Karnal are being guided for their thesis research work.

Personnel

- Scientific
- Technical
- Administrative
- Skilled Supporting Staff
- Appointments/Promotions
- Transfers/Joinings


29 वाँ
ना दिवस


हिन्दी चेतना माह


29 वाँ

Scientific

Sr. No.	Name of Scientist	Designation
1.	Dr. B.K. Joshi	Director
2.	Dr. D.K. Sadana	Pr. Scientist
3.	Dr. B. Parkash	Pr. Scientist
4.	Dr. R.K. Vijh	Pr. Scientist
5.	Dr. Anand Jain	Pr. Scientist
6.	Dr. M.S. Tantia	Pr. Scientist
7.	Dr. N.K.Verma	Pr. Scientist
8.	Dr. P.K. Vij	Pr. Scientist
9.	Dr. R.A.K. Aggarwal	Pr. Scientist
10.	Dr. P.K. Singh	Pr. Scientist
11.	Dr. R.K. Pundir	Pr. Scientist
12.	Dr. R.S. Kataria	Pr. Scientist
13.	Dr. Anil Kumar Mishra	Pr. Scientist
14.	Dr. Monika Sodhi	Pr. Scientist
15.	Dr. Jyostna Behl	Pr. Scientist
16.	Dr. Satpal Dixit	Pr. Scientist
17.	Dr. Dinesh Kr. Yadav	Pr. Scientist
18.	Dr. Manishi Mukesh	National Fellow
19.	Dr. Reena Arora	Pr. Scientist
20.	Dr. Rahul Behl	Sr. Scientist
21.	Dr. Avnish Kumar	Sr. Scientist
22.	Dr. Dinesh Kumar	Sr. Scientist (upto 18-05-2012)
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. K.N. Raja	Scientist
31.	Dr. Jayakumar S.	Scientist
32.	Dr. Sonika Ahlawat	Scientist

Technical

S. No.	Name	Designation
1.	Dr. P. S. Dangi	T (7/8)
2.	Sh. S. K. Jain	T (7/8)
3.	Dr. P.S. Panwar	T-6
4.	Sh. Sanjeev Mathur	T-6
5.	Sh. Moti Ram	T-5
6.	Sh. Harvinder Singh	T-5
7.	Sh. Sat Pal	T-5
8.	Sh. Jamer Singh	T-5

S. No.	Name	Designation
9.	Smt. Pravesh Kumari	T-5
10.	Sh. Ramesh Kumar	T-4
11.	Sh. Subhash Chander	T-4
12.	Sh. Rakesh Kumar	T-4
13.	Sh. Naresh Kumar	T-4
14.	Sh. Ashok Kumar	T-4
15.	Sh. Mahavir Singh	T-4
16.	Sh. Vijay Singh	T-4
17.	Sh. Om Prakash	T-3
18.	Sh. Ramesh Chand	T-3

Administrative

S. No.	Name	Designation
1.	Sh. Jagtar Singh	A.O.
2.	Sh. Sunil Kumar	F&AO
3.	Sh. Balkar Singh	AAO
4.	Sh. Karambir	PS to Director
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

Appointments/Promotions

1. Dr. R.S. Kataria, Sr. Scientist has been promoted to the post of Principal Scientist w.e.f. 01.01.2009.

2. Dr. Monika Sodhi, Sr. Scientist has been promoted to the post of Principal Scientist w.e.f. 28.09.2010.

3. Dr. Jyotsna Behl, Sr. Scientist has been promoted to the post of Principal Scientist w.e.f. 29.09.2010.

4. Dr. Dinesh Kumar Yadav, Sr. Scientist has been promoted to the post of Principal Scientist w.e.f. 05.05.2011.

5. Dr. Reena Arora, Sr. Scientist has been promoted to the post of Principal Scientist w.e.f. 25.07.2011.

6. Smt. Parvesh Kumari, T-4 has been promoted to the next higher grade of T-5 through five yearly assessment w.e.f. 01.07.2012.

7. Sh. Sunil Kumar has been promoted from AF&AO to the post of F&AO w.e.f. 18.12.2012 (AN).

8. Sh. Pawan Kumar Gupta has been promoted from JAO to the post of AF&AO w.e.f. 29.12.2012 (AN).

9. Sh. Balkar Singh has been promoted to the post of Asstt. Admn. Officer w.e.f. 15.06.2011.

10. Granted 2nd financial upgradation to Sh. Karambir, PS to Director w.e.f. 03.03.2013.

Transfer/joining:

1. Sh. Jagtar Singh joined NBAGR, Karnal as Admn. Officer on 14.05.2012 on inter-institutional transfer from ICAR Research Complex, Goa.

2. Dr. Anil Kumar Mishra was selected as Principal Scientist and joined NBAGR on 29.08.2012. He was promoted as Principal Scientist w.e.f. 01.01.2009 through Career Advancement Scheme.

3. Dr. Dinesh Kumar, Sr. Scientist (Biotechnology) was relieved from NBAGR, Karnal to join CABIN, IASRI, New Delhi on 18.05.2012.

4. Sh. Yoginder joined at NBAGR as Assistant w.e.f. 29.06.2012.

राजभाषा प्रकोष्ठ की गतिविधियां

राजभाषा संबंधी बैठकें

संस्थान राजभाषा कार्यान्वयन समिति की बैठकें प्रत्येक त्रैमासिक अंतराल पर नियमित रूप से दिनांक 10 मई, 21जुलाई, 18 अक्तूबर 2012 व 17 जनवरी 2013 को आयोजित की गई। निदेशक महोदय की अध्यक्षता में सम्पन्न इन बैठकों में संस्थान द्वारा राजभाषा हिन्दी में किये गए कार्यों की समीक्षा की गई। प्रत्येक बैठक में विभिन्न अनुभागों एवम् इकाईयों के प्रभारियों ने भाग लिया। दिनांक 18 अगस्त 2012 को संस्थान राजभाषा सलाहकार समिति की बैठक भी की गई, जिसमें सितम्बर–2012 में हिन्दी चेतना माह आयोजन कार्यक्रम की रूपरेखा तैयार की गई।

राजभाषा कार्यान्वयन समिति की त्रैमासिक बैठक

हिन्दी चेतना माह

वर्ष 2012 के सितम्बर माह को हिन्दी चेतना माह के रूप में मनाया गया। इस अवधि में ब्यूरो कर्मियों के लिये विभिन्न प्रतियोगिताएं आयोजित की गई। निबंध लेखन प्रतियोगिता कन्या भ्रूण हत्या – एक सामाजिक अभिशाप विषय पर थी जिसमें श्रीमती अनीता चंदा, श्री कर्मबीर मलिक, श्रीमती अमीता कुमारी ने क्रमशः प्रथम, द्वितीय तथा तृतीय स्थान प्राप्त किया। अनुवाद प्रतियोगिता में श्रीमती अनीता चंदा, श्री कर्मबीर मलिक, श्री राकेश कुमार ने क्रमशः प्रथम, द्वितीय तथा तृतीय स्थान प्राप्त किया। टिप्पणी व मसौदा लेखन प्रतियोगिता में श्री राकेश कुमार, श्री कर्मबीर मलिक, श्रीमती अनीता चंदा ने क्रमशः प्रथम, द्वितीय तथा तृतीय स्थान प्राप्त किया। वर्ष 2011–12 हेतु उत्कृष्ट हिन्दी कर्मियों का चयन किया गया, जिसमें श्री कर्मबीर मलिक ने प्रथम, श्री बाबु राम ने द्वितीय तथा श्री सोपाल, श्री विजय सिंह तथा श्री महावीर सिंह ने संयुक्त रूप से तृतीय स्थान प्राप्त किया। हिन्दी दिवस (14 सितम्बर 2012) के अवसर पर एक आशु भाषण प्रतियोगिता का आयोजन किया गया। इस प्रतियोगिता में डा. मोनिका सोढी, श्रीमती अमीता कुमारी, कु. अदिति शर्मा ने प्रथम, द्वितीय तथा तृतीय स्थान प्राप्त किया।

हिन्दी चेतना माह के दौरान प्रतियोगिता में भाग लेते ब्यूरोकर्मी

हिन्दी चेतना माह के अंतर्गत दिनांक 21 सितम्बर 2012 को ब्यूरो के स्थापना दिवस के शुभ अवसर पर हिन्दी में शोध–पत्र पोस्टर प्रदर्शनी का आयोजन किया गया, जिसमें वैज्ञानिकों तथा शोधवेत्ताओं ने बढ़–चढ़कर भाग लिया। इस प्रतियोगिता में श्रीमती करूणा असीजा व डा. पी.के सिंह ने प्रथम, डा. मनीषी मुकेश, अमित किशोर, अंकिता शर्मा, प्रवेश मुंजाल एवं मोनिका सोढी ने द्वितीय तथा प्रियंका बनर्जी, जे. जोशी, वी. दुरेजा, एस. राणा, उपासना शर्मा एस., डा. एम.एस. टाँटिया व डा. आर.के. विज ने तृतीय स्थान प्राप्त किया। हिन्दी चेतना माह के

ब्यूरो स्थापना दिवस पर आयोजित
शोध–पत्र पोस्टर प्रदर्शनी

अंतर्गत आयोजित हुई सभी प्रतियोगिताओं के विजेताओं को पुरस्कृत किया गया।

हिन्दी पत्रिका पशुधन प्रकाश का प्रकाशन

संस्थान की वार्षिक हिन्दी पत्रिका पशुधन प्रकाश के तृतीय अंक (वर्ष 2012) का प्रकाशन किया गया। इस पत्रिका में देश की विभिन्न संस्थानों/विश्वविद्यालयों के पशुविदों से प्राप्त 21 आलेखों को शामिल किया गया। पत्रिका का विमोचन ब्यूरो के स्थापना दिवस समारोह के अवसर पर किया गया। पत्रिका के द्वितीय अंक (वर्ष 2011) के प्रथम तीन श्रेष्ठ लेखों को पुरस्कृत भी किया गया। इसमें मोनिका सोढी, बी.पी. मिश्रा, एम. मुकेश, आर कपिल, पी. कुमारी, के. लेत्सुखाटे एवम् डा. बी.के. जोशी द्वारा लिखित लेख को प्रथम स्थान व डा. के.पी. सिंह को द्वितीय तथा डा. सोनिका अहलावत, डा. रेखा शर्मा और डा. मोहन सिंह ठाकुर के लेखों को संयुक्त रूप से तृतीय स्थान प्राप्त हुआ।

हिन्दी व्याख्यान आयोजन

संस्थान में स्टाफ सदस्यों का हिन्दी राजभाषा के प्रति रूझान बढ़ाने तथा साथ ही साथ जैव विविधता के प्रति जागरूक करने के उद्देश्य से दिनांक 13 मई 2012 को संस्थान में एक हिन्दी व्याख्यान जैव विविधता संरक्षण – सुरक्षित भविष्य की ओर विषय पर आयोजित किया गया। जिसमें श्री दिनेश शर्मा जी ने विषय पर अपने विचार प्रस्तुत किये।

दिनांक 18–9–12 को तिमाही हिन्दी कार्यशाला/व्याख्यान आयोजन की श्रृंखला के अंतर्गत ब्यूरो कर्मियों को तनाव मुक्ति के कारण व निदान विषय पर राजयोग शिक्षा केन्द्र से आमंत्रित बहन कु. फाल्गुनी जी ने तथा बहन कु. रेणु जी ने बड़े ही व्यवहारिक ढंग से सकारात्मक चिंतन – तनाव से मुक्ति विषय पर व्याख्यान देकर मार्ग दर्शन किया तथा ब्यूरो कर्मियों को लाभान्वित किया।

हिन्दी कार्यशाला के दौरान आयोजित व्याख्यान

ब्यूरो की वेबसाईट का द्विभाषीकरण

राष्ट्रीय पशु आनुवंशिक संस्थान ब्यूरो की वेबसाईट का द्विभाषीकरण किया गया है और अब यह वेबसाईट हिन्दी में भी उपलब्ध है। वेबसाईट के मसौदे का हिन्दी अनुवाद ब्यूरो की राजभाषा इकाई द्वारा किया गया है।

ब्यूरो की द्विभाषी वेबसाईट

एन.बी.ए.जी.आर. गीत

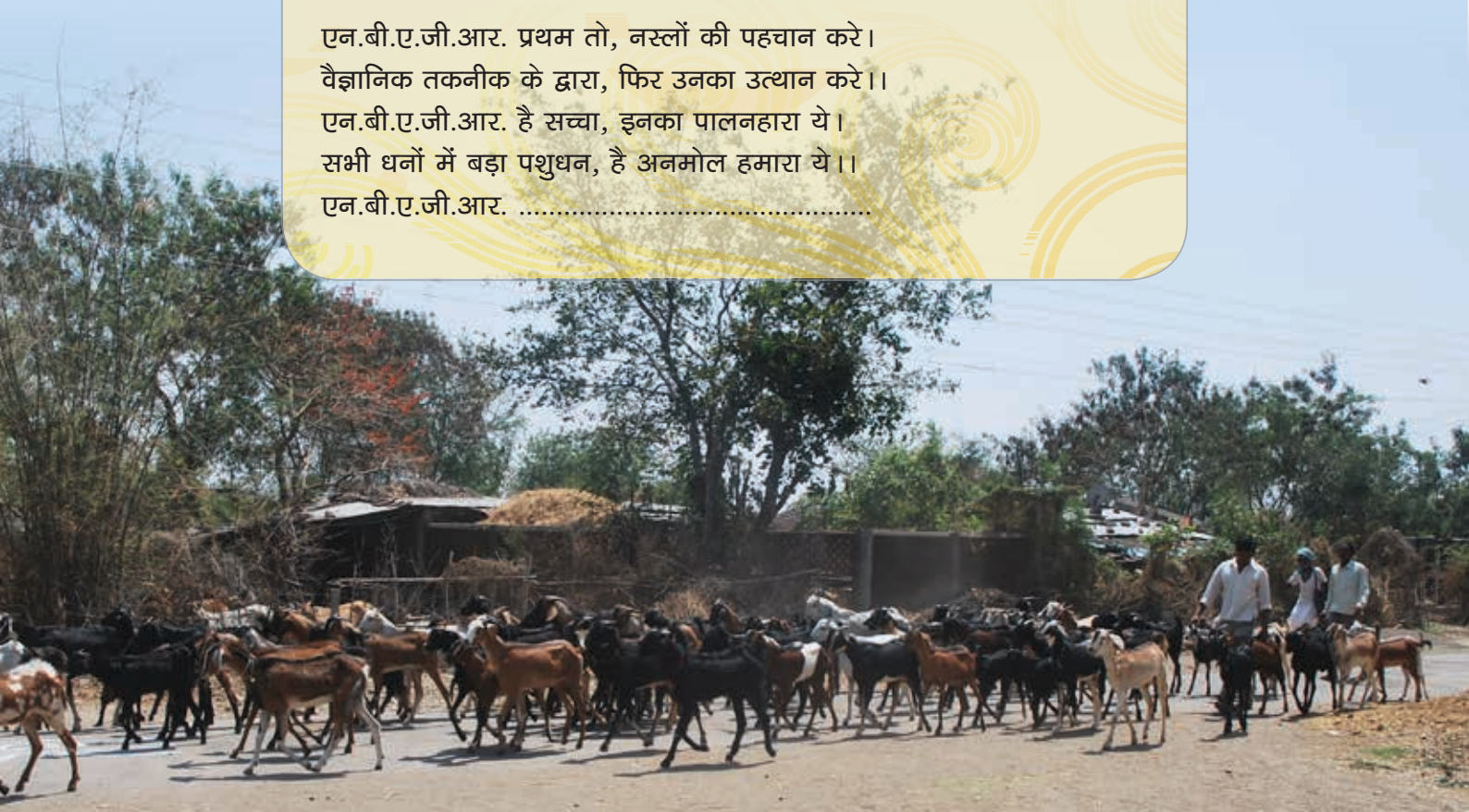
एन.बी.ए.जी.आर. –एन.बी.ए.जी.आर.
देता है ज़्यादा हमको, कम खाकर करे गुज़ारा ये।
सभी धनों में बड़ा पशुधन, है अनमोल हमारा ये।।
एन.बी.ए.जी.आर. का यही मिशन है, फूले–फले पशुधन का संसार।

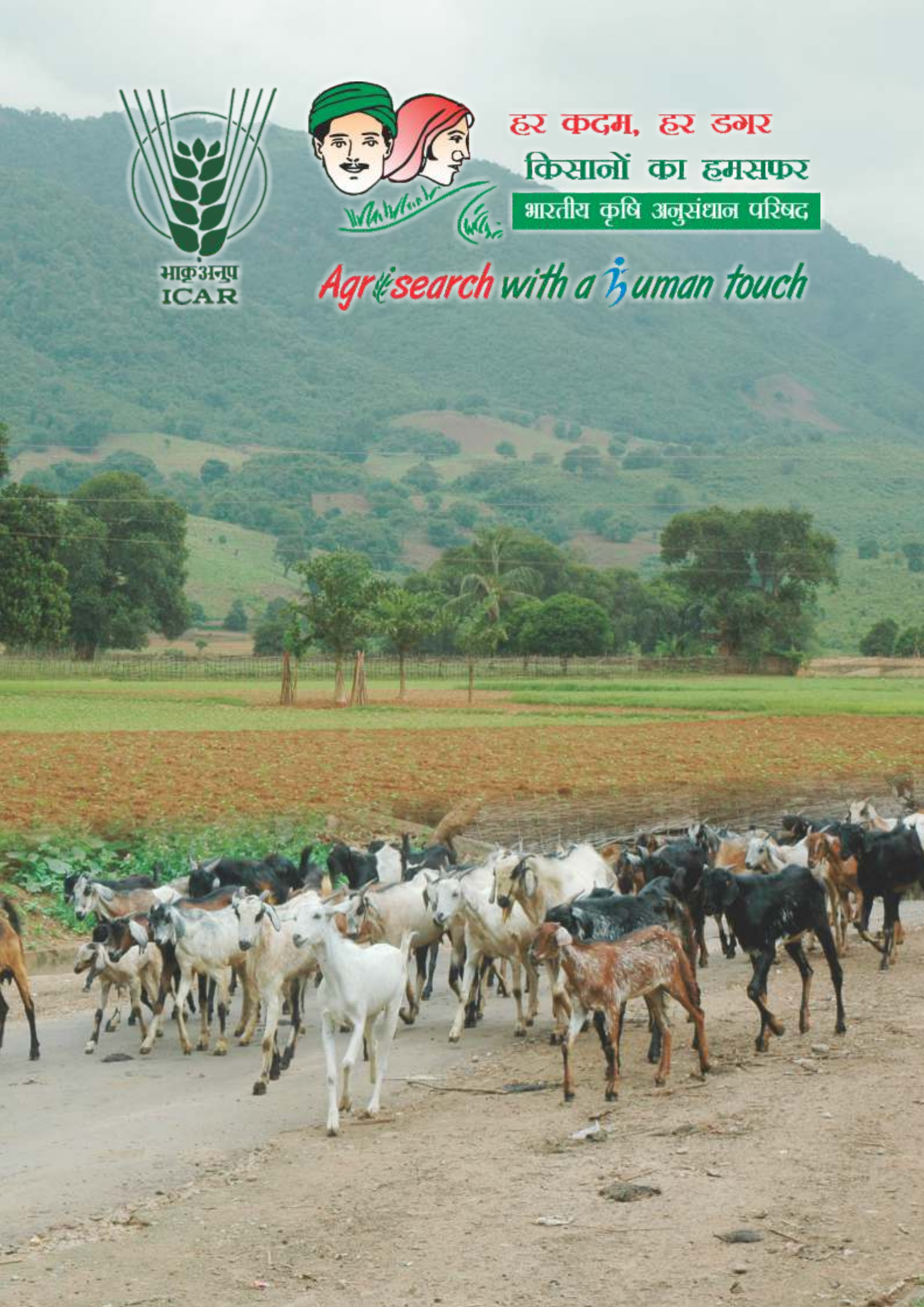
सुन्दर नस्लें हैं अपने इन, सभी पालतू पशुओं की।
गुण की ये है खान, यहाँ है सब कुछ इनका उपयोगी।।
लाखों–लाख गरीबों के, जीने का खास सहारा ये।
सभी धनों में बड़ा पशुधन, है अनमोल हमारा ये।।
एन.बी.ए.जी.आर. .....

भांति–भांति के पशुओं का, भरपूर खज़ाना हम पे है।
भारत के गाँवों की सचमुच, सुख–समृद्धि इनसे है।।
कुदरत ने उपहार दिया है, हमको बेहद प्यारा ये।
सभी धनों में बड़ा पशुधन, है अनमोल हमारा ये।।
एन.बी.ए.जी.आर.....

इस अनमोल सम्पदा को, मिलजुल के हमें बचाना है।
चुन–चुन कर उत्तम नस्लों को, आगे और बढ़ाना है।।
राष्ट्रीय पशु आनुवंशिक, संसाधन ब्यूरो का नारा ये।
सभी धनों में बड़ा पशुधन, है अनमोल हमारा ये।।
एन.बी.ए.जी.आर.....

एन.बी.ए.जी.आर. प्रथम तो, नस्लों की पहचान करे।
वैज्ञानिक तकनीक के द्वारा, फिर उनका उत्थान करे।।
एन.बी.ए.जी.आर. है सच्चा, इनका पालनहारा ये।
सभी धनों में बड़ा पशुधन, है अनमोल हमारा ये।।
एन.बी.ए.जी.आर. .....




भाकृअनुप
ICAR
हर कदम, हर डगर
किसानों का हमसफर
भारतीय कृषि अनुसंधान परिषद
Agrisearch with a human touch

NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES

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