वार्षिक प्रतिवेदन
ANNUAL REPORT
2017-18

भाकृअनुप–राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो
करनाल–132001 (हरियाणा) भारत
ICAR-National Bureau of Animal Genetic Resources
Karnal-132001 (Haryana) INDIA

With Best Compliments

Director, ICAR-NBAGR

वार्षिक प्रतिवेदन
ANNUAL REPORT

2017 - 18

रा.प.आ.सं.ब्यूरो

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

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

वार्षिक प्रतिवेदन
ANNUAL REPORT
2017-18

भाकृअनुप-राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो
ICAR-National Bureau of Animal Genetic Resources

Credit Line...

Published by

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

Compiled by

Dr N K Verma, Pr. Scientist & I/c, PME Cell
Dr Sonika Ahlawat, Scientist
Dr Jayakumar S, Scientist

Editors

Dr N K Verma, Pr. Scientist & I/c, PME Cell
Dr R S Kataria, Pr. Scientist
Dr A K Mishra, Pr. Scientist
Dr Saket Kumar Niranjan, Sr. Scientist
Dr Jayakumar S, Scientist
Dr Sonika Ahlawat, Scientist

Photographs

I/C, P&E Unit

Assistance

Dr P S Dangi, A.C.T.O.
Ms Indu Bala, Steno Gr.III

Printing

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

Contents

History and Profile

Research Accomplishments

Research Projects and Publications

Capacity Building

Other Activities

Personnel

हिन्दी खण्ड

From Director's Desk ...

As the Director of ICAR- NBAGR Karnal, a premier Institute of national and international repute, I feel pleasure to present the Annual Report which has glimpses of the achievements made in the areas of research, training, extension, education and technology management during 2017-18.

Since its establishment on 21 September 1984, the institute is continuously working to identify and manage the genetic potentials of Indian farm animal genetic resources. ICAR-NBAGR is the only institute of the country catering to breed identification, characterization, evaluation, conservation, utilization and their registration. During the glorious journey of scientific excellence since 1984, we have characterized and registered 41 cattle, 13 buffalo, 28 goat, 42 sheep, 7 horse and ponies, 9 camel, 7 pig, 1 yak, 1 duck, 1 geese, 1 donkey and 18 chicken breeds so far. A brief report of overall achievements made during the year 2017-18 has been presented through this document.

During the year, phenotypic and genotypic characterization of non-descript cattle population of Kerala and Tamil Nadu, Manda buffalo of Odisha, Chitarangi sheep of Punjab and Rajasthan, Dumba sheep, Bidri and Nandidurga goats of Karnataka and Yak population of Ladakh was carried out through field surveys. In addition, some more projects were initiated on phenotypic as well as genetic characterization of cattle, buffalo, sheep and goat populations/ breeds. A1A2 allelic and genotypic profile has also being generated which I hope will add value to our indigenous cattle and buffaloes. Attempts were also made to identify candidate genes and pathways underlying meat quality in Mandya sheep and endurance trait in high altitude adapted Zanskar ponies.

Conservation is an important mandate of NBAGR under which conservation of Sahiwal and Hariana cattle through Gaushalas is in progress and a total of 46 calves (5 Sahiwal and 41 Hariana) were born. For *ex- situ* conservation, fibroblast cell lines of Manipuri horse and Kutchi camel were generated and preserved. In the National Gene Bank at NBAGR, semen doses of Dangi, Rathi, Khillar and Nagori cattle breeds were added.

Under the Network program on AnGR, 10 new breeds/populations have been selected for characterization. These efforts will help in identification of new populations and make them eligible for breed registration. Institute is also providing consultancy services of cytogenetic screening and disease testing (BLAD, DUMPS, Citrullinemia and Factor XI deficiency) of breeding males to various agencies of the country.

Institute Research Committee (IRC) meetings were held on time to review the progress of on-going projects and approve the final report of completed projects. New proposals proposed were also screened and improved through in-house discussions. Bureau is currently running

22 research projects including five externally funded and one National Fellow project. A total of 33 research papers and 12 technical/ popular articles were published in national and international journals of high impact factor. Five books, five monographs and twenty four book chapters were also published during the reported period. The institute has also contributed to capacity building by organizing five training programs for research workers, teachers, field veterinarians and officials of animal husbandry departments. The expertise of bureau scientists was recognised at various scientific fora where they participated and presented their work.

Scientists of the Bureau participated actively to support some of the national programmes like Mera Gaon Mera Gaurav, Jai Kisan Jai Vigyan and Rashtriya Swachhta Abhiyan. Five exhibitions on AnGR were organized at various places to showcase institute's activities and sensitize farmers about the benefits of indigenous animal genetic resources. Dr. T Mahapatra, Secretary (DARE) & DG, ICAR and Deputy Director General Dr. J K Jena, visited the bureau and appreciated our work. Foundation Day of Bureau, Biodiversity day, Republic Day, Independence Day, Vigilance Week, Hindi Pakhwada were celebrated at NBAGR campus with full enthusiasm. For the first time NBAGR has started "Breed conservation awards" for people, institutes and organization involved in keeping and rearing indigenous registered livestock breeds.

I am grateful to Dr. T Mahapatra, Secretary (DARE) & DG, ICAR, Dr. J K Jena, DDG (AS), Dr R S Gandhi, ADG (AP&B) and Dr Vineet Bhasin, Pr. Sci., ICAR, New Delhi for their support for the overall development of this Institute. Guidance received from Research Advisory Committee is gratefully acknowledged. With a great sense of pride and satisfaction, I congratulate all the scientists, technical, administrative and other staff members of the institute for their fabulous contribution in the progress of the institute. At the same time, I would also like to thank the editorial committee which shaped the Bureau's achievements in the form of this document. We always welcome the suggestions and criticism for our further improvement.

(ARJAVA SHARMA)
DIRECTOR

EXECUTIVE SUMMARY

ICAR-National Bureau of Animal Genetic Resources has been the nodal institute working for the benefit and upliftment of indigenous livestock and poultry breeds, in the country. It has a broader mandate of 1) Identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country; and 2) coordination and capacity building in animal genetic resources management and policy issues. Three Divisions - 1) Animal Genetic Resources 2) Animal Genetics, and 3) Animal Biotechnology have been created in 2013 to achieve the institute's mandate. In addition, two units namely- Livestock Information & Management and Network Project are also functioning to support the Institute's activities.

Total expenditure under different heads (Capital, Revenue and Pension & retirement benefits) was Rs. 1318.49 Lakhs against the total receipt of Rs. 1335.3 Lakhs during financial year of 2017-18. Under Network project, total expenditure was Rs. 76.6 Lakhs, against Receipt of Rs. 77.0 Lakhs. Bureau could raise the revenue of Rs. 35.66 Lakhs during 2017-18 through its different activities.

Nine new breeds of indigenous livestock and poultry – one of cattle, two of goat, and one each of horse, pig, yak, geese, duck and chicken – were registered by ICAR-NBAGR. Five breeds were from NE region of the country. The institute has first time registered the indigenous breeds of yak, duck and geese. Total number of registered indigenous livestock and poultry breeds have reached 169.

Under the newly assigned mandate, study for evaluating livestock policies and programmes for the management of AnGR in Haryana and Punjab was initiated this year. Questionnaire based information on activities of animal husbandry was collected from Farmers/livestock keepers and other stakeholders.

Eight indigenous sheep breeds/populations of India were classified based on seven morphometric traits using classical - discriminant functional analysis (DFA), and heuristic - artificial neural networks (ANN) and support vector machine (SVM) methods. In the binary partition 1-to-1 and 1-to-Rest, the SVM model performed the best over the other methods.

Manda and Sambhalpuri buffaloes were surveyed in Odisha state. Manda are distributed in Koraput district of Odisha. Manda possesses small and compact body. Body colour is light blackish-brown. Horns are long and heavy with typical shape. These are excellent draught animal for ploughing in hard laterite soil. Milk yield ranges from 2 to 4 kg /day. Sambalpuri buffalo is found in Sambalpur district of Odisha and adjoining districts of Chhattisgarh. Dwindling population of Sambalpuri buffaloes in native tract is cause of concern. Various biometric traits of Odisha buffaloes could reveal distinct grouping by discriminant analysis.

Characterization of Nandidurga and Bidri goats of Karnataka was completed. Nandidurga goats are distributed in Chitradurga, Tumkur and Davangere, whereas Bidri is distributed in Bidar and Kalaburagi districts of Karnataka. Nandidurga is white, whereas, eyelids are brown or black. Ears are leafy and pendulous. In Bidri goats, coat colour, muzzle, eyelids and hooves are Black. Ears were pendulous. Both goats were reared for meat purpose only.

During survey in Nubra (Ladakh) region of Jammu & Kashmir, local yak population was characterized. They are reared by Buddhist community located for milk, meat, manure, hair fibre and transport. Yaks of Nubra are medium and moderate. Coat colour is dark brown to black. Horns are curved and placed laterally upward and backward. Ears are small. Pelvis is wider than shoulder region. Most yaks are reared under pastoralism. Preference of cross-hybrids was evident in the region and was a significant cause of decline of yak population.

Native donkey population was characterized in Ladakh region of Jammu & Kashmir. Ladakhi donkey is reared by Buddhist communities for transportation and manure. Animals are medium sized and docile. Coat colour varies from light to dark grey, brown and black with light coloured or white belly. Animals are sure footed and able to track easily in night also. Donkey population has largely declined due to fading utility and decline human concern.

Chitarangi sheep was surveyed and characterized in Fazilka, Muktsar districts of Punjab, Sri Ganga Nagar district of Rajasthan. It is a carpet wool type sheep population. Chitarangi is medium to large in size. Coat colour is white with tan patches around the eyes, muzzle and on the ear. Serrations of different shape and depth are available on distal end of ear pinna. Average annual greasy wool production is 1.5 to 2 kg. Similarly, survey was conducted for Dumba sheep distribution and characterization. It is found mainly in Jaipur, Nagaur and Ajmer districts of Rajasthan. Coat colour is white and brown in majority. Ears are large in size, pendulous and drooping. Dumba is characterized by the deposition of fat in the tail. It is mainly reared for rituals (Qurbani).

Surveys were conducted for characterization of lesser known cattle populations (Vandharvi, Zari and Kamma) of Telangana state. Vandarvi of Warangal district is white colour. Face is long and concave. Horns are long and curved. Bullocks are used for agricultural work. Daily milk yield ranges from 1.0 to 2.5 kg. Jhari cattle are grey in majority. Body is small and cylindrical shape. Long face is the major character for differentiation. Body is smaller than Ongole cattle. Hump is moderate in bullocks and small in cows.

Germplasm repository at National Gene Bank, ICAR-NBAGR is being strengthened by preserving diversified form of germplasm (semen, embryos, DNA, epididymal sperms and somatic cells). Total 23975 semen doses of 8 cattle breeds and 400 somatic cell doses each of Katchi camel and Marwari horse were added for cryopreservation.

Manipuri Horse and Kutchi camel fibroblast cell lines were generated from skin explants for somatic cell banking. Ear marginal tissues of Manipuri horse and Kutchi camel were utilized for establishment of cell lines by attachment cell culture method. Primary culture was established using explants culture technique using fibroblast specific media. The cells were cryopreserved from 3rd to 6th passage.

Under the project for developing a model of sustainable improvement vis-à-vis conservation of indigenous cows in Guashalas. Three Gaushalas of Haryana were selected for the genetic improvement and conservation of Hariana and Sahiwal cows. A total of 52 of Hariana and 4 of Sahiwal were inseminated with maintain breed purity. Total 46 calves were born. In Sahiwal, daily milk yield ranged from 4.0 to 9.0 kg, whereas in Hariana ranged from 1.0 to 4.0 kg. Two health camps were also organized.

During genetic analysis Nandidurga and Bidri goats of Karnataka, all the markers were found polymorphic. Observed heterozygosity confirmed the sufficient level of diversity in both populations. Any large or recent genetic bottleneck was absent. 2D coordinate analysis showed both populations as distinct.

Microsatellite markers based data analysis of five Odisha buffalo populations indicated that Manda was highly diverged from all other populations. Structure analysis revealed Manda and Murrah being most distinct. Paralakhemundi had maximum admixture of Kalahandi buffalo. Median joining network indicated sharing of haplotypes between Chilika and swamp buffaloes. Chilika had more number of breed specific haplotypes also.

In order to genetically characterize Chitarangi and Dumba sheep, 237 and 243 distinct alleles, respectively were identified across the 24 markers. The mean F_{IS} (within population inbreeding estimates) was 0.096 and 0.043 in these two populations, indicating deficiency in the number of heterozygotes.

Transcriptomic profiles of skeletal muscles of Bandur and local sheep of Karnataka revealed a total of 20568 differentially expressed transcripts. Among these, 1236 were significantly down regulated and 602 up regulated in Bandur. All the differentially expressed genes could be classified into 132 Gene Ontology (GO) terms for biological process, 146 terms for cellular components and 117 terms for molecular functions. Prominent pathways detected that were relevant to meat quality.

To speculate the role of methylation in crossbred cattle fertility, the methylation profile of meiosis specific genes in spermatozoa of Sahiwal, HF and HF crossbred (Frieswal) was assessed. Higher DNA methylation was observed in DAZL, BvH and PIWIL1 genes of Frieswal bulls with poor sperm motility. To assess the functional effect, the expression of Boule, DAZL and BvH genes was significantly higher in HF, Sahiwal and good motility crossbred bulls as compared to Frieswal bulls with poor semen motility as control.

Genome wide SNPs and INDELs were identified in four yak populations -Arunachali, Himachali, Ladakhi and Sikkimi. Total SNPs identified at RD10 were 256051, 241934, 312518 and 150425, respectively. Overall, 579575 SNPs were of high quality with coverage of 9.42%. Ladakhi and Sikkimi yak populations were found to be distinct.

Transcriptome analysis of Zanskar PBMCs during endurance exercise at high altitude was generated to identify differentially expressed genes before and after endurance exercise at high altitude. A total of 646 genes were found to be differentially expressed in Zanskar ponies during exercise.

Functional profile of HSPs genes in Chokla, Magra, Marwari, and Madras Red sheep was assessed under normal and stressed condition. During genotyping of 5 selected loci for SNPs were found to carry selective advantage for heat tolerance. Genotypes at 2 loci were found significantly affecting the T3 hormone concentration in these sheep. Gene expression of HSPs was found to be the highest in Madras Red and least in Marwari.

Allelic and genotypic profile for thirteen known variants of beta casein was estimated across Indian native, exotic and crossbred cattle. Amongst the 13 known variants, other than A1/A2 only B variant (ser122 arg) was observed across the three cattle types. Expression analysis of beta casein in milk of Karan Fries was also carried out. Trials to ascertain the effect of BCM7 and BCM9 in mice (diabetes progression) was completed and samples were collected for further analysis.

EXECUTIVE SUMMARY

Genotyping by Sequencing (GBS) data generated in 17 buffalo populations (625 animals) was utilized to estimate linkage disequilibrium. Total 23,306 SNPs were genotyped. Genetic distance block of 20-25 kb was found for riverine buffaloes and 25-50 kb for the swamp buffaloes, assuming r^2 greater than 0.2. Number of SNPs - 1,50,000 for riverine and 1,20,000 for swamp buffaloes were determined to be required for an association mapping.

Total 23,306 SNPs were analysed for identification of admixture among 17 buffalo breeds/populations. There was high degree of admixture for most of the buffalo populations of the country except Chilika, Mehsana, Toda, Assam and Manipuri. Spatial genetic analysis allowed the grouping of all the populations into eleven groups, largely by region-wise.

Genome Wide Association Studies was carried out based on SNP markers and phenomic data on milk traits of 1763 daughters of the 12 sires. The Manhattan plot suggested that the surrounding genomic region had a strong association with the milk yield trait. BLUP and BLUE of the trait based on SNP effects were also estimated. After availability of SNP effects, the predicted value of the trait can be estimated.

Milk transcriptome was generated for different lactation stages of buffaloes. Major pathways of up regulated genes were MAPK signalling pathway (III vs I stage), calcium regulation in the Cardiac ((III vs II stage), BDNF Signalling Pathway (II vs I) and exercise induced circardian regulation (II vs I) during different stages of lactation. *De novo* assembly of the buffalo transcripts was also carried out.

Loci of different lethal genetic diseases including Jersey Haplotype (JH1), Holstein haplotypes -HH3, HH4 and Holstein cholesterol deficiency (HCD) were characterized in Indian cattle population. Two mutant alleles-JH1 and HH4 in heterozygous condition were identified in Jersey and Holstein genetic groups, respectively. PCR based protocols were developed for screening of JH1 and HH3 in cattle.

Institute also provides the genetic defect/disease testing services to the different government agencies. During the reported period, 344 bulls/males were screened for chromosomal defects. 142 bulls were screened for genetic diseases. One bull was found to carry the chromosomal defect. Rs. 8,30,500/- was generated as revenue.

Under Network project, 9 new populations have been undertaken for characterization and 2 breeds are being conserved in their habitat.

A total of 7 research projects were completed during last year. At present 22 research projects including five externally funded and one National Fellow projects are running in the institute.

Total 33 research papers were published in National and International Journals of high impact factor. Twelve technical/popular articles were published. Five each of books and monographs were also published by the institute.

One each training of Short Course and Model Training Course was conducted for scientific and academic staff. Two training programmes were organized for upscaling the skill of administrative, technical and supporting staff of ICAR institutes.

Scientists of the Bureau participated in Mera Gaon Mera Gaurav and visited various villages and created awareness among farmers on their doorsteps and field. Seven exhibitions on AnGR were organized at various places to showcase institute's activities and sensitize farmers about the benefits of indigenous animals. Institute also celebrated different occasions like Foundation Day of Bureau, Biodiversity day, Republic Day and Independence Day, Jai Kisan Jai Vigyan, Rashtriya Swachhta Abhiyan, Vigilance Week, International yoga day, Agricultural Education Day, Hindi Pakhwada in its premises.

In the Bureau library, to keep track of the current scientific/technical developments different journals including 23 foreign and Indian journals were subscribed.

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

A contingent of 22 staff members of NBAGR participated in the ICAR (North Zone) games. Basket Ball and Volley Ball Smashing teams reached up to semi-final round. Bureau staff participated in the various events of Annual Sport Meet-2018 organized on the occasion of Republic day.

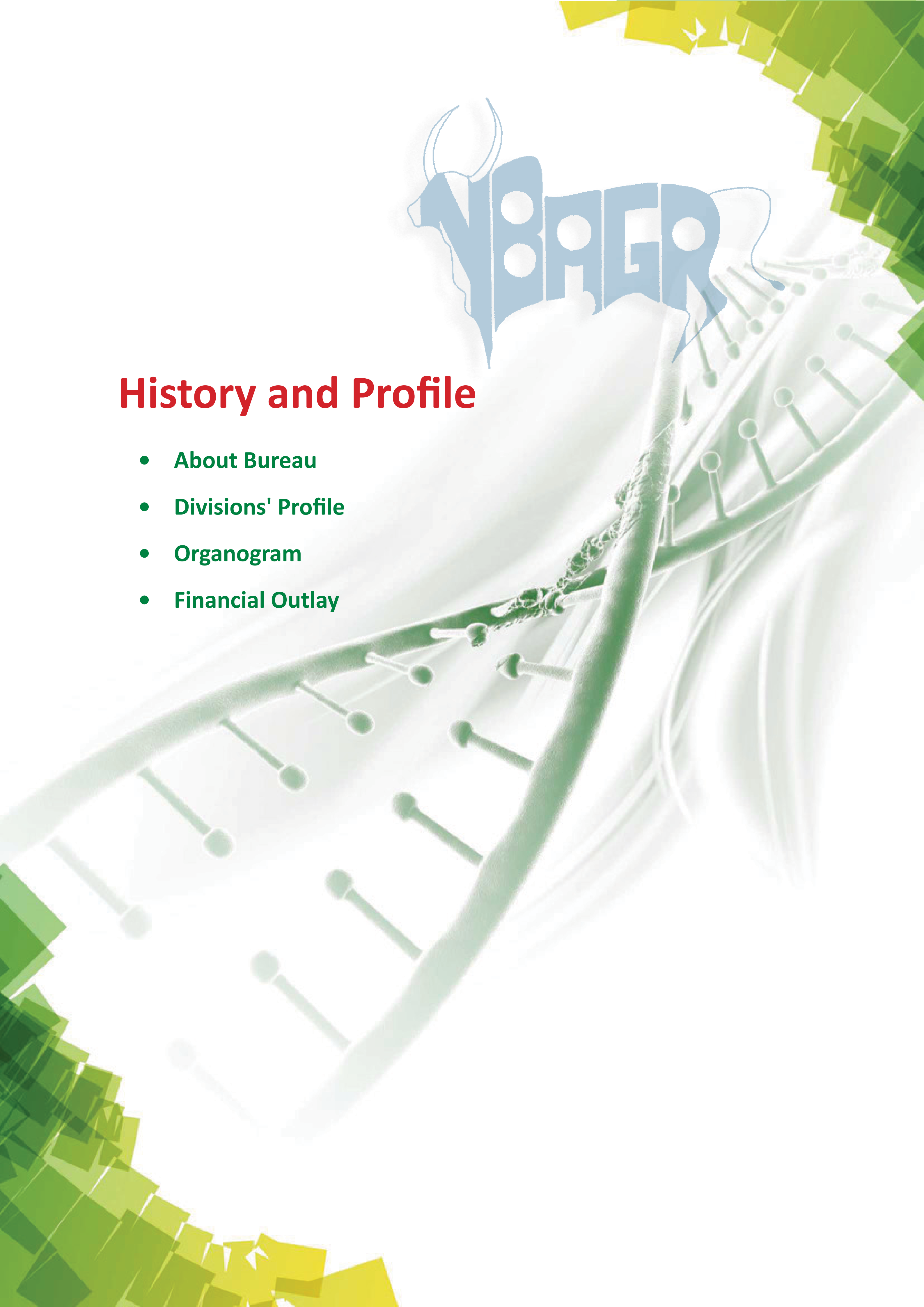
A number of distinguished persons including Secretary DARE & Director General ICAR, Deputy Director General (Fisheries & Animal Sciences), ICAR visited the institute.

Scientists were deputed for training programmes within the country and attended the workshops, symposia and conferences.

NBAGR scientists being the PG faculty of Animal Genetics & Breeding, Animal Biotechnology and Animal Biochemistry disciplines to ICAR-National Dairy Research Institute were actively involved in teaching various courses. The scientists are regularly guiding the students of different institutes and universities, including ICAR-NDRI for masters and PhD degrees.

At present 29 scientific, 16 technical, 17 administrative and 4 skilled staff persons are working at the Institute. Two scientists and four technical staff got their promotions to the next higher grade. Two staff members joined, two transferred and one superannuated during the year.

* * *



History and Profile

- About Bureau
- Divisions' Profile
- Organogram
- Financial Outlay

HISTORY AND PROFILE

About Bureau

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

MANDATE

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

OBJECTIVES

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

Divisions' Profile

Animal Genetic Resource Division

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

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

Animal Genetics Division

The present Animal Genetics Division is a transformed form of National Institute of Animal Genetics (NIAG) which was co-established with National Bureau of Animal Genetic Resources initially. Animal Genetics Division was established in the year 1996 and was formally approved in 2014 by the Indian Council of Agricultural Research with the objective 'Molecular, immunological, biochemical, cytogenetic characterization and candidate gene analysis of livestock species'. Scientists working in the fields of cytogenetics, immunogenetics, and molecular genetics became the part of Animal Genetics Division. The division has presently five principal scientists, three senior scientists, one scientist Senior Scale, one technical officer, one steno grade III and one skilled supporting staff.

During the period under report, scientists from this division completed three IRC and one DBT funded research projects successfully. Four IRC approved research projects are in progress. In addition to this, one ICAR-AGRI Consortia Research Platform project on Genomics is also running in the division. One of the important activities of the division is to provide consultancies/services for testing the breeding bulls for any inheritable abnormality. The research findings have been published in reputed journals of high impact factor.

Scientists also participated in national and international conferences and fetched awards for their presentations. Apart from this, scientists being the part of NDRI faculty were involved in teaching and guiding the M.Sc and Ph.D students.

Animal Biotechnology Division

Animal Biotechnology Division was established in 2014, by the orders of the council reorganizing the erstwhile DNA Fingerprinting Unit. Currently the division has a strength of six scientists, three technical and one skilled supporting staff. The division has the objective of 'Evaluation of functional genes/biomolecules for enhancing AnGR utilization'. The scientists of the division are working in the areas of mandated institutional activities. Various institute and externally funded projects on genetic characterization of livestock species are running with emphasis on utilization of genomic tools for the identification and evaluation of genes and transcripts associated with various production/disease resistance/ adaptation traits. At present there are two externally funded collaborative as well as four institute projects running or recently completed in the division. During last one year, under the National Fellow project on heat stress adaptation, remarkable achievements have been made through identification of unique transcripts and polymorphic loci to understand the molecular basis of thermal adaptation in indicus cattle and buffalo. In another externally funded, NASF project on A1A2 beta casein milk proteins, mice trials have been conducted by injecting BCM7 and BCM9 peptides as well as feeding A1 and A2 type beta casein milk diet and enormous data is being generated through proteomic and transcriptomic studies in order to confirm the role of A1 and A2 beta casein milk protein variants on health. During last one year work has also been carried out in sheep, helping in identification of differentially expressed genes and pathways associated with muscle tenderness, fat metabolism and ion transport in Bandur mutton sheep. While working on another institutional project on understanding the molecular basis of subfertility in cattle, scientists of the division have been able to document the variations in the number of methylated CpG sites in *Boule* gene promoter of crossbred, purebred indicus and exotic cattle, which could be the important reason for poor post thaw sperm motility in frozen semen. While working on the genetic characterization of buffaloes of Odisha state, hybrids of riverine and swamp have been identified among Chilika buffaloes. Microsatellite allelic diversity and mitochondrial D-loop sequencing indicates Manda being a unique population among Odisha buffaloes, deserving to be registered as new breed. Work of being carried out in indicus and crossbred cattle also is generating new data to understand the genetic basis of tick resistance. Being faculty in the Animal Biotechnology at NDRI, Karnal, scientists of the division are also involved in teaching and student guiding activities. Students and scientists of the division have received SOCDAB young scientist, best publication in Journal of Livestock Biodiversity and several poster presentation awards at various fora. Through publishing quality research papers in the international journals of high repute, the division topped the list again.

Livestock Information Management Unit

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

Network Project Unit

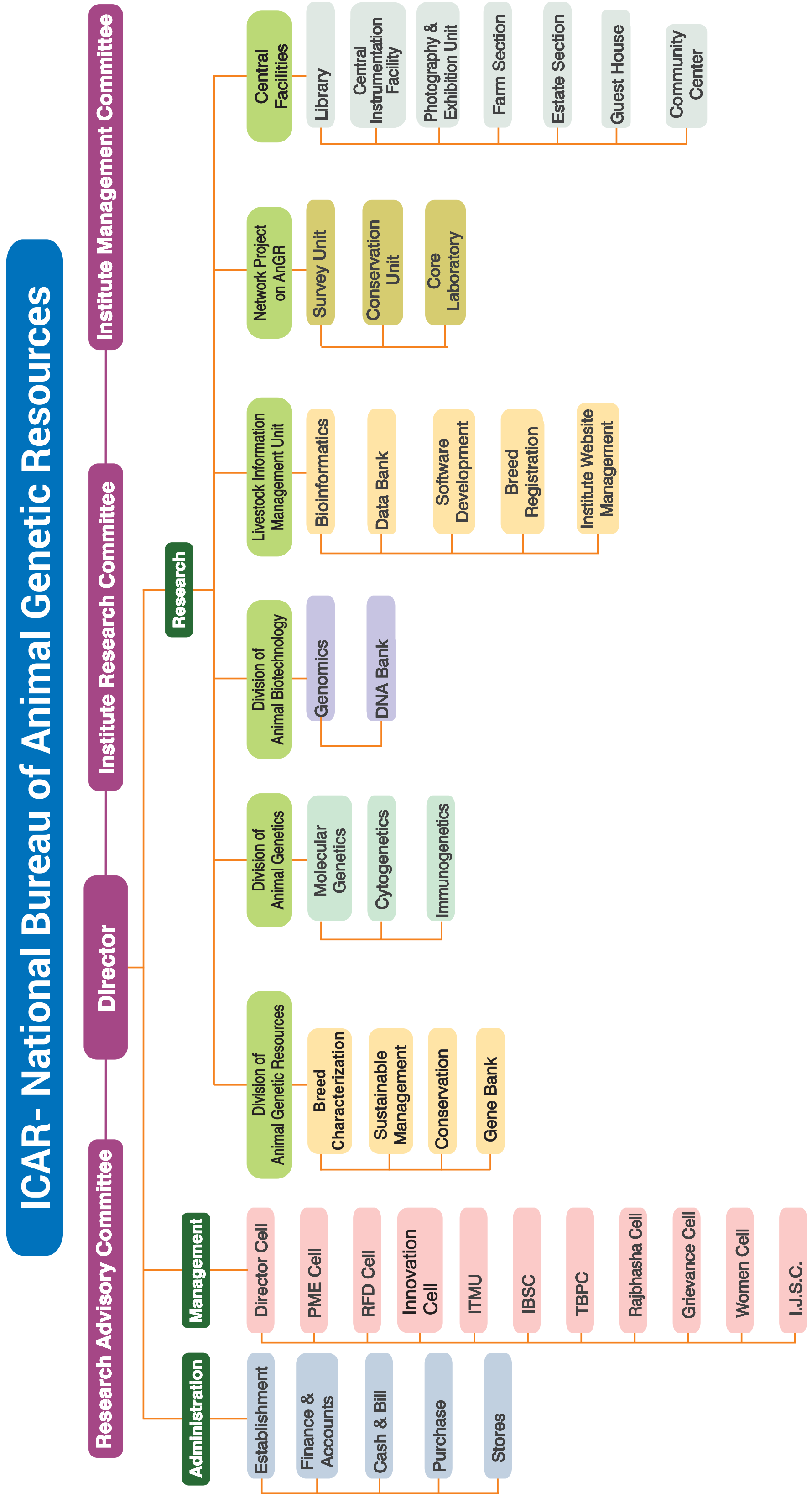
The Network project was initiated in 1996 with the following objectives:

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

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

* * *

Organogram


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

Financial Outlay

Budget Estimate under Grants & Network Project of NBAGR for financial year 2017-18 along with expenditure

(Rs. in Lakhs)

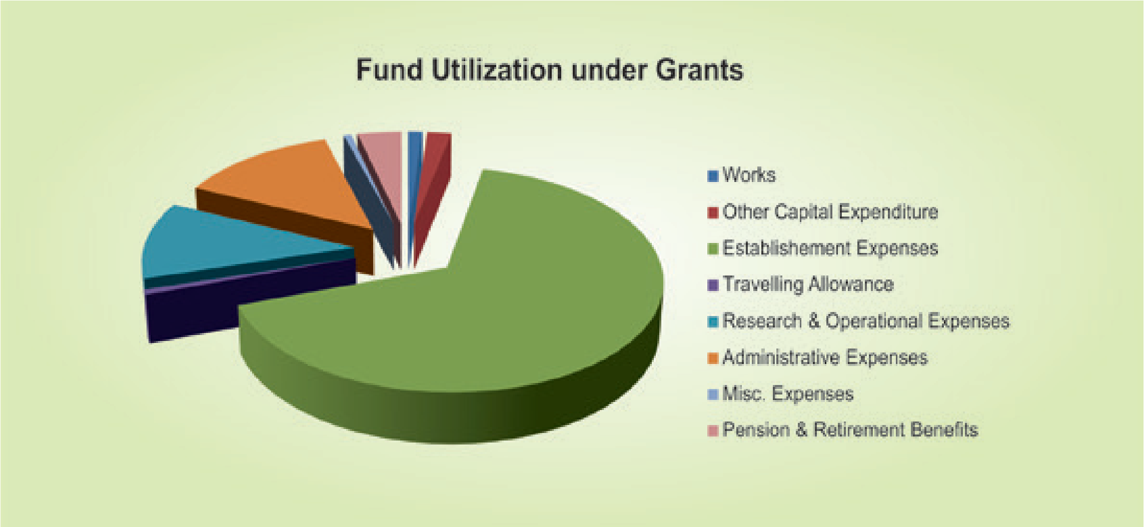
S. N.	HEAD	Grants		Network Project	
		RE	Exp.	RE	Exp.
1.	**Capital**				
	i) Works	15.80	15.77	0.00	0.00
	ii) Other capital expenditure	28.00	27.62	0.00	0.00
	Total Capital	43.80	43.39	0.00	0.00
2.	**Revenue**			77.00	76.60
	i) Establishment expenses	877.00	875.34	0.00	0.00
	ii) Traveling Allowance	10.00	9.76	0.00	0.00
	iii) Research & Operational expenses	157.00	151.69	0.00	0.00
	iv) Administrative Expenses	185.00	180.06	0.00	0.00
	v) Miscellaneous expenses	10.00	8.47	0.00	0.00
	Total Revenue	1239.00	1225.32	77.00	76.60
3.	**Pension & Retirement benefits**	52.50	49.78	0.00	0.00
	Grant Total	**1335.30**	**1318.49**	**77.00**	**76.60***

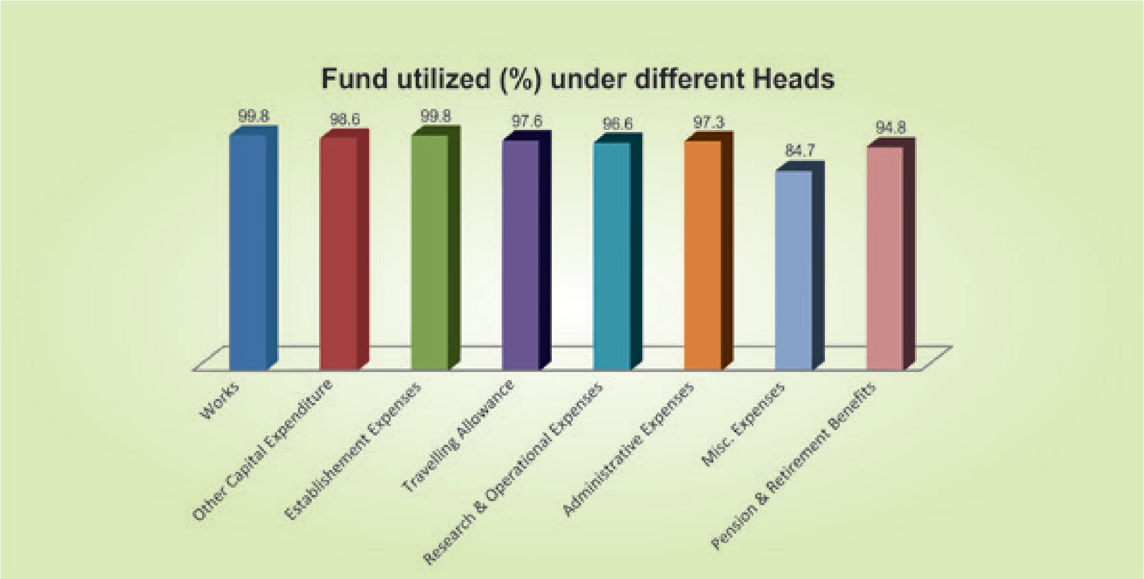
*Includes Releases of Rs.68.50 lakhs

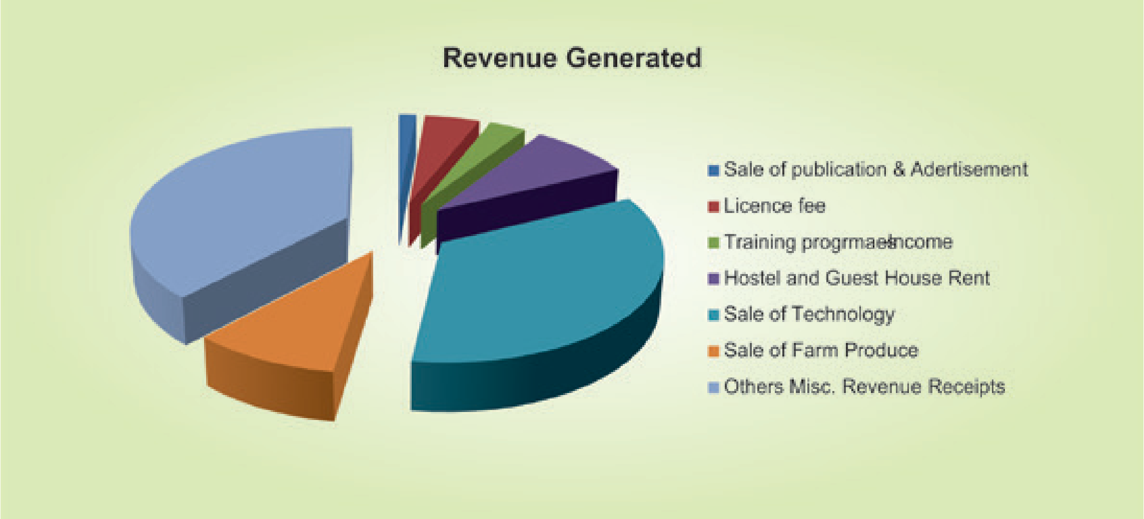
Revenue Generated during the year 2017-2018

S. N.	Head of Account	Amount (Rs)
1.	Sale of Publication & Advertisement	50,850
2.	Licence fee	1,65,394
3.	Training Programs - Income	1,11,000
4.	Hostel and Guest house rent	3,07,907
5.	Sale of Technology	12,30,260
6.	Sale of farm Produce	3,45,399
7.	Others Misc. Revenue Receipts	13,55,688
	Total	**35,66,498**

Target Achieved : 35.66 Lakhs


Fund Utilization under Grants
Works
Other Capital Expenditure
Establishement Expenses
Travelling Allowance
Research & Operational Expenses
Administrative Expenses
Misc. Expenses
Pension & Retirement Benefits


Fund utilized (%) under different Heads
99.8
98.6
99.8
97.6
96.6
97.3
84.7
94.8
Works
Other Capital Expenditure
Establishement Expenses
Travelling Allowance
Research & Operational Expenses
Administrative Expenses
Misc. Expenses
Pension & Retirement Benefits


Revenue Generated
Sale of publication & Adertisement
Licence fee
Training progrmae Income
Hostel and Guest House Rent
Sale of Technology
Sale of Farm Produce
Others Misc. Revenue Receipts

Research Accomplishments

- Livestock Information Management
- Identification & Characterization of AnGR
- Conservation of AnGR
- Genetic Characterization of AnGR
- Genomics & Evaluation of AnGR
- Network Project on AnGR

Livestock Information Management

New Registered Breeds of Indigenous Farm Animals

Breed Registration Committee in its meeting held on 4th August, 2017 at New Delhi approved registration of nine new breeds of livestock and poultry. This includes one breed of cattle, two breeds of goat, and one breed each of horse, pig, yak, geese, duck and chicken. The institute has registered first time indigenous breeds of yak, duck and geese. Now total number of indigenous breeds in the country is 169, which includes 41 cattle, 13 buffalo, 28 goat, 42 sheep, 7 horse, 9 camel, 7 pig, 18 chicken and one each of yak, duck, geese and donkey.

Lakhimi Cattle: Lakhimi cattle of Assam are distributed in entire state and reared for milk and draught purposes by local people. Total population is about 79 Lakhs. Animals are small sized, horned and have relatively short legs. Coat colour is variable, mainly brown and grey. Hump is medium in size and the backline is slightly curved. Udder is small and bowel shaped. Bullocks are excellent draft animals especially for carting and ploughing especially in the muddy fields for paddy cultivation. Lactation milk yield ranges from 270 to 375 kg.

INDIA_CATTLE_0200_LAKHIMI_03041

Salem Black Goat: Salem Black goats of Tamil Nadu are reared by Vanniyar and Kongu vellala Gounder communities for meat, skin and manure in Salem, Dharmapuri, Krishnagiri and Erode districts of Tamil Nadu. Estimated population is about 86 thousand. These goats are tall, lean and leggy. Colour is black. Ears are medium, semi-pendulous having leaf-like appearance. Both males and females have horns that are medium in size, curved upwards and backwards. In males, neck is thick, broad and well placed. Early sexual maturity, multiple births and low mortality are main features of this breed.

INDIA_GOAT_1800_SALEMBLACK_06027

Sumi-Ne Goat: Sumi-Ne Goat of Nagaland also known as "Nagaland long hair goat" is reared by Sumi tribes in traditional open range system with almost zero input. Estimated population is about 4,500. It is a medium sized goat reared mainly for its silky fibre. Coat colour is white with black patches on head, neck and legs. Head is straight. Ears are horizontal. Horns are pointed, small sized and curved backwards. Beard is present. Long silky fibres obtained from these goats are used by local people for making traditional items with socio-cultural significance.

INDIA_GOAT_1400_SUMINE_06028

Kachchhi-Sindhi Horse: This indigenous horse breed is native to Kachchh district of Gujarat and Jaisalmer and Barmer districts of Rajasthan. Total population is about 4 thousand. Unique features include roman nose appearance of face, ears curved at tips but not touching each other, 56 to 60 inch height, short back, short pastern bone length, broader hoof for better grip and docile temperament. Coat colour is mainly bay. Famous for its 'Rewal chal' as it performs with great speed and stamina covering long distance. The horse possess excellent drought and heat tolerance capacity in arid and semi arid region.

INDIA_HORSE_0417_KACHCHHISINDHI_07007

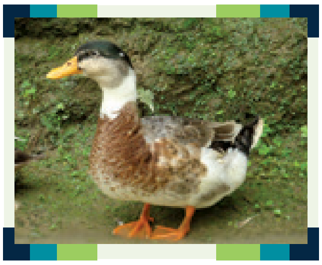
Zovawk Pig: Zovawk pig is distributed in Mizoram with an estimated population of about 39 thousand. It is reared by Mizo community for pork and manure purposes. Animals are black with white spot on forehead, white patches on belly and white boots. Erect ears, concave snout, pot belly, concave top line and long bristles on mid-line are characteristics of the Zovawk pig. Average body weight is 54 kg in males and 59 kg in females.


INDIA_PIG_2700_ZOVAWK_09007

Arunachali Yak: Native tract of Arunachali yak includes West Kameng and Tawang districts of Arunachal Pradesh. These are reared by Monpa community for milk, meat, fibre, transportation and manure. Estimated population of Arunachali yak is about 14 thousand. Predominantly black in colour with medium sized and compact body. Legs are short and stocky. Horns are mostly curved, black in colour and are bigger in males than females. Horizontal ear is typical characteristic of Arunachali Yak. Brisket, belly, ribs, lateral parts and legs are covered with long hair. Adult body weights ranges between 206 to 416 kg. Males are massive and aggressive. Milk production is about 1kg per day.


INDIA_YAK_2300_ ARUNACHALI_16001

Pati Duck: Pati ducks are reared in backyard production system in rural areas of Assam. Estimated population is 18.21 lakhs. These are squat in posture. Plumage is dark brown in drakes with greyish black head; tail with black and white feathers. Ducks are solid brown. A white ring may or may not be present at neck in both sexes. The bill, shank and feet are predominantly yellow. Pati ducks are used for meat, egg and ritual sacrifices. The average body weight is 1.58 kg.


INDIA_DUCK_0200_PATI_11001

Kashmir Anz Geese: Native tract of Kashmir Anz geese is Srinagar, Bandipora, Ganderbal, Baramulla and Budgam districts of Jammu and Kashmir. Estimated population is more than 13,000 birds. They are reared for meat, eggs, and feathers, and as a hobby in areas located around the water bodies. Colour of the plumage is cinnamon, white, and a mixture of cinnamon and white. Adult body weight is 3.82 and 3.34 kg in male and female, respectively. The goose lays about 12 white-shelled eggs/year each weighing about 137 g. Kashmir Anz geese are hardy, disease resistant and foragers requiring minimum inputs for rearing.


INDIA_GEESE_0700_KASHMIRANZ_18001

Hansli Chicken: Hansli chicken is reared in Mayurbhanj and Keonjhar districts of Odisha for game (fighting) and meat purposes. Estimated population is about 12,000. Birds are tall and slim, and have majestic look. Plumage is predominantly black. Males have golden yellow or red hackle and saddle feathers. Comb is pea type. Spur is present in males. Beak is small, strong and stout. Wattles are small and rudimentary; plenty of hackle feathers flow over the shoulder in males. Average egg production is 67 per year with an egg weight of 46 g. Average body weight is about 3.8 kg in males and 2.5 kg in females.


INDIA_CHICKEN_1500_ HANSLI_12018

Identification & Characterization of AnGR

Cattle Populations of Telengana State

To characterize and establish breed characters of Vandharvi and Kamma cattle, survey was conducted in Mahbubnagar and Vikarabad districts. A total of 90 animals of different age and sex were recorded for different physical and morphometric characteristics from 13 villages. Management practices, utility and socio-economic parameters were recorded from 22 farmers of these two districts. It was observed that in this area only bullocks are reared and used for different agricultural operations and cows are maintained in different areas.

Kamma cattle: Kamma bullocks look like Ongole breed but are lighter in colour and smaller in size. Body colour was grey with light black spots on hump and neck. Face was shorter and concave or flat. Tail was short and above the hock. Horns were small and stumpy. In these areas, only bullocks were available and used for different agricultural operations. Cows were bred in Golkunda area. Management was semi intensive including partly grazing and stall feeding. Telega, Madiga, Lambadi, Kapollu, Edigi, Gaundlu communities are rearing this cattle.

Kamma bullock

Vandharvi cattle: Vandharvi cattle are found in Warangal district. Telega, Golu, Lambadi, Munurkapnlu and Vajai communities are rearing this cattle breed. Vandharvi bullocks were white in body colour. Body was larger as compared to other cattle populations available in this area. Face was longer and concave type. Horns were longer and curved. Ears were horizontal. Hump and dewlap were moderate. Tail was upto hock with black switch. In surveyed areas, only bullocks were available for agricultural work and cows were bred in different areas. Daily milk yield ranged from 1.0 to 2.5 kg.

Vardharvi cow

Jhari cattle: To characterize and establish the breed characters of Jhari cattle, survey was conducted in Adilabad (3 village), Asifabad (4 villages) Nirmal (1 village) and Jagithiyar (2 village) districts. Information on different physical characteristics (84 animals), management practices, utility and socio-economic parameters (32 farmers) from 10 villages of 4 districts were recorded. Animals

Jhari cattle

were reared on extensive system of management i.e. grazing only. Farmers provide supplement feeding to the bullocks only at home. Breeding was natural. It was observed that in this area mixed population of cattle is available, some of them Ongole graded and others non-descript cattle. Among the non-descript cattle, there is one group which was observed to be uniform and can be considered for further study.

Jhari cattle were grey (85%) in colour, body was small and cylindrical shape. Face, which is longer and convex type, is the major character for differentiating it from other cattle. The other differentiating characters were horns i.e. longer in length and thin at the base as compared to Ongole or its grades. Body was smaller as compared to Ongole or its type. Hump was moderate in bullocks and smaller in cows. Dewlap was small. Face was concave in majority of the cases and longer as compared to body proportion with other cattle. Muzzle (86%) and eyelids (91%) were black. Ears were smaller in length and horizontal in orientation. Tail was above hock with black switch (88%), not touching the ground. Legs were long and strong. Udder was small, not developed and mostly bowl shaped. Teats were 6-10 cm long and mostly funnel type. Temperament was docile.

Buffalo Populations of Odisha State

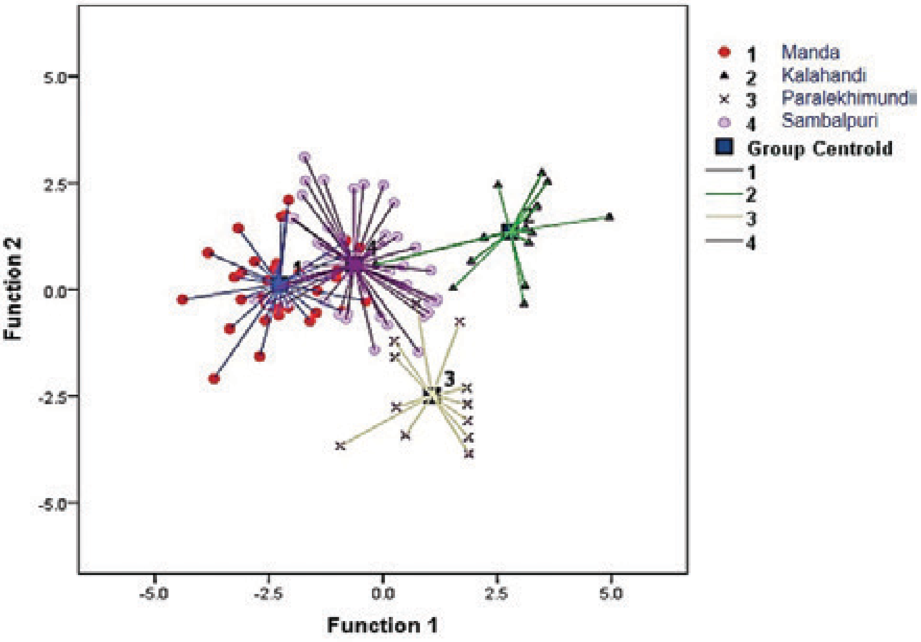
Manda buffalo: Manda buffaloes are distributed in the Koraput district of Odisha. Buffaloes surveyed in this region have phenotypic variability from other Odisha buffaloes and have uniform physical characters. Information on 18 body biometric traits of 69 adult male and female Manda buffaloes was recorded. During survey it was observed that Manda buffaloes are uniformly small with compact body. Horns are long and heavy which seems typical to the population. Body colour is light blackish brown. Animals are hardy and mainly maintained by farmers for draught purpose and also to some extent for milk and dung. Milk yield in Manda buffaloes is low ranging between 2-4 kg per day with an average of 2.5 kg. Animals are maintained on extensive system of management and are purely dependent on grazing and dry fodder. Age at first calving is invariably 4 years with a calving interval of 1.5-2.5 years. On an average, a bullock pair has the capability of ploughing around 1 acre of land in a day. It serves as an excellent draught animal for ploughing small fields of hard red laterite soil of this area. Their draught capacity for transportation is 10 quintal/day and up to 8-10 km without showing any signs of stress. A pair of bullocks is sold at a price of Rs. 30,000 to 50,000 and serves as a source of income to the farmers. The herd size varies from 5-20 adult buffaloes with an average of 8 animals per family. Total estimated buffalo population in Koraput district is around 20,000, out of which 80-90% are Manda type. Considering current scenario, the population deserves to be recognized and registered as a separate breed.

Male and female of Manda buffalo

Sambalpuri buffaloes

Sambalpuri buffalo: During visits to the breeding tract in Sambalpur, Jharsuguda, Bargarh, Deogarh and Boudh districts, Sambalpuri type buffaloes were observed mainly in Naktideul and Redhakhol blocks of Sambalpur. Buffaloes in adjoining Bargarh and Jharsuguda districts bordering Chhattisgarh had body features similar to recorded in Chhattisgarhi buffaloes. Frequent exchange of animals between two states in the region confirmed it. Phenotypic characters and body measurements were recorded. Dwindling population of Sambalpuri buffalo in its native tract is a cause of concern, major reasons observed for which were mechanization of farm operations, and choice of Murrah for milk production. Animals are maintained mostly on extensive system of rearing having milk potential of 2-4 litres per day. Animals are hardy and good for draft purpose.

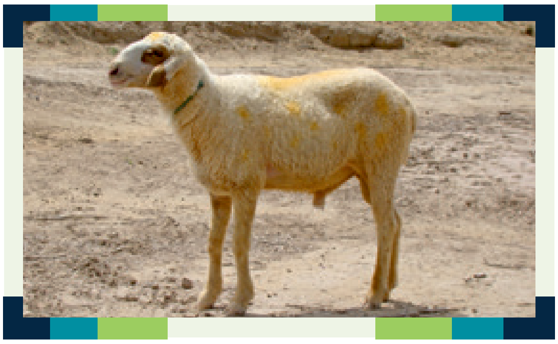
Analysis of data on body measurements of 17 biometric traits recorded on 148 animals of Sambalpuri, Manda, Paralakhemundi and Kalahandi buffaloes of Odisha could reveal distinct grouping of populations by discriminant analysis. Except body length and horn circumference, all other traits varied significantly between the 4 buffalo populations of Odisha at 1% level of significance.



Discriminant analysis based on body measurements of Odisha buffalo populations

Sheep Populations of Northern States

Chitarangi sheep: Chitarangi is a carpet wool type sheep population, distributed in Fazilka, Muktsar district of Punjab, Sri Ganga Nagar districts of Rajasthan and nearby areas. It is also known as Shamaki wali and Ratani sheep. Chitarangi animals are medium to large in size. The coat colour and face is white with tan colour patches around eyes, muzzle and on ear. The light brown, chocolaty and black colour patches were seen in flocks. Serrations of different shape and depth are visible on distal end of ear pinna in all the animals, which is the characteristic of this breed. The average adult body weight of males and females were 56.27 ± 1.28 and 46.16 ± 0.50 kg, respectively which varies from 39 to 95 kg in males and 26 to 74 kg in females. The overall body length, height at wither, chest girth, paunch girth, face length, face width, ear length and tail length were 72.54± 0.24, 73.70 ± 0.22, 86.52 ± 0.31, 88.66 ± 0.38, 20.25 ± 0.07, 9.48 ± 0.04, 18.03 ± 0.09 and 22.19 ± 0.17 cm, respectively. Sheep are primarily maintained on grazing, however, 55.36% farmers provide concentrate to sheep especially during breeding season, to the pregnant ewes, lambs and during scarcity period. The sheep are generally shorn thrice a year in the month of February- March, June- July and October- November. The majority of farmers reported average annual greasy wool production 1.5 to 2 kg. The cost of Feb- March clip wool is higher which varies from Rs. 80 to 230; followed by June-July (Rs. 30-140) and Oct-Nov clip (Rs. 20-100). The Feb- March clip is white in colour and others are canary. Marketing age of male lambs was reported as 6 months by 66.07% sheep farmers and the cost of surplus lambs was reported as Rs. 3000 to 6000 by 55.36% farmers. The ram-ewe ratio is 1:34.33 and age at first mating in rams is about 12-15 months as reported by majority of sheep breeders and age at first lambing is 17 to 18 months reported by 71.43% of farmers. The main lambing season is January to March and minor is from August to October with an average of 80 to 90% annual lambing.



Chitarangi male

Chitarangi female

Dumba sheep: Dumba is found mainly in Jaipur, Nagour and Ajmer districts of Rajasthan. The animals of Dumba are also available in Delhi, Malerkotla tehsil of Punjab and Muzzfarnagar districts of UP. Main objective of rearing Dumba is for Qurbani purpose or earning of money during the Eid festival. Biometry and body weight of Dumba reflects that it is large in size. The coat colour is white and brown; however some black animals/ and mixture of black- white and brown –white were also seen in flocks during survey. The sheep are characterized by the deposition of fat in the tail. Ears are large in size, pendulous and drooping. Majority of farmers reported that twinning varied from 1 to 2%. The price of these animals is very high as

Dumba male

Dumba female

claimed by sheep owners. Adult animals are sold at the rate of Rs. 60000 to 125000 and lambs at Rs. 25000-40000. The average adult body weight of males and females were 83.89 ± 3.95 and 58.76 ± 1.79 kg, respectively which varies from 50 to 124 kg in males and 35 to 96 kg in females. The overall body length, height, chest girth, paunch girth, face length, face width, ear length and tail length were 71.88 ± 0.55, 76.07 ± 0.60, 93.38 ± 0.79, 94.78 ± 0.85, 20.86 ± 0.18, 9.59 ± 0.08 and 17.69 ± 0.22 cm, respectively. The average flock size was 16.04 (range: 2 to 65). The flocks consisted of 15.88 Dumba and 0.16 other sheep. The Dumba flocks comprised of 2.08 rams, 10.32 ewes and 3.48 lambs. The majority of sheep farmers kept sheep in covered area. The sheep are maintained on intensive system with no grazing. Farmers provide concentrate and fodder to these sheep. The major fodder was loom, leaf of Ardu and Rijika. Breeding is through natural service. The average rams per flock is 1.28. The lambing percentage of about 95 was reported by 63.64% of the farmers.

Classification of Indigenous Sheep Populations Based on Morphometric Traits

Classification of eight sheep breeds (Kolhapuri, Lonand, Marwari, Munjal, Muzaffarnagri, Madgyal, Sangamneri and Solapuri) was made by taking pairs of breeds (1-vs-1), a single breed against the rest (1-vs-R) and all the breeds. Methods of classification included classical discriminant functional analysis (DFA), artificial neural networks (ANN) and support vector machine (SVM). Sheep aging between 2-8 teeth, having been profiled on seven morphometric traits viz. body weight, body length, height at withers, chest girth, paunch girth, ear length and tail length, were included in the data set for the classification. Training and test data set ratio consisted of 70:30. Thirty experiments were conducted using the tuned parameters on each set of data. Mean (±S.D.) accuracy of classification of thirty experiments was calculated.

Experiments on SVM were conducted using 'e1071' package in R software. Parameters of SVM model were tuned on the breed data. Values of Gamma parameter (γ) were taken in the range 10e-6 to 10e-2 and that of Cost parameter (C) were taken in the range 2e1 to 2e10 for finding tuned parameter values providing the best results for each set of data. Experiments on ANN were conducted using 'nnet' package in R software. The package uses a single hidden layer in ANN. Two parameters were tuned using 10-fold cross validation method. Number of nodes in the hidden layer - 'size' was tuned in the set (3, 5, and 10). Parameter 'decay' was tuned in the set (0.1, 0.01, and 0.001). The parameter values providing the best classification results were stored for each set of data. According to the type of binary partition one-to-one (1-to-1) in female

Correct classification rates (%) using DFA, ANN and SVM (one to rest partition)

Type of partition	DFA	ANN	SVM
Lonand-vs-R	0.936±0.001	0.948±0.005	0.946±0.004
Solapuri-vs- R	0.864±0.004	0.896±0.009	0.897±0.008
Madgyal -vs- R	0.897±0.009	0.914±0.008	0.923±0.009
Kolhapuri -vs- R	0.897±0.009	0.901±0.007	0.935±0.007
Sangamneri-vs- R	0.899±0.002	0.929±0.009	0.924±0.006
Marwari-vs- R	0.991±0.003	0.996±0.001	0.994±0.003
Munjal-vs- R	0.931±0.008	0.948±0.005	0.959±0.007
Muzaffarnagri-vs- R	0.959±0.009	0.954±0.003	0.967±0.006

data, the DFA gave least assignment accuracy (%) in Solapuri-vs-Madgayal (0.802±0.031). The corresponding values were 0.714±0.029 and 0.812±0.031 in ANN and SVM models. Overall, the SVM model performed best followed by DFA and ANN models. In the binary partition one-to-rest (1-to-R), the least assignment accuracy (%) was in Solapuri-vs-R. The DFA, ANN and SVM model accuracy were 0.857±0.005, 0.886±0.006 and 0.896±0.008 respectively. Highest accuracy were observed in Marwari-vs- R (≥99 %). Overall, the SVM model performed best followed by ANN and DFA models.

Goat Populations of Karnataka State

Information on morphological, socio economic, management and performance parameters was collected on Nandidurga and Bidri goats. Survey was conducted in Chitradurga, Challakere, Hiriyur, Holalkere, Hosdurga and Molakal Muru taluks of Chitradurga district for Nandidurga goats; and in Bidar, Bhalkhi and Humanabad taluks of Bidar district for Bidri goats. There was uniformity and purity within both populations of goats. .

Nandidurga goat: Nandidurga goats are distributed in Chitradurga, Tumkur and Davangere districts of Karnataka. Total goat population of breeding tract is 6.6 lakhs. Estimated population of Nandidurga goat is 1,78,000. Average flock size is 29.6 (12-93). Flocks are stationary. Goats are housed in kutcha sheds during night and are raised only on grazing. Coat colour is white and eyelids are brown or black. Ears are leafy and pendulous. Milking is not done as these goats are reared for meat. Twining is common. Adult weight varies from 30 to 50 kg in males and 26 to 40 kg in females.

Nandidurga goat

Bidri goat: Bidri goats are distributed in Bidar and Kalaburagi districts of Karnataka. There is uniformity and purity within Bidri population. Total goat population of breeding tract is 5.2 lakh and estimated Bidri population is 1,10,000. Average flock size is 74.3 (21-130). Flocks are stationary. Housing is in kutcha open sheds during night. Coat colour is black, muzzle, eyelids and hooves are black. Ears are pendulous. Goats are reared for meat only. Adult weight varies from 31 to 47 kg in males and 24 to 40 kg in females and twinning is commonly observed.


Bidri goat

Body measurements (cm) and adult weight (kg) of Nandidurga and Bidri goats

Parameter	Nandidurga				Bidri			
	Male (46)		Female (172)		Male (20)		Female (43)	
	Avg. ± SE	Range	Avg. ± SE	Range	Avg. ± SE	Range	Avg. ± SE	Range
Chest-girth	81.47±2.40	70-98	75.07±1.02	61-90	80.75±2.12	68-89	77.12±0.69	64-87
Body length	59.65±1.56	48-69	55.31±0.87	44-63	58.17±1.46	52-71	56.09±0.63	47-70
Height at withers	79.40±1.83	72-95	71.92±0.72	62-82	79.25±1.79	72-89	74.84±0.66	64-83
Horn size	20.33±1.54	11-30	15.79±0.73	7-23	16.44±1.85	9-26	13.72±0.67	6-20
Ear length	16.36±0.41	13-19	15.38±0.29	12-20	16.25±0.37	15-18	16.28±0.22	12-19
Tail length	21.29±0.91	13-26	18.90±0.43	17-29	17.17±0.65	14-21	16.70±0.46	11-23
Adult weight	38.92±2.95	26-56	30.11±1.03	24-41	36.78±2.76	23-52	32.36±0.90	19-45

Yak Population of Ladakh (J&K)

North Trans-Himalaya – the world's highest inhabited region with extreme climatic conditions – occupies high altitude areas (>3000 meter MSL) of Ladakh (J&K) and Lahaul-Spiti (Himachal Pradesh) of Indian Territory. This cold-arid region is well known for possessing distinctive flora and fauna adapted to the high altitude conditions - hypoxia, low temperature and high UV radiation. Breed surveys were conducted in different villages of Nubra and Sham valleys of Ladakh to characterize local yak populations and documenting their production system.

Yak and yak-cattle crosses in Ladakh of Jammu & Kashmir are about 54 thousand (Livestock census, 2012), however, pure yak may account less in number. Yaks in Nubra and other regions of Ladakh are reared by Buddhist community located at higher altitudes for milk, meat, manure, hair-fibre and transport purposes. Yaks of Nubra are medium in size and moderate in temperament. Coat colour is dark brown to black with glossy sheen. Skin, muzzle, eyelids, tail switch are black, horns are grey to black. Few yaks also possess white patches on small to large part of the coat and switch. Occipital bone is prominent. Forehead and nasal bone are straight, hump is small. Dorsal ridge is prominent in males. Dorsal line is convex on wither (ridge) and concave on back. Limbs are small and cylindrical. Horns are curved and placed laterally upward and backward with pointing tip. Ears are medium and horizontal. Pelvis is wider than shoulder region. Flank, lower belly and thigh regions are covered with long hair. Tail is small with long hair and set high. Different morphometric traits

Male yak of Ladakh

Female yak of Ladakh

were measured for male and females which are given in the table below. Udder is very small and bowl shaped. Male and female attain sexual maturity at 3 years of age. Demo starts calving at about 4 years of age and calves every alternate year and produces 7-8 calves in life time. Open breeding is preferred; no selection is carried out generally. Males are castrated at the age of 8 years. July-August months during summer is major breeding period, whereas calving occurs during April-May. Milk production of yak is 0.5 to 1.0 Kg/day. Lactation period ranges from 6 to 8 months only. Female yak (Demo) is milked mostly once in morning. Milk upto 2 months is used solely for feeding of calf. Herd size is 6 to 30. Most of the yaks are reared under pastoralism and migrate towards high land pastures in April and remain there upto October/November. FMD outbreaks are common; vaccination for FMD is followed in November and April months. Skin diseases are also prevalent. Cross-hybrids of yak are being largely preferred over the yak in most of the visited area, particularly to increase milk and make them adaptable to lower altitude. Cross-hybrids (using yak as a male) are maintained mostly for F1 generation (Dzo/Dzomo), and other generations (Garu/Garamo (F2), Giri/Girimo (F3)) in some cases. Dzomo produces 2-4 Kg milk/day. Dzo is used for ploughing and transport purposes.

Morphometric traits (in cm) of Yaks of Ladakh

Morphometric Trait	Adult Male (n=40)		Adult Female (n=65)		Dimorphism index
	Mean ± SD	C.V.	Mean ± SD	C.V.	
Horn length	45.42±6.70	14.8	31.93±5.13	16.1	1.42
Horn circumference	23.37±2.83	12.1	15.58±1.89	12.1	1.50
Distance between horns	20.40±3.53	17.3	16.00±1.79	11.2	1.28
Face width	22.41±2.61	11.7	18.46±1.50	8.1	1.21
Face length	45.93±4.43	9.7	41.64±3.04	7.3	1.10
Ear length	12.66±1.20	9.4	12.48±0.89	7.2	1.01
Height upto elbow	58.9±4.47	7.5	53.73±4.02	7.5	1.09
Height at wither	111.24±10.27	9.2	100.86±7.27	7.2	1.10
Body length	116.61±13.83	11.9	106.86±9.04	8.5	1.09
Chest girth	160.85±17.23	10.7	147.2±11.37	7.7	1.09
Paunch girth	161.82±17.07	10.6	146.20±11.96	8.2	1.10
Tail length (without switch)	38.53±5.57	14.5	36.25±4.76	13.1	1.06
Tail length with switch	67.53±7.98	11.8	62.45±7.82	12.5	1.08

Donkey Population of Ladakh (J&K)

Total donkey population in district of Leh is about five thousand. Ladakhi donkey is reared by Buddhist communities – Tsering, Tashi, Sonam, Namgyal, Tundup, Dorje; mostly in rural areas. It is used primarily as a pack animal for transportation of manure/fuel-wood/fodder/construction/trekking-camping materials by local people and food-logistics supply by Indian Army and, secondarily for manure. Animals are medium sized and docile.

Morphometric traits (in cm) of adult donkeys of Ladakh

Morphometric Trait	Adult Male (n=15)			Adult Female (n=54)			Dimorph. Index
	Mean±SD	Range	CV%	Mean±SD	Range	CV%	
Height at wither	94.27±3.75	87-101	3.98	93.85±3.8	86-106	4.05	1.01
Body length	95.53±5.66	82-103	5.92	97.46±7.37	81-116	7.56	0.98
Heart girth	101.6±5.14	93-115	5.05	102.96±5.58	92-118	5.41	0.99
Paunch girth	111.07±8.69	100-128	7.82	109.55±6.5	97-121	5.93	1.01
Face length	46.07±2.6	42-51	5.64	47.28±2.88	42-58	6.09	0.97
Face width	20.07±1.16	18-22	5.78	19.19±1.48	15-25	7.71	1.05
Ear length	21.33±1.72	19-25	8.06	22.39±1.99	17-26	8.89	0.95
Neck length	27.27±3.58	22-32	13.13	27.51±4.21	17-36	15.30	0.99
Chest width	21.63±2.21	19-26	10.22	19.92±1.74	14-25	8.73	1.09
Tail length-with switch	50.53±6.93	41-63	13.71	51.47±5.91	36-67	11.48	0.98
Fore arm length	39.13±2.39	33-42	6.11	38.4±2.52	34-44	6.56	1.02
Fore arm circumference	20.5±2.02	18-26	9.85	19.85±2.0	16-30	10.08	1.03
Canon length (FL)	17.2±1.37	15-19	7.97	17.37±1.65	14-21	9.50	0.99
Canon circumference (FL)	12.43±0.83	11-14	6.68	11.94±0.55	10.5-13	4.61	1.04
Pastern length (FL)	7.37±0.48	7-8	6.51	7.17±0.64	5-8	8.93	1.03
Pastern circumference (FL)	12.25±0.61	11-13	4.98	11.65±0.68	10-13	5.84	1.05
Hoof length (FL)	5.43±0.46	5-6	8.47	5.25±0.56	4-7	10.67	1.03
Hoof circumference (FL)	22.57±1.4	21-25	6.20	21.9±1.3	20-25	5.94	1.03
Gaskin length	42.4±3.14	35-47	7.41	41.26±2.93	32-46	7.10	1.03
Gaskin circumference	25.23±2.09	23-30	8.28	24.38±2.41	20.32	9.89	1.03
Canon length (HL)	25.8±1.47	24-29	5.70	25.89±1.34	23.29	5.18	1.00
Canon circumference (HL)	13.12±1.23	11-15	9.38	12.69±0.89	11-16	7.01	1.03
Pastern length (HL)	6.87±0.64	6-8	9.32	6.62±0.77	5-9	11.63	1.04
Pastern circumference (HL)	12.54±1.05	11-15	8.37	12.14±0.69	10-13	5.68	1.03
Hoof length (HL)	5.1±0.57	4-6	11.18	5.1±0.52	4-6	10.20	1.00
Hoof circumference (HL)	20.85±1.68	17-23	8.06	20.33±1.42	17-23	6.98	1.03
Estimated body weight (kg)	82.88±9.28	64-100		78.97±18.03	44-127		1.05

Male Ladakhi donkey

Female Ladakhi donkey

Coat colour varies from light to dark brown and black with light coloured or white belly. White mark around muzzle and mouth and white ring around eyes are observed in most of the animals irrespective of sex. Hair coat is medium and curly, and dense on lateral sides of the body. Nasal bone is straight to slightly concave. Forehead is flat to convex. Various morphometric characteristics of Ladakhi donkey are given in table. In females, age of first breeding is 3.5-4 years and first foaling is 4.5-5.5 years. Major season of breeding and foaling is March-June. Ladakhi donkey foals alternate year and produce 5-7 foals in her lifetime. Open breeding is preferred, no selection is carried out. Milk is used for feeding of foals only. Herd size is 1-6 donkeys per household. Animals are mostly housed in enclosures or animal houses (kutchha or pucca) either along with other livestock or separately during night. Some households keep them loose during night also. Animals are raised on grazing in summer. During winter and snow, stored fodder (Alfa-alfa) and crop residues are provided. During pregnancy and calving, Barley a mixture of wheat, salt, mustard oil (chhak), jiggery along with dried fodder is provided. No vaccination is done. Tympany, skin or eye diseases are observed in few cases. As uniqueness, the Ladakhi donkey has ability to cross small ridges easily (Bonchangs) and can travel 15-20 Km in 5-6 hrs with 40-50 Kg load in high terrain. Animals are sure footed and track easily in night also. Donkey manure is mixed with human and cattle manure and considered to be good for soil fertility.

Evaluation of Livestock Policies and Programmes for the Management of AnGR in Haryana and Punjab States

With extension of the mandate of the Bureau, a new project "Evaluation of livestock policies and programmes for the management of Animal Genetic Resources in Haryana and Punjab states" was initiated in July 2017 in collaboration with GADVASU, Ludhiana. Two sets of questionnaires were developed for collecting information from farmers/livestock keepers and veterinarians. Three districts each in Haryana (Karnal, Hisar and Palwal) and Punjab (Tarn Taran, Ferozpur and Ludhiana) were selected for the study. Existing policies and programmes of AHD Haryana and Punjab states were collected. Information from 16 farmers attending Kisan Mela at GADVASU was collected using the questionnaires. One visit was also made to Tarn Taran district of Punjab and from 21 villages, a total of 42 farmers were interviewed to collect information as Q-1 and four VOs as per Q-2. All kinds of farmers keeping cattle, buffalo, goat, pig and poultry were consulted for their activities of animal husbandry and problems faced by them were also recorded.

Conservation of AnGR

Ex situ Conservation

The germplasm repository at NBAGR is being strengthened by preserving diversified form of germplasm (semen, embryos, DNA, epididymal sperms and somatic cells). The germplasm procured during this year is given in the following table.

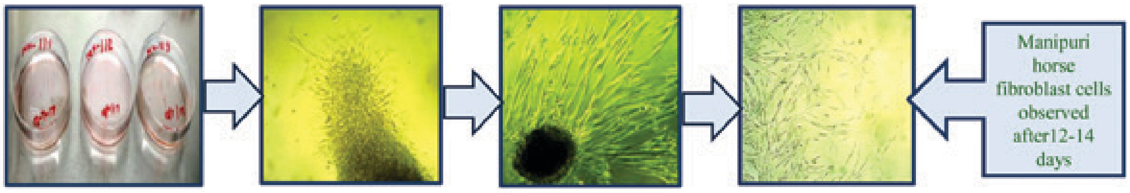
Germplasm cryopreserved during 2017 - 18

Germplasm	Species	Breed	No. of doses/ vials
Semen	Cattle	Kankrej	500
		Gir	500
		Sahiwal	500
		Bargur	3000
		Dangi	6000
		Rathi	2475
		Khillar	7000
		Nagori	4000
Somatic Cells	Camel	Kutchi	400
	Horse	Marwari	400
Total			24775

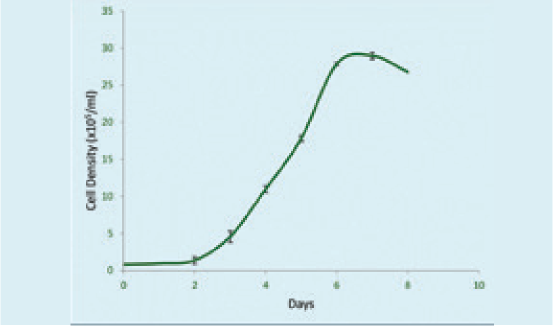
Somatic Cell Banking

Manipuri horse and Kutchi camel: Fibroblast banks propose a practical approach to preserve precious livestock genetic resources due to advancement of cell culture techniques. In addition, skin cells offer an attraction because of easy accessibility, non-invasiveness and without any limitations of sex or age of animal. Ear marginal tissues from 8 Manipuri horses and 6 Kutchi camels were utilized for establishment of cell lines by attachment cell culture method followed by cell cryopreservation technique. Primary culture was established using explant culture technique with fibroblast specific media (HiFibroXL™). At about 10-14 days, epithelial-like and fibroblast-like cells could be seen sprouting from the margins of explants of both Manipuri horse and Kutchi camel. Fibroblast-like cells showed typical fusiform morphology with centrally located oval nuclei. Initially epithelial and fibroblast cells grew together but during subsequent passages, fibroblast cells grew rapidly and replaced the epithelial cells. Passaging of cell lines for both Manipuri horse and Kutchi camel was continued using DMEM+Ham's F12 (1:1) media with 10% FBS. Cells exhibited radiating, flame like or whirlpool like migrating patterns and density dependent inhibition during cell proliferation. The growth curve at passage-5 represented typically S-shaped as the cell population passed through a lag phase, a logarithmic phase and a plateau phase with population doubling time of 27.9 hrs and 31.37 hrs with multiplication rate of 0.86 population doubling/24 hrs and 0.76 population doubling/24 hrs for Manipuri horse and Kutchi camel respectively. The cells were cryopreserved from 3rd to 6th passage stocking at least 75 cryogenically-preserved vials (1×10^6 cells/ml) per animal.

These newly established cell lines of Manipuri horse and Kutchi camel preserves the genetic



Explant culture of fibroblast cells



Growth curve of fibroblast cells

resources at the cellular level and provides invaluable materials for genomic, post-genomic and somatic cell cloning research.

Conservation of Sahiwal and Hariana Cattle at Gaushalas

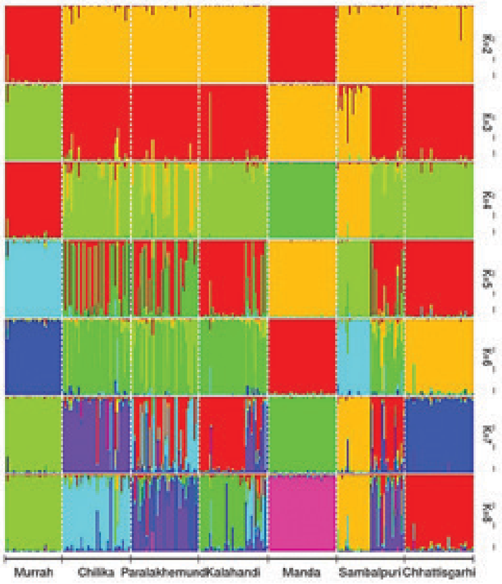
Cows of Hariana and Sahiwal breeds and their grades were identified in the 3 selected Gaushalas (Shri Krishan Gaushala Jundla, Nising and Uplana) based on physical characteristics and health soundness. Identified cows were ear tagged and kept in separate enclosures at respective Gaushala. Among the identified cows, 52 cows of Hariana and 4 of Sahiwal were inseminated with elite male semen of Hariana and Sahiwal, respectively. State Animal Husbandry Department, Karnal has provided liquid nitrogen containers to all the three Gaushalas. They are refilling liquid nitrogen every month in LN2 containers to these Gaushalas. All the selected cows were given deworming treatment and mineral mixture supplementation. Two health camps were organized in all the three Gaushalas with the help of State Animal Husbandry Department, Karnal. In Jundla Gaushala, cows were examined by ultrasonography for their reproductive status and accordingly, treatment was given. The Controlled Internal Drug Release (CIDR) treatment was applied to 10 cows and 4 pregnancies were confirmed in Hariana cows. A total of 46 (5 Sahiwal (4 F + 1 M) and 41 Hariana (24 F +17M)) calves were born. In Sahiwal, fortnightly daily milk yield ranged from 4.0 to 9.0 kg. In Hariana, fortnightly daily milk yield ranged from 1.0 to 4.0 kg. Birth weight of Sahiwal calves ranged from 14 to 18 kg and in Hariana, it varied from 12 to 20 kg.

Hariana calves born in Gaushala

Genetic Characterization of AnGR

Genetic Diversity of Odisha Buffalo Populations

Genotype data generated for 20 microsatellite markers on 48 animals each of five Odisha buffalo populations- Chilika, Kalahandi, Paralakhemundi, Sambalpuri and Manda as well as mitochondrial D-loop sequence of 24 animals of each breed/ population was used to delineate the genetic structure and evolutionary lineages. Microsatellite markers based data analysis indicated Manda being genetically highly differentiated from all other buffalo populations of Odisha.

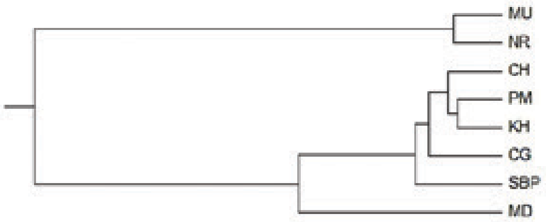


Clusters inferred from STRUCTURE 2.3.4 (admixture model) including five Odisha buffalo populations and Murrah alongwith Chhattisgarhi buffaloes

When compared, Chhattisgarhi buffalo, however, was closer to other Odisha buffaloes. Same was reflected in F_{st} based principal component analysis also. Nei's genetic distance based phylogenetic analysis also showed clustering of Odisha and Chhattisgarhi buffalo together, whereas Murrah and Nili Ravi grouped together into distant cluster. Within Odisha buffaloes, Manda grouped separately, again indicating this being a distinct population fit for registration as new buffalo breed.

Breed-wise Fst based genetic differentiation of Odisha with other buffaloes

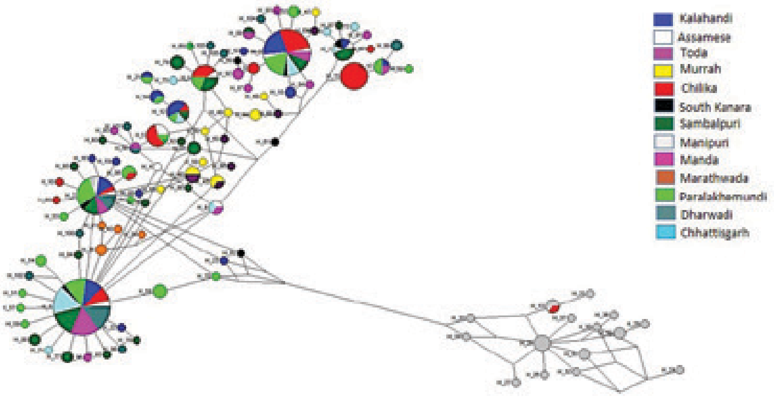
Murrah	Nili Ravi	Chilika	P'mundi	K'handi	Manda	S'puri	Ch'garhi	
0.000								Murrah
0.035	0.000							Nili Ravi
0.143	0.157	0.000						Chilika
0.146	0.152	0.031	0.000					P'mundi
0.149	0.166	0.028	0.023	0.000				K'handi
0.210	0.219	0.093	0.079	0.087	0.000			Manda
0.147	0.161	0.040	0.042	0.037	0.083	0.000		S'puri
0.167	0.183	0.048	0.045	0.037	0.085	0.045	0.000	Ch'garhi



Phylogenetic analysis using microsatellite allelic diversity based Nei's genetic distance

(MU-Murrah, NR-Nili Ravi, CH-Chilika, PM-Paralakhemundi, KH-Kalahandi, CG-Chhattisgarhi, SBP-Sambalpuri, MD-Manda)

Microsatellite allelic frequencies based structure analysis carried out on five Odisha breeds and including Murrah and Chhattisgarhi buffalo at K=7, having maximum support, partitioned the populations into 7 groups,



Median joining network analysis based on mitochondrial haplotype sharing among different buffalo populations

Manda and Murrah being most distinct. Paralakhemundi had maximum admixture of Kalahandi buffalo.

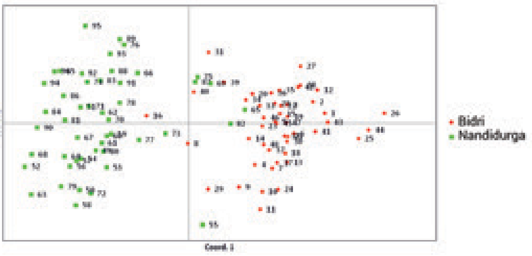
Evolutionary studies using mitochondrial D-loop sequencing of Odisha buffaloes and comparative analysis using median joining network with other reported Indian riverine and swamp buffaloes indicated three major haplotypes being shared by riverine buffaloes. Manipuri swamp buffaloes with unique haplotypes were grouped separately. Most interesting part was sharing of haplotypes between Chilika and swamp buffaloes. Chilika had more number of breed specific haplotypes also. Phylogenetic analysis also grouped riverine and swamp buffaloes into distinct clusters but within riverine buffaloes, Odisha buffaloes grouped into a different sub-cluster.

Genetic Diversity of Chitarangi and Dumba Sheep

Different measurements of within breed genetic variations viz. observed and effective number of alleles (Ne), observed (H_o) and expected heterozygosity (He) along with polymorphism information content (PIC) of different microsatellite loci and within population inbreeding estimates (FIS) were estimated for Chitarangi and Dumba sheep. The microsatellite loci amplified were observed to be polymorphic in the investigated population. All the markers were found to be highly informative with average PIC value of 0.71. A total of 237 distinct alleles were identified across the 24 markers in Chitarangi sheep and 243 distinct alleles in Dumba sheep. The observed number of alleles ranged from 4 (OarAE129) to 16 (CSSM31) with a mean of 9.875 in Chitrangi and 5 (BM757) to 19 (BM1314, CSSM31) with a mean of 10.125 in Dumba. Effective number of alleles was lower than the observed number of alleles in both populations and ranged from 1.612 (CSSM47) to 8.828 (CSSM31) with a mean value of 4.171 in the former and 1.246 (CSSM47) to 8.860 (OarCP0049) with a mean value of 4.852 in the latter. The average observed heterozygosity values and expected heterozygosity values were 0.636 and 0.712 in Chitrangi and 0.689 and 0.749 in Dumba, respectively. The estimates of allele diversity (mean number of observed alleles) and gene diversity (mean expected heterozygosity) implied the presence of substantial amount of genetic variability in these populations. The mean F_{IS} (within population inbreeding estimates) was 0.096 and 0.043 in the two populations indicating deficiency in the number of heterozygotes. The observed positive F_{IS} in the investigated sheep populations might be due to the non-random mating and use of fewer rams for the breeding purpose. The existence of population substructure (Wahlund effect) due to sampling from different flocks in different villages of the distribution area appears to be the most probable explanation.

Genetic Diversity Status of Nandidurga and Bidri Goats

Population genetic parameters were calculated based on the genotype data generated by using a battery of 23 microsatellite markers. All the markers were polymorphic and a total of 189 and 195 alleles were detected across these loci in Nandidurga and Bidri goats, respectively. An exact test for genotypic linkage disequilibrium yielded no significant *P* values and therefore, independent assortment of all the loci was assumed. Reasonable polymorphism in Bidri goats was evident as the mean number of observed alleles was 8.48±0.88 with ILSTS033 showing the highest number (16) of alleles. Expected number of alleles varied from 1.043 (OarJMP29) to 8.804 (OMHC1) with mean of 3.58±0.44. Similarly, Nandidurga population had 8.22±0.66 mean observed number of alleles. Estimates of observed heterozygosity, 0.58±0.06 and 0.60±0.05 for Bidri and Nandidurga confirmed the sufficient level of diversity in the two populations. Heterozygote deficit in these populations was also not significant being 3.9% in Bidri and 2.5% in Nandidurga goats. Any detectably large, recent genetic bottleneck was also absent. Distinctness of the two goat populations can be assumed on the basis of assignment tests and Principal Coordinate Analyses.



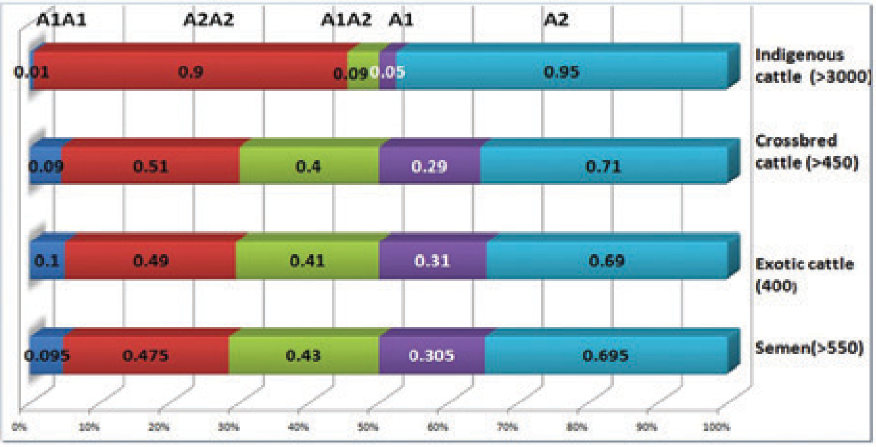
2D plot of the Principal Coordinate Analysis depicting relative positions of two goat populations

Genomics & Evaluation of AnGR

β-casein Variants in Indian Cows and Health Implication of A1/A2 Milk

A1/A2 alleles of β- casein gene in Indian cattle: The allelic frequency of A1/A2 allele of β casein was estimated in more than 4000 animals including Indian native (30 breeds), crossbred, exotic cattle and semen samples. The breeding bulls' semen samples were collected from semen stations/ livestock development boards of different states. The analysis revealed that the frequency of A1 allele was highest in exotic cattle (0.31), followed by semen samples (0.30) and crossbred cattle (0.29). Indian native cattle revealed the minimum frequency of A1 allele (0.05). The A2A2 genotype was predominant in all the analyzed cattle types and ranged from 0.49 (exotic cattle) to 0.90 (Indigenous cattle) with an average frequency of 0.59. On the other hand, A1A2 genotype was in higher proportion in exotic and crossbred cattle as well as semen samples with an average frequency of 0.41 and a range of 0.40-0.43. The comparative proportion of A1A2 genotype in Indian native cattle was much lower (0.09). The frequency of least common genotype A1A1 was minimum in indigenous cattle (0.01) and highest in exotic cattle (0.1). Allelic and genotypic profile for thirteen known variants of β casein was estimated across more than 1500 samples of Indian native, exotic and crossbred cattle. Amongst the 13 known variants, other than A1/A2 only B variant (ser 122 arg) was observed across the three cattle types. The frequency of B allele was highest in crossbred cattle (0.19) followed by exotic (0.13) and Indian native cattle (0.04).

Expression analysis of β-casein in milk somatic cells of Karan Fries: A total of 56 animals, 36 of Karan Fries and 20 of Sahiwal cows maintained at NDRI, Karnal were selected to check the

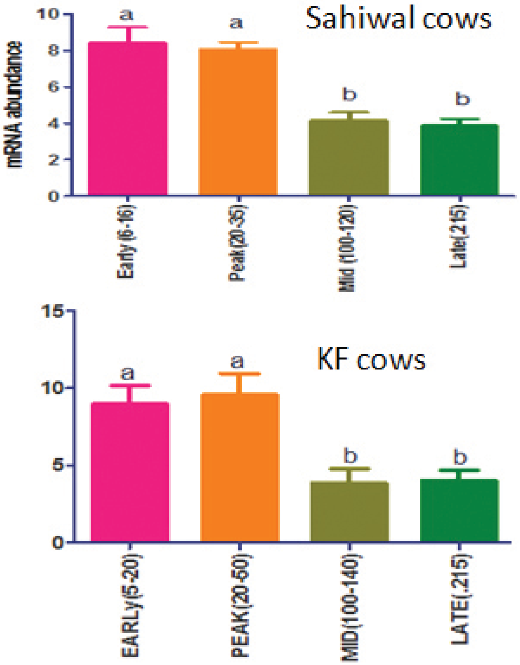


Allelic and genotypic frequencies of A1/A2 variant β casein in Indian native, exotic, crossbred cattle and semen samples

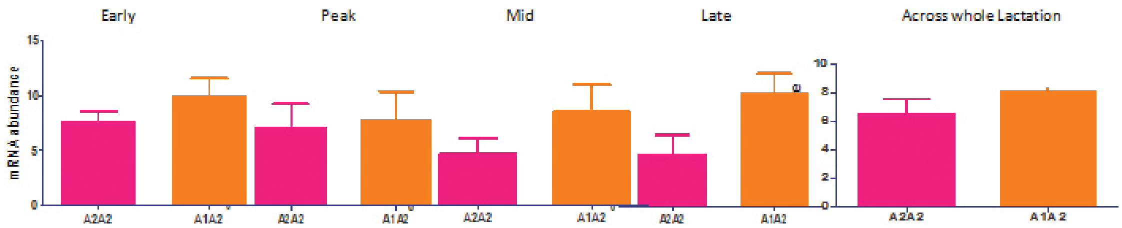
expression profile of β-CN across the lactation stages. These animals were selected on the basis of data of their previous parities and their milk yield records of current parity. The data showed that the selected animals were able to complete all the lactation stages before involution. Milk samples were collected during different stages of lactation early (5-15- days), peak (20-50 days), mid (100-140 days) and late (>215 days) lactation to isolate somatic cells. For Karan Fries cows, two genotypes (A1A2 and A2A2) and for Sahiwal cows, only one genotype (A2A2) could be traced across the lactation stages for sample collection, as number of KF cows with A1A1 genotype is low and for Sahiwal, none of the animal showed A1A1/A1A2 genotype.

Analysis of β-casein mRNA expression data (based on CT values) revealed that in both Sahiwal and Karan Fries, the expression of β-casein was significantly (P=0.0014, P<0.05) higher in early and peak lactation stage than mid and late stages. The mRNA abundance at peak with mean value 9.8 was highest followed by early with mean 8.9 and then further subsequently decreased in mid and late lactation stages. The mean value of mRNA at early and peak was almost similar, hence no significant difference was observed.

Further the Karan Fries animals were also grouped on their genotype basis to delineate the differential expression of β-casein in A2A2 genotype and A1A2 genotype throughout the lactation. Being in dry stage, the animal belonging to A1A1 genotype could not be included in the study. No significant (P<0.05) difference in the expression of β-casein across A2A2 and A1A2 genotypes at different stages of lactation was observed. However the



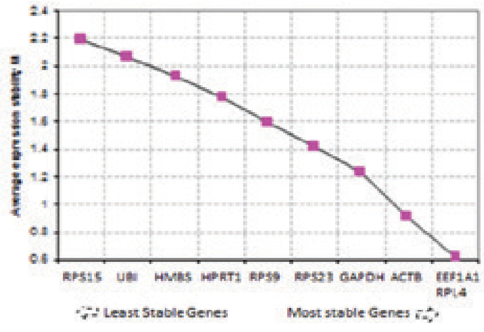
Relative mRNA level of β-casein gene in Karan Fries and Sahiwal milk somatic cells during different lactation stages. *a and b represent the statistical difference (P=0.0014)*



Relative mRNA level of β-casein gene in** KF **milk somatic cells in A2A2 and A1A2 genotypes. *Statistical difference in expression was determined by the unpaired t-test. (P<0.05)*

mRNA abundance in case of A1A2 animals was high in comparison to A2A2.

Identification of internal control genes: For evaluation of potential internal control across different lactation stages of Karan Fries, 10 candidate genes (EEF1A1, RPS15, RPS9, HPRT1, HMBS, UBI, GAPDH, RPL4, RPS23, and ACTB) were chosen. geNorm analysis was used to rank candidate reference genes according to their expression stability in milk derived milk somatic cells of *KF*. The lower M value is indicative of higher expression stability of a gene. Stepwise exclusion method resulted in ranking of ICGs in decreasing stability order as EEF1A1=RPL4> ACTB>GAPDH> RPS23> RPS9>HPRT1> HMBS> UBI> RPS15. EEF1A1 and RPL4 genes were ranked as most stable with lowest M values and RPS15 was least stable. Further, Normfinder analysis was also used to identify ICGs. The analysis identified EEF1A1 and ACTB as most stably expressed genes and most stable to least stable genes were, ACTB> EEF1A1> RPL4> GAPDH> RPS23> UBI> HPRT1> RPS9> RPS15>HMBS. EEF1A1 and ACTB were found to be best combination of genes with stability value of 0.193.



Ranking of reference genes based on** geNorm **and *Normfinder analysis*

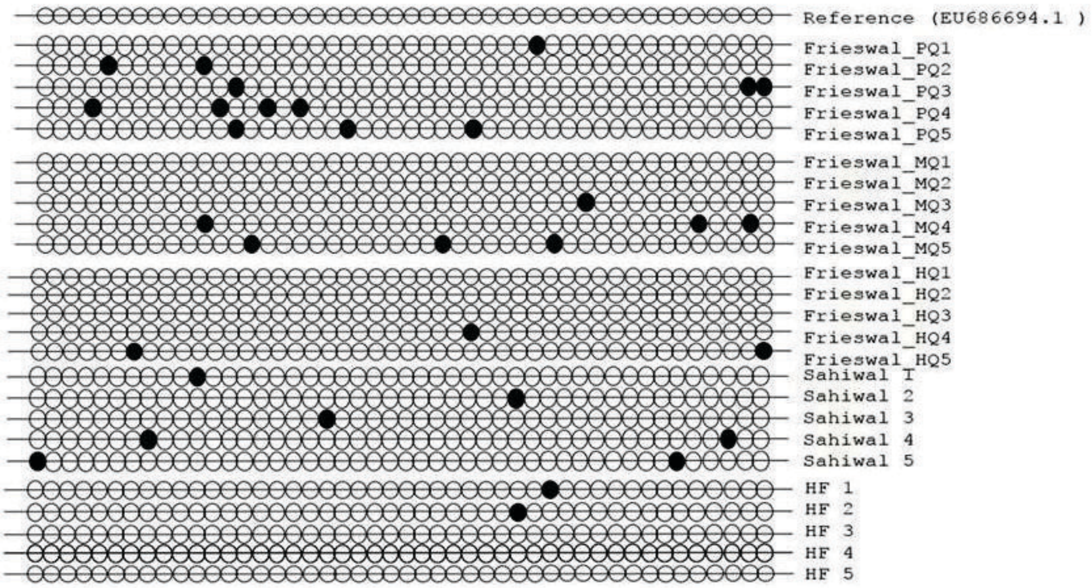
Association of BCM7/9 with diabetes in mouse model: Work on animal trials was initiated at ICAR-NDRI, to establish experimental evidence for the cause and effect relationship of BCM7 peptide with disease progression in mice model. BCM7/9/7+9 was administered by intra peritoneal injection to four different groups of animals (8-10 animals in each group) in different concentrations ranging from 50ug to 400ug (50, 100, 200 and 400ug), till the symptoms for hyperglycemia appeared. Later, the animals were euthanized and different tissues have been collected for further analysis. Also, whole milk powder of different beta casein genotype variants has been prepared and studies related cause and effect relationship of A1A1, A2A2 and A1A2 milk with disease progression in mice model are underway. Comparative profiling of milk phenomic data in cows of A1A, A2A2 and A1A2 genotypes across different cattle populations is being carried out to reveal association of phenomic data with specific genotype if any.

Methylation Status of *DAZL* Gene Promoter With Varying Semen Motility in Bulls

Epigenetic modifications (DNA methylation, histone modifications, chromatin remodelling) are regarded as key players influencing gene expression. *DAZL* gene plays an important role in germline development and gametogenesis. The methylation and mRNA expression level of this gene have been significantly negatively correlated in the testes of cattle-yaks hybrids and their parents. The methylation profile of *DAZL* gene promoter in bull spermatozoa was analyzed in an attempt to evaluate its role in crossbred cattle subfertility. Semen samples from Sahiwal, Holstein Friesian and Frieswal bulls (Sahiwal X Holstein Friesian) with varying semen motility parameters were collected and DNA was isolated. Methylation specific primers were used to amplify part of promoter and exon 1 of *DAZL* gene using bisulfite converted DNA. The amplified products were sequenced after cloning in pTZ57R/T vector. Sequence analysis revealed significantly higher DNA methylation of *DAZL* gene in Frieswal bulls with poor motility (28.26%) as compared to medium (15.21%) and high motility phenotype (6.52%). In purebred counterparts, Sahiwal and Holstein Friesian, epigenetic marks were more in the former (15.21%) than the latter (4.34%) but in both cases, the values were lower as compared to the poor motility Frieswal bulls. This suggests that differential hypermethylation of the CpG islands could possibly influence reproductive parameters in bovines.

Genome Wide Diversity of Indian Buffaloes

Linkage disequilibrium analysis: For biallelic markers, one of the most commonly used measures for LD is r^2, the square of the correlation coefficient between two indicator variables – one representing the presence or absence of a particular allele at the first locus and the other representing the presence or absence of a particular allele at the second locus. The linkage disequilibrium values for the Indian buffaloes (riverine as well as swamp buffaloes) are not known. The data generated using Genotyping by Sequencing (GBS) was utilized to estimate the values of linkage disequilibrium. A total of 625 animals belonging to 17 different breeds/populations (Assam, Manipuri, Banni, Bhadawari, Chilika, Jaffarabadi, Kalasthi, Kerala, Mehsana, Surti, Murrah, Nagpuri, Nili Ravi, Pandharpuri, UP,



Position of methylated CpG sites in different groups (PQ: Poor motility, MQ: Medium motility, GQ: Good motility, HF: Holstein Friesian)

Tarai and Toda) were utilized for the purpose. By GBS, a total of 23,306 SNPs were genotyped and were common to all individuals. The estimation of linkage disequilibrium was done using PLINK software v 1.9.

The various distance bins, number of SNP pairs analysed and average r² obtained for each distance for riverine and swamp buffaloes is given in the following tables.

Statistical information for LD over various distances in riverine buffaloes

Distance	Number of SNP pairs	Average r^2
0-5 kb	17539	0.32
5-10 kb	19791	0.29
10-20 kb	23725	0.25
20-25 kb	25607	0.23
25-50 kb	37177	0.18
50-100 kb	57250	0.13

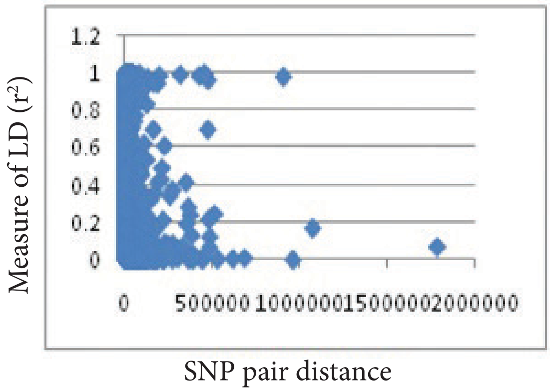
Statistical information for LD over various distances in swamp buffaloes

Distance	Number of SNP pairs	Average r^2
0-5 kb	14553	0.33
5-10 kb	16203	0.31
10-20 kb	19113	0.27
20-25 kb	20546	0.25
25-50 kb	26541	0.21
50-100 kb	37415	0.17

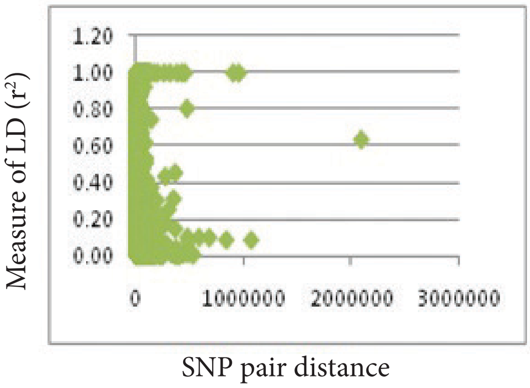
Breed wise linkage disequilibrium analysis was also carried out for Manipuri and Assam buffaloes (Swamp) and all other 15 buffalo populations (Riverine). The values of distance beyond 20-25 kb yield r^2 values were less than 0.2. Though there is no fixed criterion for the value of r^2 to be statistically significant but it is generally assumed that the r^2 should be greater than 0.2 for its usage in linkage disequilibrium utilisation for genome wide association studies. Thus, the values for LD are between 20-25 Kb distance for both riverine and swamp buffaloes.

The graphs reveal how fast LD decays across the genome with distance. It is useful to determine the number of markers needed for an association mapping experiment. If we take only the genetic distance with r^2 value of greater than 0.2, we get the genetic distance block of 20-25 kb for the riverine buffaloes and value of 25-50 kb for the swamp buffaloes. This translates to approximately 1,50,000 SNPs to be required for riverine buffaloes and approximately 1,20,000 SNPs shall be required for swamp buffaloes.

Taking into account the requirement for the Genome Wide Association Studies, we have completed SNP identification with High Density Buffalo chip for Murrah buffaloes. The chip consists of 675,000 SNPs and shall be utilised for the creation of a reference family of



LD decay in riverine buffaloes



LD decay in swamp buffaloes

Linkage disequilibrium in Indian buffaloes

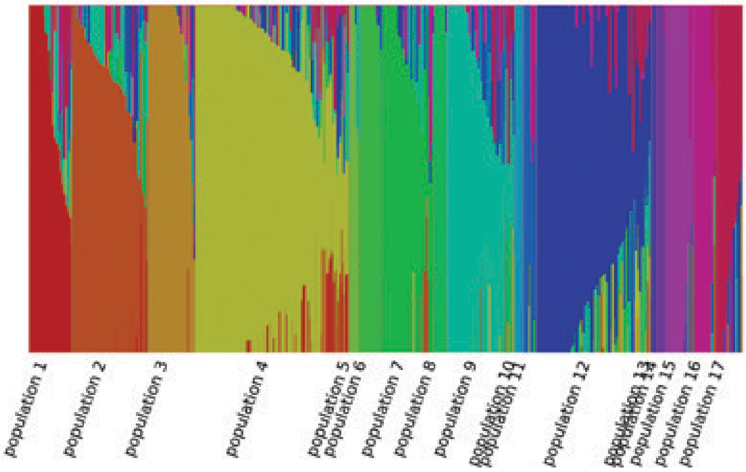
Breeds	Number	0-5Kb		5-10Kb		10-20Kb	
		SNP pairs	Average r^2	SNP pairs	Average r^2	SNP pairs	Average r^2
Assam (Swamp)	15	13401	0.36	14856	0.34	17400	0.30
Banni	31	16486	0.33	18563	0.30	22190	0.26
Bhadawari	40	17095	0.35	19321	0.32	23211	0.28
Chilika	12	11468	0.41	12693	0.38	14828	0.34
Jaffarabadi	45	17436	0.34	19680	0.30	23604	0.26
Kalasthi	39	17117	0.38	19346	0.35	23250	0.31
Kerala	15	16806	0.36	18984	0.33	22076	0.30
Manipuri	8	8281	0.48	8672	0.46	10402	0.42
Mehsana	40	16821	0.36	18871	0.33	22898	0.29
Murrah	86	16981	0.35	19733	0.32	23661	0.27
Nagpuri	33	17466	0.34	19703	0.31	23620	0.27
Niliravi	41	17480	0.32	19031	0.29	21657	0.25
Pandhpuri	40	17323	0.33	19058	0.30	23440	0.26
U P Buffaloes	90	17461	0.32	19712	0.29	23645	0.25
Surti	41	17500	0.34	19747	0.31	23679	0.27
Tarai	18	16390	0.34	17647	0.31	22078	0.27
Toda	31	16104	0.38	19017	0.35	22801	0.31
Total	**625**		**0.36**		**0.33**		**0.29**

buffaloes under the National Bovine Genome Centre (indigenous breeds) under the Mission of Enhancement of Bovine Productivity being implemented by DADF.

SNP based diversity analysis in buffaloes: A total of 23,306 genome wide SNPs were analysed for identification of admixture among buffalo breeds/populations. The data was analysed using software Faststruct with K =17 i.e the number of populations belonging to different geographical locations. The admixture proportions for each of the populations were estimated using ancestry coefficients.

The analysis reveals high degree of admixture for most of the buffalo populations of the country except Chilika, Mehsana, Toda, Assam and Manipuri. The buffaloes of Manipur and Assam are primarily swamp buffaloes. Although the sampling was done purely on phenotypic characteristics, still there are few animals that are crosses of riverine x swamp buffaloes. The spatial genetic analysis of the SNP data on diverse breeds of buffalo grouped all the populations into eleven different entities.

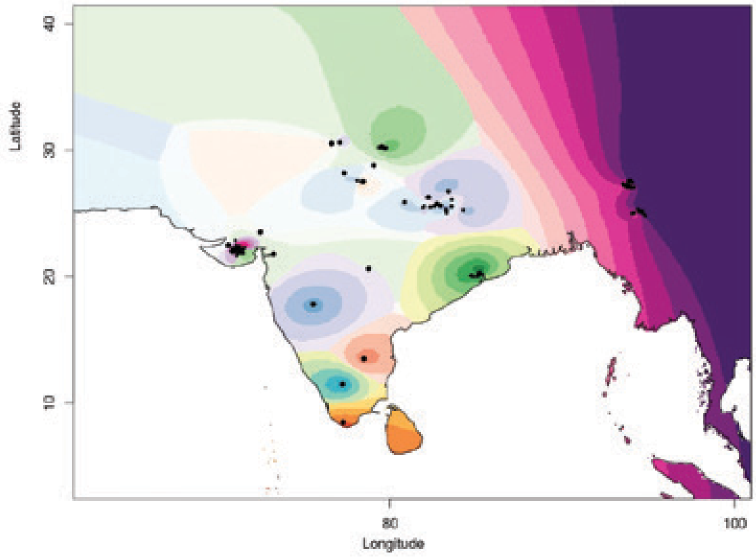
The first group consists of swamp buffaloes of North East region of Assam and Manipur, the second group of Chilika buffaloes, the third group of Murrah and Nili Ravi buffaloes, the fourth group of Surti, Mehsana, Nagpuri and Banni buffaloes. Kerala buffaloes, Toda and Kalasthi buffaloes forming separate clusters or groups. Tarai and Bhadawari form two separate groups and rest of the UP buffaloes formed two groups. Thus, there were in all 11 groups based on their ancestry coefficients.



Admixture among diverse buffalo populations of India

1= Banni, 2= Bhadawari, 3= Chilika, 4= Murrah, 5= Jaffarabadi, 6=Kalasthi, 7=Kerala, 8= Mehsana, 9= Nagpuri, 10= NiliRavi, 11= Pandharpuri, 12= UP buffaloes, 13= Surti, 14= Tarai, 15= Toda, 16= Assam, 17= Manipuri

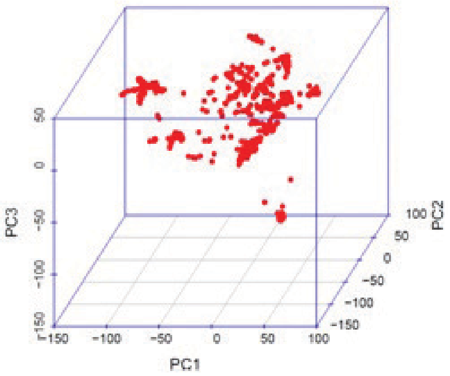
Genome wide association studies in buffalo: The phenotype data which was recorded from the field and belonged to the daughters of the 12 sires was analyzed using identified SNP markers which were genome wide in nature. Genotyping by Sequencing (GBS) method was utilized to identify the genome wide markers. Owing to the very nature of the technique, the SNPs may not be common in all the individuals on which the data was generated. The technique of imputation was used to get all the SNPs genotyped across 1763 buffaloes for which the phenotypic data was generated. Imputation was carried out using half sib design as the sires to which these daughters belonged were also sequenced at 10X coverage. The daughters were imputed with the sires' sequence data to which they were born. The imputation was carried out using Beagle version 4.0 software. Data on 1763 buffaloes was obtained with



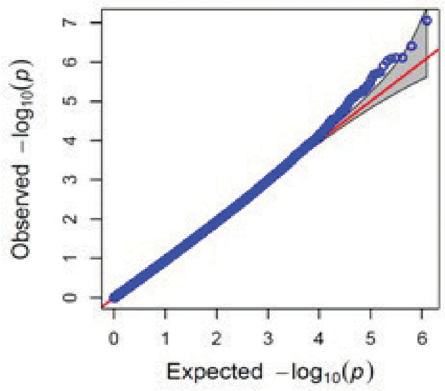
Estimation of admixture proportion in buffaloes by using ancestry coefficients

1253973 SNPs genotyped. Gapit software, an R package was used which utilises Efficient Mixed Model Association (EMMA) R package, P3D-Population parameters previously defined. The EMMA R package uses the EMMA algorithm to reduce computational time when estimating variance components in the mixed linear model (MLM). Compressed mixed linear model was used for the GWAS. The GWAS was utilized to identify the SNPs which were significantly associated with the traits of interest. More so, the Infinitesimal model by including large number of SNP markers for the quantitative traits and estimating the effect of each SNP is used for prediction of breeding value of individuals based on the genotype only. Identifying the genetic potential of individuals is one of the ultimate goals of genetic researchers especially in large ruminants and this potential can be incorporated into selection programs. Gapit software which utilizes the CMLM method developed for GWAS can be efficiently used for genomic prediction and selection, and can provide accurate predictions with a dramatic reduction in computational time.

The data was analyzed using CMLM with 1763 buffaloes with known genotypes (obtained from GBS and imputation) and several traits for which the phenotype data was generated in the field. The traits of economic interest were :



Principal component analysis for milk yield



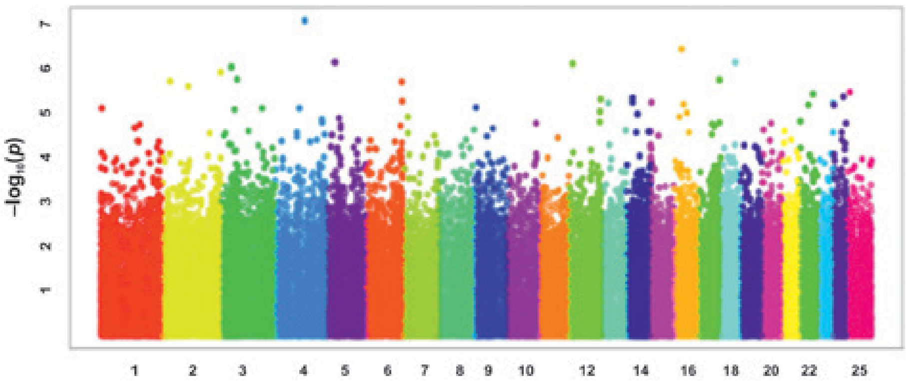
Quantile-quantile (QQ) plot of P-values for milk yield

Milk yield, Fat percentage, Protein percentage, Somatic cell count (as indicator of mastitis), Age at first calving and age at first heat (functional traits), Total fat (synthetic variable), Total protein (Synthetic variable).

We utilized the Kinship matrix obtained from the SNP markers and used the Principal Component analysis to take care of the structuring of data. The mixed linear model (MLM) included both fixed and random effects. We included individuals as random effects which provides MLM the ability to incorporate information about relationships among individuals. This information about relationships was conveyed through the kinship (K) matrix, which is used in MLM as the variance-covariance matrix between the individuals. When a genetic marker-based kinship matrix (K) is used jointly with population structure, it improves the statistical power compared to population structure only.

Three dimensional PCA diagram is depicted for the trait milk yield which is being shown as the representative trait in the present analysis.

The quantile-quantile (QQ) plot for the trait milk yield in buffaloes presents the assessment as to how well the model used in GWAS accounts for population structure and familial relatedness. The negative logarithms of the P- values from



Manhattan plot for milk yield in buffaloes

the models fitted in GWAS are plotted against their expected value under the null hypothesis of no association with the trait. Most of the SNPs tested are probably not associated with the trait. the majority of the points in the QQ-plot should lie on the diagonal line. Deviations from this line suggest the presence of spurious associations due to population structure and familial relatedness, and that the GWAS model does not sufficiently account for these spurious associations. It is expected that the SNPs on the upper right section of the graph deviate from the diagonal. These SNPs are most likely associated with the trait under study. By default, the QQ-plots in GAPIT show only a subset of the larger P-values (i.e. less significant P-values) to reduce the file size of the graph.

The Y-axis is the observed negative base 10 logarithm of the *P*-values, and the X-axis is the expected observed negative base 10 logarithm of the *P*- values under the assumption that the *P*-values follow a uniform [0,1] distribution. The dotted lines show the 95% confidence interval for the QQ-plot under the null hypothesis of no association between the SNP and the trait.

The Manhattan plot is a scatter plot that summarizes GWAS results. The X-axis is the genomic position of each SNP, and the Y-axis is the negative logarithm of the P-value obtained from the GWAS model (specifically from the F-test for testing H0: No association between the SNP and trait). Large peaks in the Manhattan plot (i.e., “skyscrapers”) suggest that the surrounding genomic region has a strong association with the trait. Manhattan plot for the entire genome and individual Manhattan plots for each chromosome can be drawn.

Each chromosome is colored differently. SNPs with stronger associations with the trait have a larger Y-coordinate value. The size of the first chromosomes being wider as they are large and metacentric chromosomes.

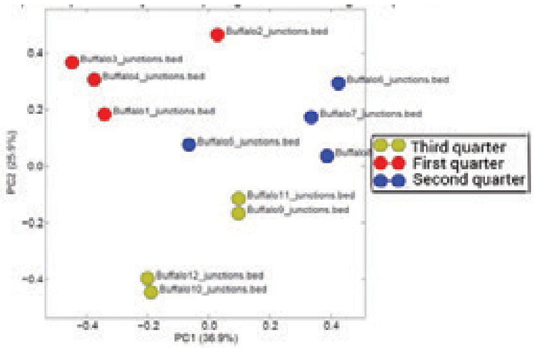
We estimated the Best Linear Unbiased Prediction and the Best Linear Unbiased estimates of the trait based on SNP effects. Once the SNP effects are available, the predicted value of the trait can be estimated by only the knowledge of the genotypes. These genotypes can be generated at birth, allowing the selection of the individuals with higher genetic merit at an early stage. However, this shall require the development of a reference family (with both genotypes and phenotypes available) and the animals whose phenotypes shall be predicted from the genotypes shall be known as inference group, a procedure known as Genomic Selection which is a routine in advanced countries for large ruminants (Cattle).

The significance level has been taken at $p < 10^{-5}$. The highly significant SNPs are being annotated for the identification of their location -whether exonic, intronic or intergenic. In case of intergenic SNPs (significantly associated), the nearest genes shall be identified.

SNPs association with various traits

Trait	Number of significant SNPs
Milk yield	132
Fat percent	147
Protein percent	208
Somatic cell count	107
Total fat	198
Total protein	169
Age at first calving	140
Age at first heat	110

Transcriptome analysis of milk in buffalo: Milk transcriptome data was generated for three stages of lactation in buffaloes viz; Initial three months (early lactation), next three months (mid lactation) and last three months (late lactation). The Next Generation sequence data was mapped on the cattle genome (the nearest relative of cattle whose sequence is available in public domain). The mapped data was then processed to find out the genes which were differentially expressed during the three lactation stages. The marker gene correlations found in the analysis have been depicted.



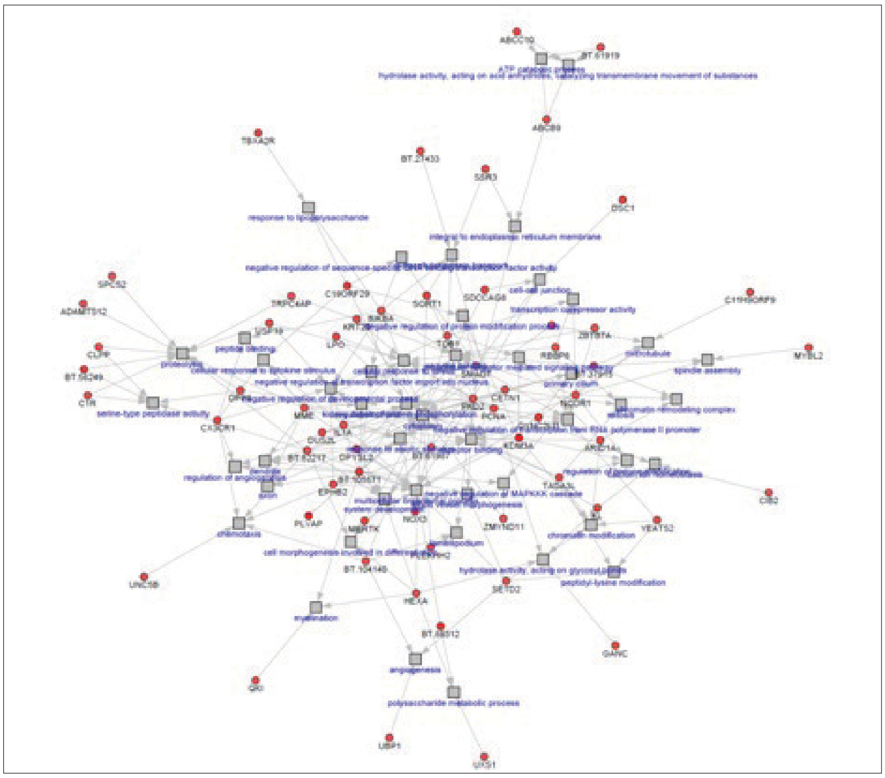
Principal component analysis - sample Log Folds - Different stages comparison

The diagram reveals that the three stages of lactation present specific set of genes being expressed. The principal component analysis of data revealed that the three stages of lactation grouped together as given.

The principal component analysis revealed that the first PC accounts for 37% of the total variance while the second PC accounts for 26% of the total variance. The up-regulated genes were associated with different Wiki Pathways. The major pathways of up regulated genes were MAPK Signalling Pathway (WP 998) between the III and I stage of lactation, Calcium regulation in the Cardiac (WP1043) for III vs II, BDNF Signaling Pathway (3141) for II vs I, exercise induced circardian regulation (WP3230) for II vs I stage of lactation. The upregulated genes between III and I (WP3231) related to senescence and autophagy, primary focal segmental glomerular disease (Wp3233) for II vs I stage of lactation, myometrial relaxaion and contraction pathways in III vs II quarter. Similarly the comparison of upregulated micro RNA and transcription factor binding sites have also been completed. The sum up of genes, microRNA and transcription factor binding sites reveal the following structure as per the Z score utilising Wiki pathways.

All the Pathways affected are in one way associated with the milk composition and or formation of milk.

In addition, *de novo* assembly of the buffalo transcripts was also carried out. The up-regulation of genes between III and I lactation and between II and I stage of lactation have also been identified and our analysis also includes the microRNAs as well as transcription factor



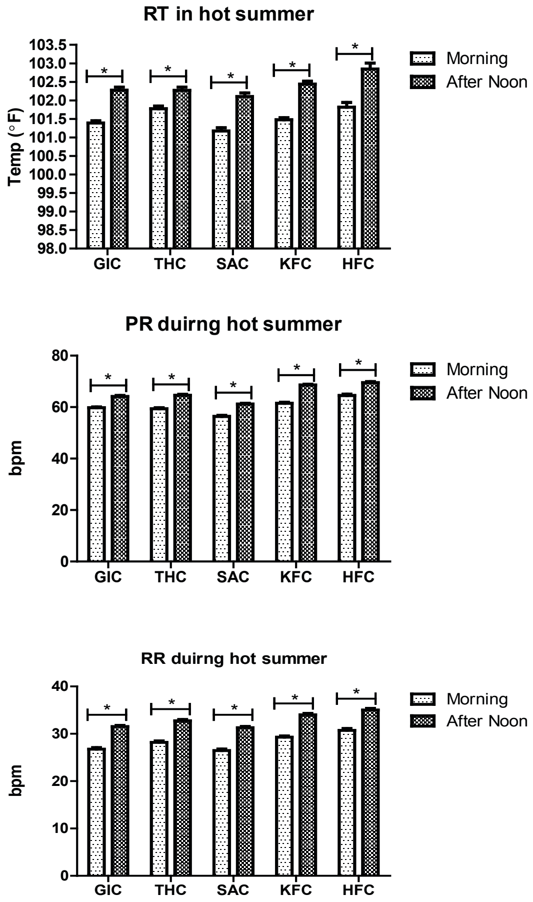
Network analysis of the genes up-regulated between II and I stage of lactation

binding sites. Similarly, the work on down-regulation of genes and associated pathways is being carried out and the genes underlying the QTL regions are being recognised which may be the candidate genes for milk traits in buffaloes.

Evaluation of milk fat as an alternative source of RNA from buffalo milk: Since no specific commercial kits are available for extraction of total RNA from Milk Fat Globules (MFG), the methodology for extraction of total RNA from buffalo milk fat was optimized. Milk fat (containing MFGs) was separated from milk by centrifugation. RNA was isolated from the two different sources namely milk and MFG using three different methods: 1) Trizol extraction method, 2) Commercial RNA isolation kit and 3) Combination of Trizol method and commercial kit. All the experiments were carried out in triplicate. Maximum yield of total RNA was obtained by Trizol method followed by purification using filter columns in both milk and fat. Least amount of mRNA was isolated using only commercial kits. However, much higher yields were obtained from buffalo milk fat as compared to skim milk, with manual method as well as commercial kits. Quality and integrity of the samples from both methods was comparable. The A260/280 ratio was observed to be between 1.9 and 2.05 in all cases. The quantitative-PCR (qPCR) was performed on cDNA derived from both milk and fat RNA, using the specific primers for RPS9, ACTB and CSN2 genes. Quantitative profiling of mammary gland specific genes from skim milk and fat derived RNA validated the efficiency of MFG as an alternate source of total RNA. This study confirmed that the RNA obtained from buffalo MFG was suitable for studies of mammary genes expression.

Genome Data Mining for Thermotolerance and Adaptation in Native Cattle and Buffaloes

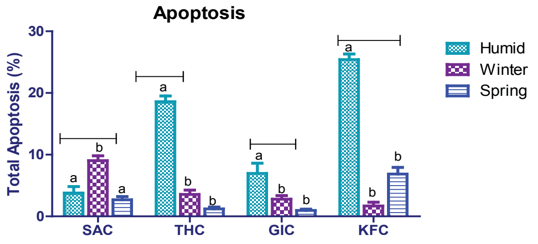
Phenomic data related to cellular, biochemical and molecular changes in heat stress: During the year, a total of 2400 physiological data with respect to respiration rate, pulse rate, rectal temp, skin temperature were recorded in animals of Sahiwal, Tharparkar, Gir (native cattle), Karan Fries (Cross-bred) , Holstein Frisian (Exotic cattle) and Murrah buffaloes across hot summer, humid, winter and spring season. These measurements were done in order to visualize the effect of heat stress at higher Temperature Humidity Index (THI) on different cattle types and Murrah buffaloes. On combining the physiological values, across breeds and seasons, it was observed that maximum respiration rate, pulse rate, rectal temp, skin temperature were recorded in hot summer afternoon. Holsten Frisian followed by Karan Fries cattle showed higher physiological values while native cattle, showed minimal physiological stress at higher THI.



*Rectal temperature (RT), Respiration rate (RR) and Pulse rate (PR) in Gir (GIC), Tharpakar (THC), sahiwl (SAC), Karan Fries (KFC) and Holstein Frsian (HFC) cattle during hot summer (THI>85; *<0.05).*

In addition to generate systematic phenotype data related to thermo-physiological parameters, efforts were also made to generate, biochemical, and hematological changes in Sahiwal, Tharparkar, Gir, Karan Fries , Holstein Frisian and Murrah buffaloes. For this, more than 1000 blood samples were collected from these breeds to generate complete blood count (CBC) profile as well as to conduct serum biochemical analysis. For haematological profile, data on various hematological parameters like white blood cells (WBCs), red blood cells (RBCs), hemoglobin (Hb), packed cell volume (PCV), etc. were generated in 5 cattle and 1 buffalo breeds exposed to different seasons and THI. The data showed season effect on several hematological parameters in different breeds. For example, both Karan Fries and Holstein Frisian cattle showed significant ($p<0.05$) decline in Hb level during summer and humid seasons (≥ 85 THI) in comparison to winter period. In Gir and other native breeds as well there was a reduction in Hb level during summer and humid seasons but the difference was non-significant ($p>0.05$). Such an effort has helped to generate systematic data on physiological, biochemical, hematological data in different cattle types and buffaloes across four different seasons, covering different THI.

The data on cellular parameters like aptoptosis and oxidative stress were generated in PBMCs of different cattle types across varying degree of THI and season. For this study, a total of 80 PBMCs samples collected during different



Comparative analysis of cellular aptoptsis in PBMCs of Sahiwal (SAC), Tharparkar (THC), Gir (GIC) and Karan Fries (KFC) cows across humid, winter and spring seasons

seasons were used to generate cellular data with respect to total apoptosis and oxidative stress in Gir, Sahiwal, Tharpakar and Karan Fries cattle across hot humid, winter and spring period (August 2017-March 2018). These measurements were done in order to visualize the effect of heat stress at higher THI on different cattle types. The mean data on total apoptosis and oxidative stress indicated higher cellular stress in PBMCs of Karan Fries cows during hot humid condition in comparison to PBMCs of native cattle. Efforts are underway to generate cellular response data in hot summer as well.

Allelic spectra in heat shock factor gene in diverse native cattle adapted to different agroclimatic regions: In continuation to our earlier effort to characterize, heat responsive genes, this year, heat shock factor gene was sequenced characterized in Indian native cattle and genotyping was carried out at two different locus: 909 and 4693. A total of 883 animals were screened for HSF-909 locus from 18 cattle breeds *viz.*, Indian cattle- Tharparkar (n=84), Rathi (n=32), Nagori (n=32), Red Sindhi (n=32), Malvi (n=32), Kankrej (n=30), Gir(n=59), Sahiwal (n=99), Hariana (n=32), Red Kandhari(n=32), Nimari(n=32), Dangi (n=26), Khillar (n=30), Ladakhi (n=30), Gaolao (n=20) and exotic/crossbred cattle- Jersey (n=36), Holstein Frisian (n=95), and Karan Fries (n=150). CC genotype was observed to be predominantly present in Indian cattle breeds with overall allelic frequency (0.895) followed by TC and TT genotypes. Whereas in exotic or crossbred cattle breeds the TC genotype was higher with frequency of 0.615 followed by CC and TT genotype with 0.237, 0.148 frequency, respectively.

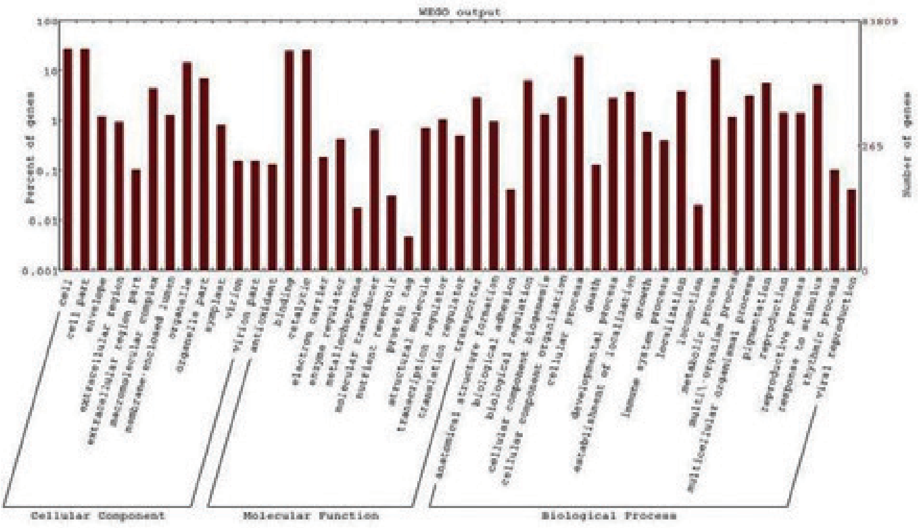
Additionally, for HSF-4693 locus, a total of 711 animals were screened from 17 cattle breeds Indian cattle- Tharparkar (n=82), Rathi (n=32), Nagori (n=32), Red Sindhi (n=32), Malvi (n=32), Kankrej (n=30), Gir(n=63), Sahiwal (n=71), Hariana (n=32), Red Kandhari (n=32), Nimari(n=32), Dangi (n=26), Khillar (n=30), Ladakhi (n=30) and exotic/crossbred cattle- Jersey(n=14), Holstein Frisian (n=48), and Karan Fries (n= 99). Analysis revealed that TT genotype was predominantly present in Indian cattle with frequency of 0.725 followed by GG and GT genotype. Such information will be vital for future genotype: phenotype association studies for theromotolerant and adaptation traits.

Expression of genes related to high altitude adaptation in jersey cows migrated from tropical condition: In this study, an effort was made to evaluate the transcriptional pattern of hypoxia related genes such as hypoxia inducing factor α (*HIF-1α*), vascular endothelial growth factor A (*VEGFA*), glucose transporter-1 (*GLUT-1*), Tumor necrosis factor-1 (*TNF-1*), glutathione peroxidase-1 (*GPX-1*), superoxide dismutase 2 (*SOD2*) *etc* in Jersey cattle transported from sea level tropical condition to high altitude hypoxia condition. For this study blood was collected from external jugular vein of 18 Jersey animals at 8 different time points *i.e.* zero week (mean sea level) and then at regular intervals (2nd, 3rd, 23rd, 40th, 80th, 86th, and 110th week) after animals were shifted to high altitude. The peripheral blood mononuclear cells (PBMC) were purified and used for qPCR based expression analysis. The analysis has helped us to understand about the expression pattern of certain genes known to be associated with high altitude adaptation. Efforts are underway to generate more information on high altitude acclimation and adaptation using molecular tools.

Cellular and transcriptional changes in heat stressed skin fibroblast of Indian native cattle and buffaloes: For this study, primary fibroblast culture established form ear pinna samples of Sahiwal cows (*Bos indicus*) and Murrah buffaloes (*Bubalus Bubalis*) were exposed to thermal stress at 42°C for 1 hour. The cells were subsequently allowed to recover at 37°C and harvested at different time intervals (0h, 2h, 4h, 8h, 16h and 24h) along with control samples. Different cellular parameters *viz.*, apoptosis, proliferation, mitochondrial membrane potential (ΔΨm), oxidative stress, along with expression pattern of heat responsive genes and miRNAs were determined. The cell viability and proliferation rate of heat stressed fibroblast cells decreased significantly ($p<0.05$) for both the species. On the other hand, cellular parameters like cell cytotoxicity, apoptosis, production of reactive oxygen species and ΔΨm increased significantly ($p<0.05$) in heat stressed fibroblasts cells. The pattern heat shock proteins, inflammation/immune genes and heat responsive miRNA during pre- and post-heat stress also showed subtle differences in induction of their expression level in buffalo and native cattle fibroblast cells (Fig.3). The kind of cellular response, pattern of *HSP* genes, and heat responsive miRNA before and after heat stress indicated better cellular tolerance of fibroblast cells derived from Indian native cows compared to riverine buffaloes.

Skeletal Muscle Transcriptome Profiling of Bandur (Mandya) Sheep

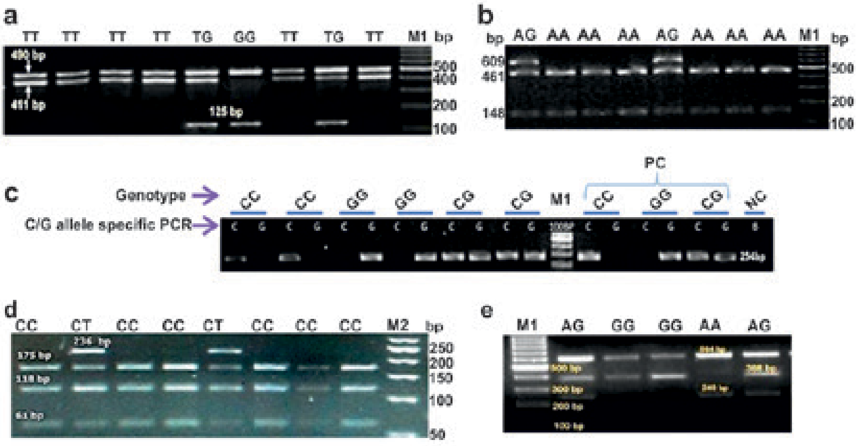
The mutton of Bandur and local sheep was analyzed for 17 amino acids and 12 fatty acids. Bandur had a significantly higher level of oleic acid and histidine as compared to local sheep. The high throughput RNA sequencing technique was used to establish the transcriptomic profiles of skeletal muscles of Bandur and local sheep of Karnataka. Paired end sequencing was performed on Illumina HiSeq-2000 Platform. The raw reads were filtered and mapped to the sheep genome sequence assembly Oar 3.1. A total of 20568 transcripts were observed to be differentially expressed across Bandur and local sheep. Of



Gene ontology catgories of DE genes in Bandur and Local sheep of Karnataka these, 10729 were down regulated and 1236 were significantly down regulated in Bandur ($p \leq 0.05$). Similarly, 9839 transcripts were up regulated, out of which 602 were significant. All the DE genes could be classified into 395 functional categories using DAVID which included 132 Gene Ontology (GO) terms for biological process, 146 terms for cellular components and 117 terms for molecular functions. A total of 25 annotation clusters were identified with enrichment score of > 0.76 and $p<0.05$. The significantly enriched clusters were involved with nucleic acid binding, RNA catabolic process, cellular response to stress, regulation of protein polymerization, muscle development and regulation, actin and cytoskeleton organization, as well as amino acid phosphorylation. As expected, 99 GO terms were related to muscle or protein and fat metabolism. Prominent pathways were detected that are relevant to meat quality were AMPK signaling pathway, Adipocytokine signaling pathway, PPAR signaling pathway, Biosynthesis of amino acids, Calcium signaling pathway, Lipid metabolism, Muscle development and differentiation and Ketone body metabolism. The data was also used to identify a large number of SNPs across the two groups of sheep. The results provide information of candidate genes and pathways that contribute to the differences in meat quality of Bandur and local sheep.

Molecular and Physio-biochemical Evaluation for Heat Stress in Indian Sheep

The research was conducted to study how thermo-tolerance is modulated by HSP90 and HSP70 gene polymorphism and its association with hemato-physio-biochemical parameters, supported by their expression profiles in Chokla, Magra, Marwari, and Madras Red sheep breeds. The reference values for all the breeds for each hemato-physio-biochemical parameter was generated both under normal and heat stressed condition and their adaptability percentage was calculated. Least square analysis was carried out which revealed significant effect ($P < 0.05$) of season and breed on all the physiological parameters, i.e., temperature, respiratory rate and pulse rate (a.m. and p.m.), as well as hematological parameters like Hb, packed cell volume, total erythrocyte count (TEC), neutrophil/ lymphocyte (N/L) ratio, and total leukocyte

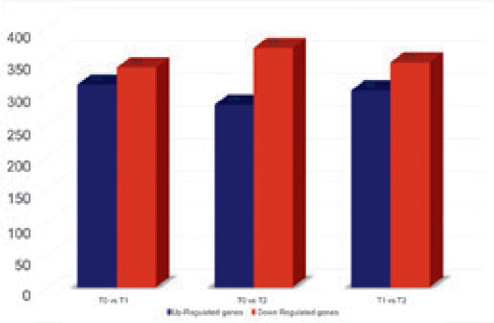


Electrophoretic patterns obtained by genotyping: a. SNP1 genotyped by tetra-primer ARMS PCR b. SNP2 by PCR-RFLP with Hpy CH4 III restriction enzyme. c. SNP4 by allele specific PCR. d. SNP3 by PCR- RFLP with Taq α I restriction enzyme. e. SNP5 by tetra-primer ARMS PCR.

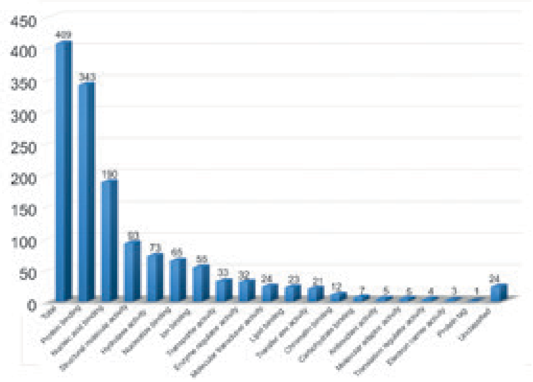
count (TLC). There was a significant influence ($P < 0.05$) of breed on biochemical parameters such as glucose, SGOT, phosphorous, triglyceride, and cholesterol. HSP90 and 70 genes were characterized by direct sequencing and 13 single-nucleotide polymorphisms (SNPs) were identified. Phylogenetic analysis of HSP 90 (93.6%) and HSP70 (96%) gene fragments revealed that these genes are highly conserved among different livestock species. Tetra-primer amplification refractory mutation system PCR, PCR-RFLP, and allele-specific PCR genotyping protocols were developed and large-scale genotyping of five SNPs was carried out for 50 DNA samples of each breed. A significant difference ($P < 0.05$) of rectal temperature (a.m.), respiratory rate (p.m.), triglyceride, and total protein was observed at SNP01; albumin at SNP2; pulse rate (p.m.) at SNP3; and rectal temperature (p.m.), pulse rate (p.m.), Hb (g/dL) and N/L ratio at SNP4 and TLC at SNP5. Predominant allele was found to be superior in most of the SNPs indicating the selection acting in directional manner (positive selection). TACCA combination of alleles of SNP1-SNP2-SNP3-SNP4-SNP5 was found to be of selection advantage for the identification of animals more adaptable to heat stress. A total of 80 plasma samples (10 animals per breed and per season) of Chokla, Marwari, Magra and Madras Red breed were used for the estimation of cortisol, T3 and T4 level by ELISA. The cortisol level was found to be higher in high THI (84) condition than lower THI (65). There was no significant effect ($P<0.05$) of cortisol level among breed, season and 5 identified SNPs of HSP90AA1 and HSP70 genes. Both T3 and T4 had significantly higher ($P<0.05$) mean values during winter season (low THI) and the genotypes of SNP1 and SNP2 were significantly effected ($P<0.05$) in case of T3 only. Gene expression analysis revealed higher expression in less adapted animals with Madras Red < Magra < Chokla < Marwari expression pattern. The results obtained are consonance with the expression profiles of different HSP genes generated in different cattle and buffalo breeds in which lower HSP expression was observed in more adaptable native animals during periods of stress.

Evaluation of Zanskar Ponies for Endurance at High Altitude of Ladakh

RNA seq based transciptome data of 9 PBMCs samples (3 each from pre-exercise (T0), post-exercise (T1) and post recovery period (T2) groups) was generated to identify the genes up- or down-regulated before and after endurance exercise at high altitude among Zanskar ponies. A total of 646 genes were found to be differentially expressed in Zanskar ponies before trial (T0) and after endurance exercise trial (T1) and 2 hr post-trial (T2). Ribosomal protein such as S21 (*RPS21*), S15A *(RPS15A)*, S28 (*RPS28*), S13 (*RPS13*), S6 (*RPS6*), S24 *(RPS24)*, L37 *(RPL37)*, L35A (*RPL35A)*, L34 (*RPL34)*, L27A *(RPL27A)*, L35 *(RPL35)*, L23 *(RPL23)*, L31 *(RPL31)* and L5 *(RPL5)* genes were among the top up-regulated genes. Beta-2-Microglobulin (B2M), an immune related gene involved in the presentation of peptide antigens to the immune system also showed an increased expression in T1 and T2 groups in comparison to T0 group. Several immune related genes such as *CXCL16, CCL5, DQA, DRB, MHCB3,* TNF receptor superfamily member 1B (*TNFRSF1B*), cathepsin W (*CTSW*), cathepsin S (*CTSS*), Integrin alpha L (*ITGAL)* were also found to be up-regulated in animals after trial. Increased expression of chemokines such as chemokine (C-X-C motif) ligand16 (*CXCL16; FPKM T1: 116.349*) and C-C Motif Chemokine Ligand 5 (*CCL5;*



Up-regulated and down-regulated differentially expressed genes (DEGs) in Zanskar ponies under endurance trial (T0: Before exercise, T1: immediately after trial; T2: 2 hr post-trial)



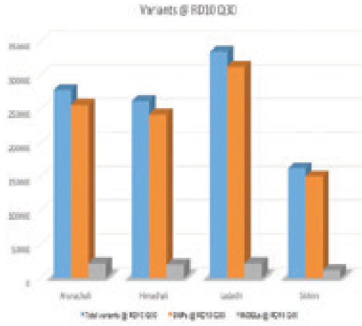
Top ontology terms for molecular functions

FPKM T2:3604) after trial treatment indicated strong inflammatory response in horses during stress conditions. These chemokines actively participate in cell cycle regulation and induce strong immune response. Data suggested significant induction of hypoxia inducible factor 1A (*HIF-1A*). The anti-inflammatory superoxide dismutase 1 (*SOD1*) also showed increased expression in T1 and T2 groups after exercise.

The up-regulated genes in Zanskar ponies were classified in terms of most significant biological processes and molecular functions enriched in the data set. Top biological processes were metabolic process (311 genes), biological regulation (276 genes), localization (244 genes), response to stimulus (216 genes), unicellular organismal process (164 genes), multi-organism process (159 genes), cell communication (157 genes), and cell proliferation (65 genes). Similarly, major molecular functions identified were; protein binding (343 genes), nucleic acid binding (190 genes), structural molecule activity (93 genes), hydrolase activity (73 genes), nucleotide binding (65 genes), ion binding (55 genes), transporter activity (33 genes), enzyme regulator activity (32 genes), molecular transducer activity (24 genes), lipid binding (23 genes), and transferase activity (21 genes). Some of the important molecular pathways impacted were glucagon signaling pathway, NF-kappa B signaling pathway, B cell receptor signaling pathway, antigen processing and presentation, natural killer cell mediated cytotoxicity, RNA transport and protein export.

Genome Wide Diversity in Indian Yaks

Indian yaks belonging to Arunachali, Himachali, Ladakhi and Sikkimi yak were used for the identification of genome wide SNPs and INDELs using Illumina TrueSeq chemistry on Illumina HiSeq 2000 platform. The number of SNPs genotyped in Arunachali, Himachali, Ladakhi and Sikkimi yaks at RD 10 were 1,04,188, 67,032, 49,665 and 33,782, respectively. Overall, a total of 5,79,575 high quality SNPs along with 50,319 INDELs were identified with a coverage of 9.42% in the Indian yaks. Corresponding values for observed and expected heterozygosity were 0.3362 and 0.2981; 0.3435 and 0.2992; 0.3136 and 0.3073; 0.2831 and 0.2817, respectively.



Variants identified in Indian yaks (RD10)

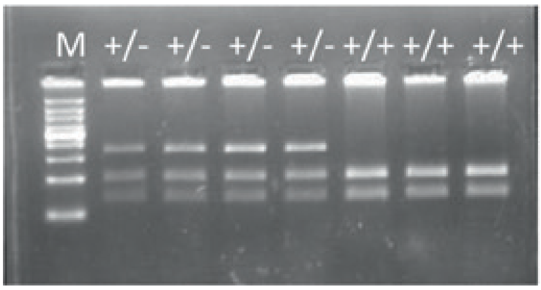
The F_{IS} value was 0 in case of Arunachali and Himachali yaks, whereas it was found to be 0.022 in Ladakhi and 0.015 in Sikkimi yaks. The genetic distance based on genome wide SNPs in the Indian yaks revealed that Ladakhi and Sikkimi yak populations are distinct.

Karyotyping and DNA Testing for Genetic Defects in Indian Livestock

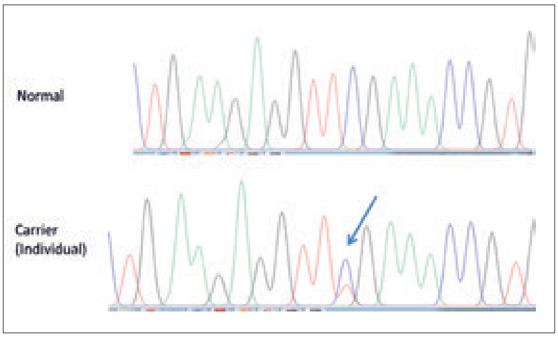
Loci of five lethal genetic diseases – Congenital vertebral malformation (CVM), Jersey Haplotype (JH1), Holstein haplotypes -HH3, HH4 and Holstein cholesterol deficiency (HCD) – were characterized for the presence of mutant allele(s) in Indian cattle population. PCR products for each disease were amplified and sequenced in five different genetic groups- Jersey, Jersey Crossbred, Holstein Frisian (HF), HF Crossbreds and indigenous *Bos indicus* comprising 10 male samples in each group.

Two mutant alleles -JH1 and HH4 in heterozygous condition were identified in Jersey and Holstein genetic groups, respectively. Lethal JH1, originated through a point mutation in CWC15 gene causes early embryonic death of foetus in Jersey cattle. Sequencing and PCR-RFLP by TaqαI enzyme confirmed the presence of JH1 allele with heterozygous condition in seven animals from 40 Jersey bulls screened. The HH4 is also a lethal mutation at GART gene, causing the embryonic death in cows of Holstein origin. Sequencing and PCR-RFLP by MseI enzyme indicated the presence of HH4 mutant allele in two males out of 100 bulls of Holstein origin (HF and HF crosses) screened. These are first reports about the presence of lethal JH1 and HH4 mutations in Indian cattle population, specifically in exotic type. Novel PCR based tests including PCR-RFLP protocols were developed for screening of JH1and HH4 mutations. These PCR based tests developed would be helpful for rapid screening of the genetic diseases in Indian cattle, specifically of exotic origin.

Services for chromosomal screening and DNA testing for genetic diseases- BLAD, FXID, Citrullinemia and Deficiency of uridine mono phosphate synthase (DUMPS, in HF/HFX only) was provided to different government agencies of J&K, HP, Uttarakhand, Punjab, Haryana, Rajasthan &UP states and Indian Army. Total 344 bulls/males (125 cattle, 219 buffalo), one buffalo female, 17 breeding pigs and 5 breeding dogs were screened for chromosomal defects. Total 142 bulls of cattle (93) and buffalo (49) were screened for genetic diseases. One bull was found to carry the chromosomal defect. Total Rs. 8,30,500/- was received as a revenue to the institute from these services provided under the project during the period.



PCR-RFLP Test for JH1 mutation in Jersey bull



Chromatogram of wild homozygous (normal) and Heterozygous (carrier) animal for JH1 loc

Network Project on AnGR

Project was initiated in VIII plan for characterization of breeds. During IX and X plan, conservation activities were also initiated along with characterization of breeds. Genetic characterization was also commenced in IX plan by establishing 3 core labs. During XI plan, project activities were shifted to buffalo genomics to establish baseline information of buffalo genome. In XII plan, focus was again shifted to basic mandate of the Bureau and 18 new breeds/populations have been undertaken for characterization and 4 at risk breeds for conservation. In 2017-20, 9 new populations have been undertaken for characterization and 2 breeds are being conserved in their habitat.

Livestock and poultry breeds for characterization and conservation under Network Project

Sr. No.	Species	Breed/population	Centre
Characterization			
1.	Cattle	Vandarvi Kamma	WASSAN (NGO), Telengana
2.		Kathani	BAIF, Pune
3.	Goat	Balangir	
4.		Sojat	RAJUVAS, Udaipur
5.	Duck	Manipuri	CAU, Imphal
6.	Chicken	Poonchi	SKUAST, Jammu
7.	Camel	Marwari and Sindhi	NRCC, Bikaner
Conservation			
8.	Camel	Kharai	Sahjeevan (NGO)
9.	Chicken	Ankleshwar	AAU, Anand, Gujarat

* * *

Research Projects & Publications

- Research Projects
- Publications
- Awards

Research Projects

Completed IRC Projects

1. Haplotypic diversity of Indian cattle breeds based on Y-Chromosome specific markers - Indrajit Ganguly and Sanjeev Singh - April, 2014 to March, 2017, extended up to March, 2018.
2. Phenotypic and genetic characterization of buffalo populations of Odisha - RS Kataria, SK Niranjan, Vikas Vohra (NBAGR), Sanat Mishra and SK Das (OUAT, Odisha) - April, 2014 to March, 2018.
3. Phenotypic characterization of Chitarangi and Dumba sheep in their native tract - AK Mishra, Sanjeev Singh and Anand Jain - April, 2015 to March 2018.
4. Classification of indigenous sheep breeds of India based on morphometric traits using classical and heuristic methods - Dinesh Kumar Yadav and Avnish Kumar - April, 2016 to March, 2018.
5. Molecular and physio-biochemical evaluation of Heat Stress Protein genes in Indian sheep breeds - Sanjeev Singh, Indrajit Ganguly, KN Raja, HK Narula (CSWRI) R Venkataramanan (TANVASU) and Anita Ganguly, LUVAS - April, 2014 to March, 2018.
6. Characterization of Bidri and Nandidurga goats of Karnataka - MS Tantia, PK Vij, VS Kulkarni (UAS, Dharwar) and VB Shettar & HM Yatish (KVAFSU, Bidar) and Rekha Sharma (wef. 01.04.2017) - April, 2016 to March, 2018.

Ongoing IRC Projects

1. Deciphering the molecular basis of male sub-fertility or sterility in bovines - Sonika Ahlawat, Rekha Sharma and Sachinandan De (NDRI) and Reena Arora (from Nov.2014) - April, 2014 to March, 2018.
2. Characterization and evaluation of lesser known cattle populations (Vandharvi, Zari and Kamma) of Telangana state - RK Pundir, PK Singh and PS Dangi, Shilpi Sharma (TSBDB) and Sabyasachi Das (WASSAN-NGO) - July, 2017 to June, 2020.
3. Characterization of non-described cattle population of Kerala and Tamil Nadu - KN Raja, AK Mishra, R Saravanan (TANVAS) and K Anil Kumar (KANVAS) - October, 2017 to September, 2020.
4. Characterization of Mangadh Dahodi cattle of Gujarat - RAK Aggarwal, PK Vij, MS Tantia and Sukram Ninama; Prakriti Foundation - October, 2017 to September, 2019.
5. Identification, characterization and evaluation of mixed indigenous cattle populations of Haryana, Punjab and North-West Rajasthan - Anand Jain, DK Yadav and HK Singh (CHRS Rohtak) - October, 2017 to March, 2020.
6. Conservation of Sahiwal and Hariana cattle at Gaushalas - RK Pundir, Arjava Sharma, PK Singh, AK Mishra and KN Raja - April, 2015 to March, 2020.
7. Identification of genetic and phenotypic variation associated with tick infestation in Indian Cattle - Karan Veer Singh, Vikas

Vohra, Jayakumar S and Kamal Jaiswal, (BBAU Lucknow) - April, 2016 to March, 2019.

8. Characterization and evaluation of some non-descript buffalo populations of central and eastern India - Vikas Vohra, RS Kataria, Monika Sodhi, Karanvir Singh, PS Dangi, SV Kuralkar (PGIVAS, Akola) and R Das (VO- ARD, Tirpura) - October, 2017 to September, 2020.

9. Skeletal muscle transcriptome profiling of Bandur (Mandya) sheep - Reena Arora, Sonika Ahlawat and RK Vijh - April, 2016 to March, 2019.

10. Identification and characterization of goat germplasm of Andhra Pradesh and Telangana states - NK Verma, RAK Aggarwal, Rekha Sharma and PS Dangi - October, 2017 to March, 2020.

11. Study of the genetic variability present across the goat Major Histocompatibility complex Class II antigens - Jyotsna and NK Verma - April, 2015 to March, 2018 (Extended).

12. Genome wide diversity analysis of Indian Yak populations - Jayakumar S, SP Dixit and Karan Veer Singh - April, 2015 to March, 2018 (Extended).

13. Phenotypic and genetic characterization of yak and donkey populations of North trans-Himalayan region of India - SK Niranjan, Rahul Behl, Jyotsna Behl, M Iqbal (CAHO, Leh) and Vijay K Bharti (DIHAR, Leh) - July, 2017 to March, 2020.

14. Development of mobile application on farm animal genetic resources of India - Avnish Kumar and DK Yadav - October, 2017 to March, 2019.

15. Network Project on Animal Genetic Resources - Arjava Sharma (w.e.f.01.10.2013) Director NBAGR, Project coordinator and MS Tantia (I/c, Network Project) - 1992- Contd.

16. Evaluation of livestock policies and programmes for the management of Animal Genetic Resources in Haryana and Punjab states - PK Singh, RK Pundir, Arjava Sharma and HK, Verma (GADVASU) - July, 2017 to June, 2019.

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

External Funded Projects

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

2. Delineating beta casein variants in Indian cows and potential health implications of A1A2 milk - Monika Sodhi, M Mukesh, RS Kataria and SK Niranjan - July, 2015 to June, 2018.

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

July, 2015 to December, 2016, Extended up to 30th November, 2017.

4. CRP on Agro-biodiversity conservation of animal genetic resources - MS Tantia, PK Vij, RAK Aggarwal and Rekha Sharma - April, 2015 to March, 2017, extended up to March. 2020.

5. ICAR-AGRI Consortia Research Platform project on Genomics: - Identification of markers for economic traits and Transcriptomics study in Buffalo and goats - RK Vijh, Reena Arora, Sonika Ahlawat, Jayakumar S and SP Dixit - June, 2015 to March, 2017, extended up to March, 2020.

National Fellow Project

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

Publications

Research Articles

1. Arora R, Yadav DK, Sharma A, Pothuraju M, Tanwar N and Girdhar Y (2017) Tetra-primer ARMS-PCR assay for genotyping SNPs in ovine *GDF8* gene associated with mutton traits in sheep. *Indian Journal of Animal Sciences* 87(4): 525-528.

2. Behl JD, Sharma A, Kataria RS, Verma NK, Kimothi SP, Bhatia AK and Behl R (2017) Characterization of genetic polymorphism in Toll like receptor 9 gene in *Bos indicus* Sahiwal cattle. *Indian Journal of Animal Sciences* 87(11): 1362-1366.

3. Behl R, Niranjan SK, Behl J and Vijh RK (2017) Comparison of three types of Indian donkey populations based on morphometric characteristics. *Journal of Livestock Biodiversity* 7(1): 17-21.

4. Behl R, Niranjan SK, Behl J, Tantia MS, Arora R, Rao DMV, Reddy PP, Vijh RK and Sharma A (2017) Genetic characterization of brown type donkeys of Andhra Pradesh using microsatellite markers. *Indian Journal of Animal Sciences* 87(9): 1102-1105.

5. Behl R, Sadana DK, Behl J, Banerjee P, Joshi J, Vijh RK, Attri PN, Nadda S and Joshi BK (2017) Characterization and microsatellite analysis for genetic diversity and bottlenecks of Spiti donkeys. *Indian Journal of Animal Sciences* 87: 1221-1225.

6. Behl R, Vij PK, Behl J and Sharma A (2017) Population trends and distribution of equines in India. *Journal of Livestock Biodiversity* 7 (2): 71-77.

7. Dash S, Singh A, Bhatia AK, Jayakumar S, Sharma A, Singh S, Ganguly I and Dixit SP (2017) Evaluation of Bovine High-Density SNP genotyping array in indigenous dairy cattle breeds. *Animal Biotechnology* 1-7.

8. Dubey PK, Dubey S, Mishra SK, Arora R, Patel J,. Singh KP, Kathiravan P, Mishra BP and Kataria RS (2017) PCR-SSCP analysis of MDGI gene and its association with milk production traits in river buffalo (*Bubalus bubalis*). *Research in Veterinary Science* 115: 307-309.

9. Kaur R, Sharma A, Sodhi M, Swami SK, Sharma VL, Verma P and Mukesh M (2017) Sequence characterization of Alpha 1 isoform (*ATP1A1*) of Na^+/K^+ ATPase gene and expression characteristics of its major isoforms across tissues of riverine buffaloes (*Bubalus bubalis*). *Gene Reports* 10: 97-108.

10. Kaur R, Sodhi M, Sharma A, Sharma VL, Verma P, Swami SK, Kumari P and Mukesh M (2018) Selection of suitable reference genes for normalization of quantitative RT-PCR (RT-qPCR) expression data across twelve tissues of riverine buffaloes (*Bubalus bubalis*). *PLOS ONE* doi.org/10.1371/journal.pone.0191558.

11. Kumar M, Ratwan P, Das R, Chopra A and Vohra V (2017) Allelic diversity of butyrophilin (*BTN1A1*) gene in Indian bovines. *Indonesian Journal of Biotechnology* 22(2): 92-97.

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

13. Mishra P, Dixit SP, Aggarwal RAK, Behl J, Dangi PS and Verma NK (2017) Estimation of genetic diversity and relationship among goats of Maharashtra state. *Indian Journal of Animal Sciences* 87(8): 982-990.

14. Mishra SK, Niranjan SK, Banerjee B, Singh R, Singh RV, Kumar N and Kataria RS (2017) Genetic diversity at MHC-DRB3 locus suggests distinctness of the riverine-swamp buffalo populations in North-East region of India. *Indian Journal of Animal Research* DOI:10.18805/ijar.v0iOF.8000

15. Mukesh M, Kishore A, Sharma A, Tantia MS, Kataria RS, Mohanty AK and Sodhi M (2018) Selection of stably expressed internal control genes in circulating poly-morpho-neutrophils of periparturient Sahiwal (*Bos indicus*) cows. *Indian Journal of Animal Sciences* 88: 84-90.

16. Nigam A, Swami SK, Sodhi M, Verma P, Singh MK, Kumari P, Sharma A, Verma OP and Mukesh M (2018) Conservation of coding and untranslated regions of heat shock protein Beta-1 (*HSPB1*) gene

and its expression pattern in heat stressed peripheral blood mononuclear cells of Indian native cattle (*Bos indicus*) and riverine buffaloes (*Bubalus bubalis*). *Agri Gene* 8: 9-17.

17. Niranjan SK, Kataria RS, Sodhi M, Bharti VK, Kumar B, Garg A, Yadav MC, Sharma A, Vivek P, Giri A and Mukesh M (2018) Evaluation of physiological parameters in response to endurance exercise of Zanskar ponies adapted to high altitude of Ladakh region. *Defence Life Science Journal* 3(2): 172-176.
18. Raja KN, Saravanan R, Devendran P, Singh PK, Mishra AK and Ganguly I (2017) Cytogenetic profile of Rajapalayam dog breed of Southern India. *Indian Journal of Animal Research* DOI:10.18805/ijar.v0iOF.9132.
19. Ranjan A, Raja KN, Sinha R, Ganguly I, Gupta ID, Bhakat M and Mohanty TK (2017) Sequence characterization and SNP identification of *TNP1* gene in Indian cattle breeds. *Indian Journal of Animal Research* DOI:10.18805/ijar.v0iOF.8492.
20. Sarova N, Ahlawat S, Grewal A, Sharma R and Arora R (2018). Differential promoter methylation of *DAZL* gene in bulls with varying seminal parameters. *Reproduction in Domestic Animals* DOI: 10.1111/rda.13187.
21. Sharma A, Swami SK, Kumar M, Sodhi M, Kataria RS, Jain P, Bhatia AK, Mohanty AK, Niranjan SK, Shandilya UK, Kumari P and Mukesh M (2017) Analysis of sequence variability and expression pattern of lactoferrin gene in Sahiwal cows (*Bos indicus*) and Murrah buffaloes (*Bubalus bubalis*). *Journal of livestock Biodiversity* 7:1
22. Sharma R, Sharma H, Ahlawat S, Panchal P, Yash Pal, Behl R and Tantia MS (2017). Simple sequence repeat (SSR) genotypic data reveal high genetic diversity in Rajasthan donkey of India. *Indian Journal of Animal Sciences* 87 (12):1497-1503.
23. Singh KM, Singh S, Ganguly I, Raja KN, Ganguly A, Chopra A and Narula HK (2017). Association of heat stress protein 90 and 70 gene polymorphism with adaptability traits in Indian sheep (*Ovis aries*). *Cell Stress and Chaperones* 22: 675-684.
24. Singh KV, Jayakumar S, Dixit SP and Malik ZS (2017) Molecular characterization and genetic variability of Alpha Casein gene, *CSN1S1* in Bikaneri camel (*Camelus dromedarius*) milk. *Indian Journal of Animal Research* DOI:10.18805/ijar.B-3468.
25. Singh PK, Sankhala G and Singh PK (2017) Performance of Gangatiri cattle rearing in field conditions. *International Journal of Livestock Research* 7(3): 142-148.
26. Singh R, Kumar V, Rajesh C, Gurao A, Kulshrestha A, Sehgal M, Kaushik A, Sharma P, Mishra SK and Kataria RS (2017) Computational Analysis of HSP-60 Protein with Structural Insights into Chaperonin Containing TCP-1 Subunit 5 in Bos Taurus. *MOJ Proteomics Bioinformatics* 6(1): 00183.
27. Singh R, Mishra SK, Rajesh C, Dash SK, Niranjan SK and Kataria RS (2017) Chilika-A Distinct Registered Buffalo Breed of India. *International Journal of Livestock Research* 7: 259-266.
28. Singh R, Rajesh C, Mishra SK, Gurao A, Vohra V, Niranjan SK and Kataria RS (2018) Comparative expression profiling of heat-stress tolerance associated *HSP60* and *GLUT-*

1 genes in Indian buffaloes. *Indian Journal of Dairy Science* 71: 183-186.

29. Singh S, Mishra AK, Vohra V, Raja KN, Singh Y, Singh KM, Ganguly I and Arora R (2017) Microsatellite based genetic diversity estimation in Kajali sheep and its phylogenetic relationship with other indigenous sheep breeds. *Indian Journal of Animal Sciences* 87(9): 1097-1101.

30. Sodhi M, Kataria RS, Niranjan SK, Kumari P, Verma P, Swami SK, Sharma A, Bharti VK, Kumar B, Iqbal M, Rabgais S, Kumar P, Giri A, Kalia S, Gagoi D, Sarangi PP and Mukesh M (2018) Sequence characterization and genotyping of allelic variants of beta casein gene establishes native cattle of Ladakh to be a natural resource for A2 milk. *Defence Life Science Journal* 3(2): 177-181.

31. Vijh RK, Sharma U and Gokhle SB (2018) Creation of a large reference family with phenotype recording and genotype data generation in buffaloes. *Indian Journal of Animal Sciences* 88(2): 194-199.

32. Vohra V, Singh M, Das R, Chopra A and Kataria RS (2017) Multivariate analysis of biometric traits and their shared variance in Chhattisgarhi buffalo. *Indian Journal of Animal Sciences* 87(7): 864-870.

33. Yadav DK, Arora R and Jain A (2017) Classification and conservation priority of five Deccani sheep ecotypes of Maharashtra, India. *PLoS ONE* 12(9): e0184691.

Technical / Popular articles

1. अनिल कुमार मिश्र, आनंद जैन एवं संजीव सिंह (2017) चितरंगी : भारत के उत्तर – पश्चिमी क्षेत्र में पाई जाने वाली भेंड का मूल्यांकन एवं अध्ययन। पशुधन प्रकाश (8): 18–21.

2. करण वीर सिंह, विकास वोहरा, अवनीश कुमार एवं मनीषी मुकेश (2017) किलनी संक्रमण से दुधारू पशुओं का बचाव। पशुधन प्रकाश 8: 89–90.

3. करण वीर सिंह एवं एस जयकुमार (2017) भारतीय हिमालियन याक। पशुधन प्रकाश 8: 39–41.

4. तन्मय हजरा, पुष्पराज शिवहरे, सोनिका अहलावत, रेखा शर्मा, विवेक शर्मा एवं एन के वर्मा (2016) वर्तमान परिद्रश्य में गधों के दूध की महता : एक उपेक्षित जाती को सुरक्षित करने का आधार। दुग्ध गंगा (5): 17–19.

5. नरेश कुमार वर्मा (2017) नागालैंड की लम्बे बालों वाली बकरियों का शारीरिक लक्षण, प्रबन्धन व उपयोग । पशुधन प्रकाश 8: 28–32.

6. पुष्पराज शिवहरे, एम भगत, ऐ के गुप्ता अनुश्री मेश्राम, एन के वर्मा एवं ऐ के चक्रवर्ती (2016) दुधारू पशुओं में ग्र्भाश्योध, दुग्ध गंगा (5): 44–46.

7. बीरबल सिंह , गौरखमल, मोनिका सोढ़ी, प्रवेश कुमारी एवं मनीषी मुकेश (2017) ग्लोबल वार्मिंग एवं देसी पशुधन – संसाधन(पशुधन प्रकाश (8): 44–47.

8. मोनिका सोढ़ी , मनीषी मुकेश, प्रवेश कुमारी, रणजीत सिंह कटारिया, राकेश कुमार पुंडीर, प्रीती वर्मा, अंकिता शर्मा, विजय के भारती, शेलेश कुमार स्वामी, अरूप गिरी, प्रभात कुमार,दीपक गगोई एवं भुवनेश कुमार (2017) लदाखी गाय: लदाख की एक अनमोल गो–सम्पदा: पशुधन प्रकाश (8): 6–10

9. राकेश कुमार पुंडीर, पी के सिंह, नीलकांत सी वी सिंह, बी प्रकाश एवं अनिल कुमार मिश्र (2017) बद्री: उत्तराखण्ड की एक नई गौ–नस्ल। पशुधन प्रकाश (8): 1–5.

10. सोनिका अहलावत, नेहा, रेखा शर्मा, रीना अरोड़ा एवं एम एस टांटिया (2017) समेकित कृषि: सतत आजीविका के लिये एक उत्कृष्ट विकल्प। पशुधन प्रकाश 8: 50–55

11. शालू कुमार, हरेन्दर सिंह चौहान, आर जी बुरटे,

बी जी देसाई, आर के पुंडीर, पी एस दाँगी, एस बी यादव, जी एस साहू एवं जवाहर लाल कुलदीप (2017). भारत में गौधन का महत्व। पशुधन प्रकाश (8): 56–58.

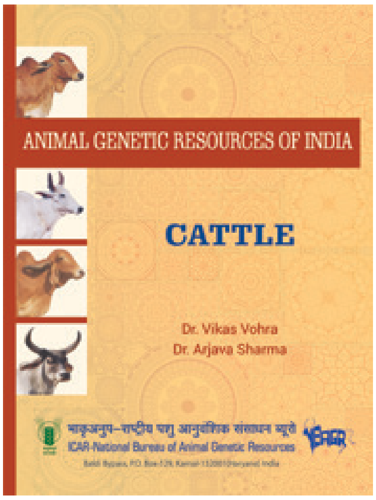
12. शालू कुमार, आर जी बुरटे, हरेन्दर लसह चौहान, बी जी देसाई, आर के पुंडीर, पी एस दाँगी एवं डी जे भगत (2017) साइलेज – अनावृस्टि में पशुओं के लिए एक पौष्टिक आहार। पशुधन प्रकाश (8): 96–98.

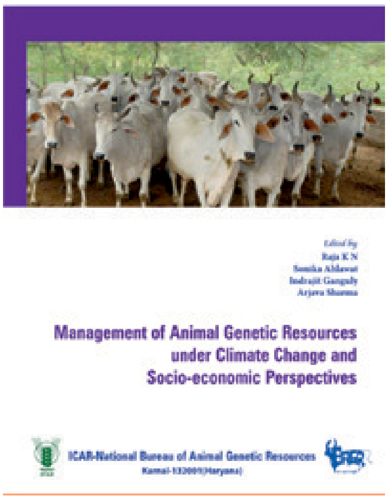
Books

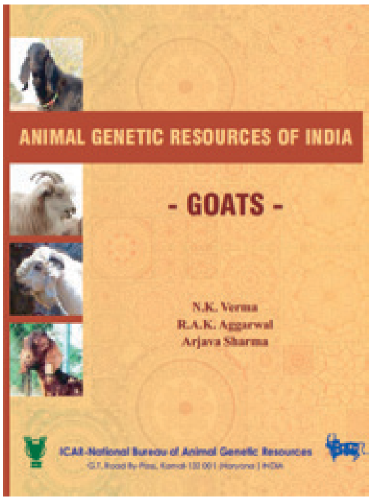
1. *In situ* conservation of Indigenous Livestock and Poultry breeds edited by Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).
2. Management of Animal Genetic Resources under Climate Change and Socio-economic Perspectives edited by Raja KN, Sonika Ahlawat and Indrajit Ganguly and Arjava Sharma (ISBN: 978-93-83537-38-9).
3. Animal Genetic Resources of India – Goats edited by NK Verma, RAK Aggarwal and Arjava Sharma (Pub. # 106/2017) Published by Director NBAGR, Karnal (ISBN: 978-93-83537-36-5).
4. Animal Genetic Resource of India – Cattle edited by Vikas Vohra and Arjava Sharma (Pub. # 109/2018). Published by Director NBAGR, Karnal (ISBN 978-93-83537-39-6).
5. Animal Genetic Resources of India: Sheep edited by AK Mishra, Vikas Vohra, Raja K N and Arjava Sharma (Pub. # 111/2018). Published by Director NBAGR, Karnal (ISBN: 978-93-83537-40-2).

Book Chapters

1. AK Mishra (2017) Indigenous poultry breeds and production system under climate change scenario in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).
2. AK Mishra (2017) Role of Goshala and NGOs in breed conservation in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).







3. Arjava Sharma and NK Verma (2017) Priortization of small Ruminant resources for Conservation in compendium of National Seminar on Small Ruminants: National Scope on upscaling production to products value addition and their safety at ICAR- NBAGR, Makhdoom, Mathura from November 9-10, 2017.

4. MS Tantia, Rekha Sharma and Sonika Ahlawat (2017) Strategies for conservation of threatened breeds and *in situ* models in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

5. MS Tantia, Rekha Sharma and Sonika Ahlawat (2017) Strategies for conservation of indigenous AnGR in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

6. MS Tantia, Rekha Sharma and Sonika Ahlawat (2017) Survey methodology for characterization of livestock and poultry populations in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

7. NK Verma (2017) Characterization of Animal Genetic Resources of India: Approaches and Implications" in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

8. NK Verma (2017) Indigenous goat breeds and impending risk to its diversity in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

9. PK Singh (2017) National watch list and early warning and response system for Indian Livestock in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

10. PK Singh (2017) State-wise breeding policy for improvement and conservation of AnGR in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

11. PK Singh and Indubala (2017). Global status of Animal genetic Resources in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

12. RK Pundir (2017) Indigenous cattle diversity and breeds at watch in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

13. RK Pundir (2017) Breed differentiation based on morphometric traits using Canonical Discrimanant analysis in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma,

Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

14. RK Pundir (2017) Role of gaushalas in conservation of indigenous cattle genetic resources in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

15. Reena Arora, Mandeep Kaur, Sonika Ahlawat and Rekha Sharma (2017) Molecular approaches for genetic diversity analysis in farm animals in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

16. Reena Arora, Mandeep Kaur, Sonika Ahlawat and Rekha Sharma (2017) Molecular Markers for Genetic Diversity Analyses of Animal Genetic Resources in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

17. Rekha Sharma, Sonika Ahlawat, Himani Sharma, Reena Arora and MS Tantia (2017) Somatic cell approach for cryopreservation in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

18. Rekha Sharma, Sonika Ahlawat, Reena Arora and MS Tantia (2017) Characterization of indigenous livestock produce: A future prospect for conservation in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

19. Rekha Sharma, Sonika Ahlawat, Reena Arora and MS Tantia (2017) Somatic Cell Banking: An alternate method for conservation of endangered species in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

20. RS Kataria, SK Mishra and SK Niranjan (2017) Identification and genotyping of functional markers for improvement of livestock in the book entitled "*In situ* conservation of Indigenous Livestock and Poultry breeds". Ed. Arjava Sharma, Jayakumar S and SK Niranjan (ISBN 978-93-83537-37-2).

21. RS Kataria, SK Mishra, Namita Kumari and SK Niranjan (2017) Diversity and evolution of immune response genes in livestock species adapted to different agro-climatic conditions in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

22. Sonika Ahlawat and Rekha Sharma (2018) Nuclear and mitochondrial marker based diversity and population structuring of Indian goats in the book entitled "Sustainable goat production in adverse environments: Volume I (Welfare, Health and Breeding)". Ed. Joao Simoes and Carlos Gutierrez, Springer.

23. Sonika Ahlawat, Rekha Sharma, Reena Arora and MS Tantia (2017) Molecular Techniques for characterization of AnGR in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

24. Sonika Ahlawat, SK Niranjan, Rekha Sharma, Reena Arora, RS Kataria and MS Tantia (2017) Biotechnological interventions for increasing bovine productivity in the book entitled "Management of Animal Genetic Resources under Climate Change and Socio-economic perspectives". Ed. Raja KN, Sonika Ahlawat, Indrajit Ganguly and Arjava Sharma (ISBN 978-93-83537-38-9).

Monographs/ Bulletin / Compendium

1. Technical bulletin on "Ladakhi Cattle: A Unique Animal Genetic Resource Adapted to High Altitude of Leh-Ladakh: Manishi Mukesh, Monika Sodhi, RS Kataria, Saket K Niranjan, RK Pundir, Preeti Verma, Ankita Sharma, Parvesh Kumari, Shelesh Kumar Swami, Arjava Sharma, Vijay K Bharti, Arup Giri, Prabhat Kumar, Sahil Kalia, Deepak Gogoi, Sarangi Prabhu, Bhuvnesh Kumar, M. Iqbal, Stanzin Rabgais, Shakil Ahmad.

2. लद्दाखी गाय लद्दाख की एक अनमोल गौ–सम्पदाभाः कृ.अ.प.–राष्ट्रीय पशु अनुवांशिक सं साधन ब्यूरो : मनीषी मुकेश, मोनिका सोढी, साकेत के निरंजन, आर एस कटारिया, आर के पुंडीर, प्रीती वर्मा, अंकिता शर्मा, परवेश कुमारी, शेलेश कुमार स्वामी, आर्जव शर्मा , विजय के भारती, अरूप गिरी, प्रभात कुमार, साहिल कालिया, दीपक गोगोई, भुवनेश कुमार, एम इकबाल, एस राबगैस, शकील अहमद

3. Goat Germplasm of Nagaland state by NK Verma, RAK Aggarwal, Pushp Raj Shivahre, N Savino and Arjava Sharma. Monograph # 101/2017 (ISBN: 978-93-83537-33-4).

4. Jain A, Kulkarni VS, Arora R and Yadav DK. Sheep Genetic Resources of India- Mouli Sheep. Monograph No102/2017 (ISBN: 978-93-83537-34-1).

5. Jain A, Kulkarni VS, Arora R and Yadav DK. 2017. Sheep Genetic Resources of India- Yalaga Sheep. Monograph No103/2017 (ISBN: 978-93-83537-35-8).

Awards

1. The prestigious Dr. P.G. Nair Award for scientific contribution in the field of identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country during last 3 years (January, 2014 to December, 2016) was conferred upon Dr. Rekha Sharma (Principal Scientist, Core Lab).

2. Second Best paper award by Pashudhan Prakash for the paper माइटोकोंड्रियल डी. एन. ए. पशुधन प्रजातियों के विकास एवं वंशावली रूप रेखा के लिए एक चिन्ह. पशुधन प्रकाश, 7:80–87 इल रीना अरोड़ा, राकेश कुमार, अंजु शर्मा, याशिला गिरधर, सोनिका अहलावत एवं रेखा शर्मा (2016).

3. Best oral presentation award to Dr Reena Arora for the paper entitled "Exploring the muscle transcriptome of Bandur sheep using RNA sequencing" presented in National seminar on Small ruminants: National scope on upscaling production to products value addition and their safety at ICAR-CIRG, Makhdoom (9-10th November, 2017).

4. Best oral presentation award to Dr Rekha Sharma for the paper entitled "Comparative milk metabolite profiling for exploring superiority of indigenous cow milk over exotic and crossbred counterparts" by Rekha Sharma, Sonika Ahlawat, RAK Aggarwal, Ajit Dua and MS Tantia, presented in National Symposium on "Sustainable management of livestock and poultry diversity for enhancing the farmers income" at RAJUVAS, Bikaner (8-10th February, 2018).

5. Prof KN Sharma Memorial award for best research article entitled "Analysis of sequence variability and expression pattern of lactoferrin gene in Sahiwal cows (*Bos indicus*) and Murrah buffaloes (*Bubalus bubalis*) by Sharma A, Swami SK, Kumar M, Sodhi M, Kataria RS, Jain P, Bhatia AK, Mohanty AK, Niranjan SK, Shandilya UK, Kumari P and Mukesh M published in Journal of Livestock Biodiversity 2017.

6. Young Scientist Award to Ravinder Singh for his presentation entitled "STR markers and mitochondrial D-loop sequence based genetic diversity analysis indicates unique population structure among buffaloes of Odisha state" in National Symposium on "Sustainable management of livestock and poultry diversity for enhancing the farmers income" at RAJUVAS, Bikaner (8-10th February, 2018).

7. Best poster award for the research entitled "Characterization and evaluation of milk colostrum derived lactoferrin of Sahiwal cows for its anti-cancerous potential by Sharma A, Sodhi M, Mohanty A, Shandilya UK, Kataria RS, Singh MK, Jain P, Niranjan SK, Bhatia AK, Kumar P, Swami SK, Mukesh M in National Symposium on "Sustainable management of livestock and poultry diversity for enhancing the farmers income" at RAJUVAS, Bikaner (8-10th February, 2018).

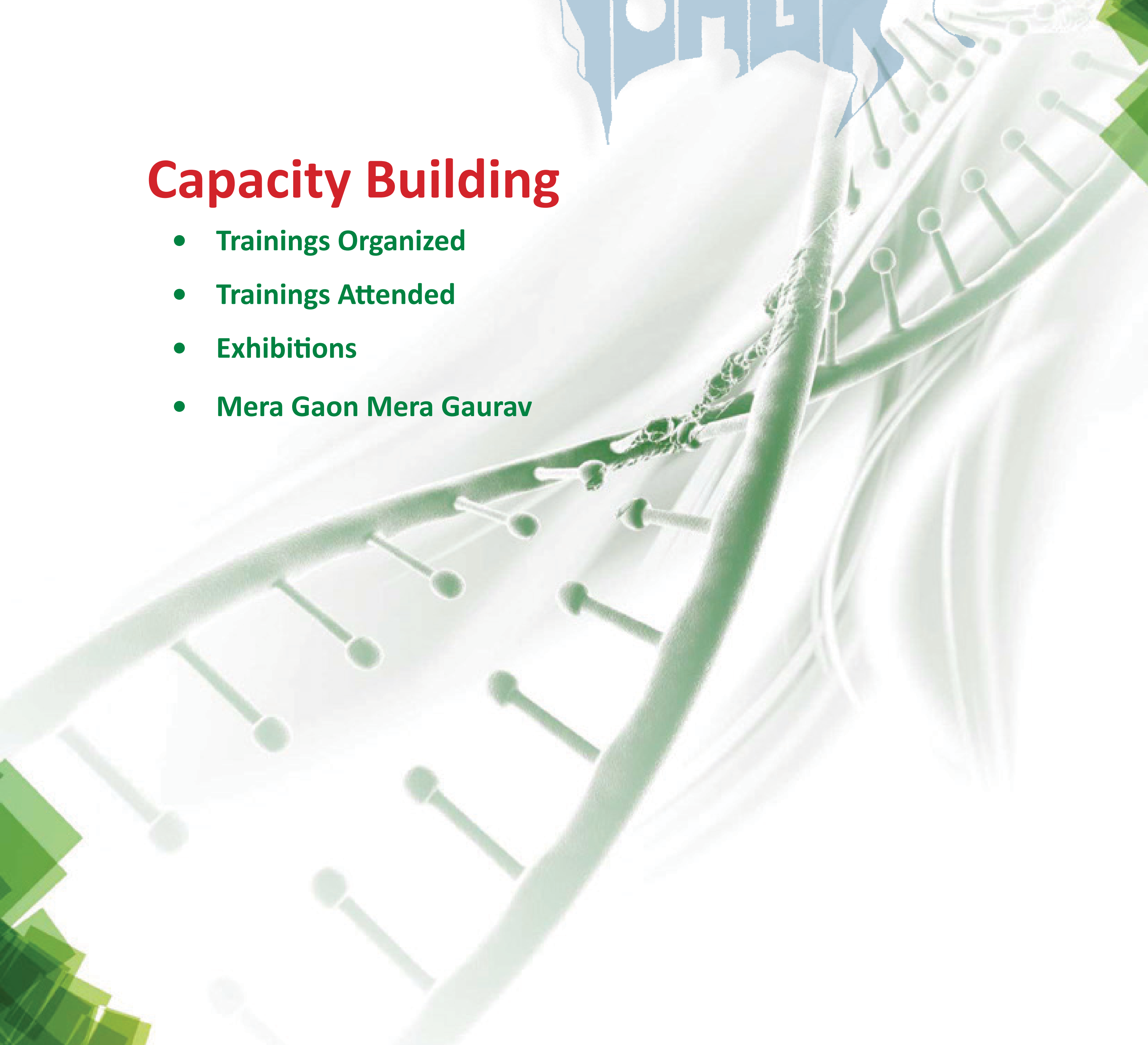
8. Second best poster award for the research entitled "My vision-corruption free India" by Himani Sharma, Mandeep Kaur, Reena Arora and Rekha Sharma during Vigilance awareness week (30th October – 4th November, 2017) at ICAR-NBAGR, Karnal

9. Dr. Avnish Kumar, Principal Scientist presented an invited lecture on the topic "Application of information technology in field survey and dairy buffalo recording system" in the International Conference on Carabao Based Enterprise Development, October 26-27, 2017 at Philippines Carabao Center, Nueva Ecija, Philippines.

10. Dr. Monika Sodhi received "Eminent Scientist Award" by Samgra Vikas Welfare Society (SVWS) on account of overall achievement and accomplishment in the field of Agriculture & Allied Sciences on June 5th, 2017

11. Best poster award for the research entitled" Delineating Indian native cattle specific allelic variants and haplotypes in lactoferrin gene: A potential candidate for disease resistance" by Sharma A, Kumar M, Sodhi M, Jain P and Mukesh M at 36th conference of International Society of Animal Genetics held at Dublin in Ireland from 16-21st July 2017.

* * *



Capacity Building

- Trainings Organized
- Trainings Attended
- Exhibitions
- Mera Gaon Mera Gaurav


WHAT NBAGR CAN OFFER
Breed certification and registration
Ex situ conserved germplasm
DNA sequencing
Parentage testing and pedigree analysis
Karyological screening and profiling
Training in the field of evaluation, characterization and conservation of AnGR
Scientific training in the field of molecular genetics and biotechnology
Consultancy planning and policy making related to characterization and conservation of AnGR
Generation of the cell lines of endangered and unique livestock germplasm
CHICKEN BREEDS OF INDIA
BREEDS OF INDIA

Trainings Organized

Following training programmes were conducted at NBAGR for upscaling the skill of administrative, technical and supporting staff of ICAR institutes.

1. A Training program on "Enhancement of professional competence of ICAR technical and administrative professionals" was conducted under ICAR-HRD program during June 27-29, 2017 at ICAR-NBAGR, Karnal.

2. Training on 'PCR based detection of beef' organized for officials of Department of Animal Husbandry, Haryana during August 28-31, 2017 at ICAR-NBAGR.

3. A Training program for Skilled Supporting Staff of ICAR entitled "कुशल सहायक स्टाफ की योग्यता वृद्धि एवं व्यक्तित्व विकास हेतु प्रशिक्षण कार्यक्रम," was conducted under ICAR-HRD during August 29-31, 2017 at ICAR-NBAGR, Karnal.

4. ICAR sponsored Short Course on "*In situ* Conservation of Indigenous Livestock and Poultry Breeds" from October 25 to November 3, 2017 for Assistant Professors and above of ICAR, SAUs and SVUs.

5. Model Training Course on 'Strategies for Conservation of Indigenous Animal Genetic Resources under Climate Change and Socio-economic Perspectives' was organized from November 23-30, 2017 for officers of SAHD, SLDB/agencies and State Biodiversity Board.

National Symposium

National Symposium on "Sustainable Management of Livestock and Poultry Diversity for enhancing the Farmers' income" was organized by Society for Conservation of Domestic Animal Biodiversity (SOCDAB) in collaboration with College of Veterinary & Animal Science, Rajasthan University of Veterinary & Animal Sciences, Bikaner (Rajasthan) from 8th-10th February, 2018.

Trainings Attended

1. Sh. Karambir Malik (PS to Director), Dr. P. S. Dangi (CTO) , Sh. S.K.Jain (ACTO), Smt. Anita Chanda (PA), Sh. Harvinder Singh (STO) and Sh. Naresh Kumar (LDC) attended training programme on "Enhancement of professional competence of ICAR technical and administrative professionals" from June 27-29, 2017 at ICAR-NBAGR.

2. Sh. Ramesh Kumar (TO) attended training programme on "Basic training on chemical analysis" from August 21-26, 2017 at ICAR-NDRI.

3. All Skilled supporting staff including Sh. Krishan Lal, Sh.Ram Sagar, Sh. Deepak and Sh.Satbir attended training programme on "कुशल सहायक स्टाफ की योग्यता वृद्धि एवं व्यक्तित्व विकास हेतु प्रशिक्षण कार्यक्रम" from August 29-31, 2017 at ICAR-NBAGR, Karnal.

4. Sh. Balwinder (Technician) attended training programme on "Automobile maintenance, road safety & behavioural skills" from September 19-23, 2017 at CIAE Bhopal.

5. Sh. Harish Arya (AO), Sh. Sunil Kumar (F &AO), Sh. Balkar Singh (AAO) and Sh. Pawan Kumar Gupta (AF&AO) attended the PFMS Training by ICICI BANK on September 22, 2017 at ICAR-NDRI, Karnal.

6. Dr. RK Pundir attended training programme on "Analysis of Animal Breeding Data and Genomic Prediction" from November 20-24, 2017 organized by ILRI at ICAR-CIRB, Hisar.

7. Technical officers, Sh. Naresh Kumar and Sh. Rakesh Kumar of Animal Biotechnology Division underwent a training programme on "Proficiency enhancement for working in biochemistry & biotechnology laboratory" from December 14-16, 2017 at ICAR- IIWBR, Karnal.

Exhibitions

1. An exhibition explaining the farm animal diversity and its utility at ICAR-IIWBR on the occasion of Seed Day on October 10, 2017.

2. An exhibition explaining the farm animal diversity and its utility at Police Line ground, Jajhar on the occasion of Livestock Show organized by Animal Husbandry Department Haryana from October 27-29, 2017.

3. An exhibition on Animal Genetic Resource of the country was organized at NDRI, Karnal during Dairy Mela on November 23-25, 2017.

4. AnGR exhibition was organised at 10th Livestock Championship, 2017 held at village Jhalan, Patiala, Punjab from December 1-5, 2017.

5. An exhibition was organised during the Kisan Mela at Sugarcane Breeding Institute (Regional Centre) Karnal held on February 17, 2018.

6. An exhibition was organised during the Krishi Unnati Mela at IARI Mela ground, New Delhi during March 16-18, 2018. The ICAR-NBAGR mobilized 16 progressive farmers from Barota village of Karnal to attend Prime Minister's address and visit of various stalls.

7. An exhibition of farm animal genetic resources was organised during Haryana's 3rd Agri-summit 2018 cum Kisan Mela at Rohtak (Haryana) held from March 24-26, 2018.

Mera Gaon Mera Gaurav

Linkages with farmers and livestock keepers were strengthened through Mera Gaon Mera Gaurav programme. Bureau team visited Narukheri, Pingli, Dadupur, Shahjanpur, Sambhli, Bras, Sirsi, Chiaro and Badshahpur villages of Karnal and delivered lectures on various aspects of Animal Husbandry. People were also sensitized about various social issues.

* * *

GENTINGPOWER

Other Activities

- Library
- Important Meetings
- Celebrations
- Distinguished Visitors


GOAT BREEDS OF INDIA
RK624

Library

The NBAGR library has been playing an important role in serving the scientists and technical staff of the bureau. Library Advisory Committee (LAC) is guiding force in the management of the library issues pertaining to purchase of scientific books/journals etc.

Books and journals worth Rs. 7, 98,306/- were procured in the library during the period. Seventeen Indian Journals and Six foreign journals have been subscribed for the benefit of scientific readers.

Total collection	4196
No. of books added	05
No. of Indian/ Foreign Journals subscribed	23
No. of Newspapers subscribed	07

Important Meetings

Research Advisory Committee

A meeting of Research Advisory Committee (RAC) was held on April 3, 2017 under the chairmanship of Dr. SL Goswami, Vice Chancellor, Banda University of Agriculture and Technology, Banda. The revised breed calendars of Cattle and buffalo breeds were released by the RAC at this occasion.

Institute Research Committee

Institute Research Committee (IRC) meeting was held on April 28-29, 2017 wherein final reports of the completed projects and new project proposals were discussed and approved. Another IRC meeting was held on September 19, 2017 to discuss the pending new project proposals.

Interactive Meet

An Interactive meet on "Animal Genetic Resources of Ladakh Region was held on May 10, 2017 at Ladakh Autonomous Hill Development Council (LAHDC), Leh-Ladakh to discuss various related issues for characterization and evaluation of Ladakh animal genetic resources especially yak, local non-descript cattle, Zanskari horse, donkey and double hump camel. Meeting was attended by Councilors of LAHDC, ADG (AP&B) and Scientists from ICAR Head Quarter, Director and Scientists of ICAR-NBAGR and DRDO- Defense Institute of High Altitude Research and Officers of AHD, Jammu & Kashmir.

Breed Registration Committee Meeting

A meeting of Breed registration Committee was held on August 4, 2017 at ICAR, Krishi Bhawan, New Delhi. Registration of nine new breeds of livestock and poultry were approved in meeting.

Celebrations

International Biodiversity Day

ICAR-NBAGR, Karnal in collaboration with SEVA, Madurai, Tamil Nadu organized International Biodiversity and Breed Saviour Award ceremony from May 21- 22 2017. Dr. J.K. Jena, Deputy Director General (AS & Fisheries) graced the function as chief guest. Twenty farmers / breeders representing various states were felicitated with Breed Saviour Award- 2015 for conserving and maintaining different indigenous livestock and poultry.

On this occasion, a poster competition on the subject "Biodiversity and its conservation" was also organized for school students and Research Scholars of ICAR-NBAGR, Karnal. In the School group, Delhi Public School (First), Tagore Bal Niketan (Second), The Millennium School and Adarsh Public School (Third) received the awards. Among research scholars Group, Ankita Sharma, Himani Sharma and Prerna Kapoor secured first, second and third positions, respectively.

Independence Day

The 70th Independence Day was celebrated on 15th August in the Bureau campus. All the staff, SRFs, RAs and their families attended the programme. Dr. Arjava Sharma, Director hoisted the tricolor and addressed the gathering. Various cultural activities were also conducted in which staff and their wards participated actively.

Foundation Day

ICAR-National Bureau of Animal Genetic Resources, Karnal celebrated its 34th Foundation Day on 21st September, 2017. Dr. K.M.L. Pathak, Vice-Chancellor, UPPDUPVV, Mathura was the chief guest and Dr. R.S. Gandhi (ADG, AP&B, ICAR) and Sh. Umesh Kumar Sharma (DGM, Canara Bank, Karnal) were the guests of honour on this occasion. The prestigious Dr. P.G. Nair Award for scientific contribution in the field of identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country was conferred upon Dr. Rekha Sharma, Principal Scientist. In technical and administrative category Sh. Om Prakash and Sh. Jita Ram, respectively were awarded. The contribution of livestock keepers in conservation of diverse breeds from different livestock species was acknowledged

by bestowing them with Breed Conservation Awards. The winners of various competitions organized during "Hindi Pakhwada" were also awarded. The best articles published in the 7th issue of "Pashudhan Prakash" were also awarded. The eighth edition of "Pashudhan Prakash" and three breed monographs on Nagaland goats, Mouli sheep and Yelga sheep respectively were released on this occasion by the chief guest, Dr. K.M.L. Pathak. The programme ended with an inspiring Foundation Day lecture delivered by the chief guest.

Republic Day

Staff and families of the Bureau celebrated 69th Republic Day on 26th January, 2018 with fervour and enthusiasm. The function was presided over by Director, Dr. Arjava Sharma. National Anthem was played after unfurling of the tricolour. Children participated in quiz and cultural program with enthusiasm and excitement.

International Yoga Day

ICAR-NBAGR, Karnal celebrated International Yoga Day and organized a Yoga camp in the Bureau premises on June 21, 2017. All the employees, RA/SRF/JRF, students/scholars along with their families attended the Yoga camp under the guidance of a well-known Yoga teacher, Sh. Dinesh Gulati and his team.

Agricultural Education Day

Agricultural Education Day was celebrated at NBAGR on December 3, 2017. The purpose of this programme was to generate awareness among the students about the career opportunities that exist in the agricultural sector. It was kept an open day for the students. The participating students (120) of five schools were briefed about the animal genetic resources of the country and the institute's research work. Dr Arjava Sharma, Director of the Bureau delivered a talk on "Livestock biodiversity and its role in national development". Students from all the schools enthusiastically participated in a quiz competition that was organized on this occasion. The teachers and students of the participating schools expressed their desire to be part of such celebrations in future as well.

Sports Events

A contingent of 22 staff members of ICAR-NBAGR participated in the ICAR Zonal (North) sports held at ICAR-IISR, Lucknow from October 30 to November 2, 2017. The contingent participated in Basket Ball, Volley Ball (smashing & shooting), Kabaddi, Badminton, Table Tennis, Carrom Board, Chess and athletic events.

As a part of Republic Day celebration, NBAGR also organized an annual sports meet for its staff from January 23-24, 2018 where most of the staff including ladies and their wards participated actively. The winners were given prizes on NBAGR Foundation Day.

Distinguished Visitors

1. Dr. T. Mohapatra, Secretary, DARE and Director General, Dr. J. K. Jena, DDG (Fisheries & Animal Science), Indian Council of Agricultural Research along with Dr. R.K. Singh, Director, ICAR-IVRI and others visited on 06.05.2017.
2. Dr. JK Jena, DDG (Animal and Fishery Sciences), ICAR; and Dr. R.S.Gandhi, ADG (AP&B), ICAR visited ICAR-NBAGR, Karnal on 22.05.2017 for participation in Breed Saviour Award ceremony organized on International Biodiversity Day.
3. Dr. Santosh Kumar Singh, Agricultural Specialist in Embassy of the USA, New Delhi visited on 10.07.2017.
4. Dr. K.M.L. Pathak, Former DDG (AS), ICAR and Vice-Chancellor, DUVASU, Mathura and Dr. R.S.Gandhi, Assistant Director General (AP&B), ICAR visited on 21.09.2017.
5. A Doordarshan Team from New Delhi visited on 24.10.2017.
6. Sh. R P Singh, Member, Governing Body, ICAR visited on 13.02.2018.
7. Dr. Shiv Tripathi and Prof. N.R. Bhusnur Math from Management Development Institute visited on 03.03.2018.

* * *

Personnel

- Personalia
- Promotions
- Joinings/Transfers
- Superannuation


स्वच्छता अभियान
USE ME

Personalia

Scientific

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

*Not physically present in NBAGR.

Technical

Sl. No.	Name	Designation
1.	Dr. P. S. Dangi	Chief Technical Officer
2.	Sh. S. K. Jain	Asstt. Chief Technical Officer
3.	Dr. P.S. Panwar	Asstt. Chief Technical Officer

4.	Sh. Sanjeev Mathur	Asstt. Chief Technical Officer
5.	Sh. Harvinder Singh	Senior Technical Officer
6.	Sh. Sat Pal	Technical Officer
7.	Sh. Jamer Singh	Technical Officer
8.	Smt. Pravesh Kumari	Technical Officer
9.	Sh. Naresh Kumar	Technical Officer
10.	Sh. Ramesh Kumar	Technical Officer
11.	Sh. Rakesh Kumar	Technical Officer
12.	Sh. Subhash Chander	Technical Officer
13.	Sh. Ashok Kumar	Technical Officer
14.	Sh. Om Prakash	Senior Technical Assistant
15.	Sh. Ramesh Chand	Senior Technical Assistant
16.	Sh. Balwinder Singh	Technical Assistant (Driver)

Administrative

Sl. No.	Name	Designation
1.	Sh.Raj Kumar	A.O.
2.	Sh. Sunil Kumar	F&AO
3.	Sh. Karambir	PS to Director
4.	Sh. Balkar Singh	AAO
5.	Sh. Pawan Kr. Gupta	AF&AO
6.	Sh. Ramesh Behl	Assistant
7.	Smt. Anita Chanda	PA
8.	Smt. Amita Kumari	PA
9.	Smt. Indu Bala	Steno Gr.III
10.	Smt. Shashi Bala	Assistant
11.	Sh. Jita Ram	Assistant
12.	Sh. Yoginder (Presently on deputation)	Assistant
13.	Sh. Satish Kumar	UDC
14.	Sh. Shiv Chander	LDC
15.	Smt. Neerja Kaul	LDC
16.	Sh. Naresh Kumar	LDC
17	Sh. Babu Ram	LDC

Skilled Supporting

Sl. No.	Name	Designation
1.	Sh. Krishan Lal	SSS
2.	Sh. Ram Sagar	SSS
3.	Sh. Deepak	SSS
4	Sh. Satbir	SSS

Promotions

1. Dr. P.S. Panwar has been promoted to the next higher grade i.e. Assistant Chief Technical Officer w.e.f. 28.02.2013.
2. Sh. Ashok Kumar has been promoted to the next higher grade of Technical Officer w.e.f. 24.02.2016.
3. Sh. Balwinder Singh has been promoted to the next higher grade of Technical Assistant (Driver) w.e.f. 18.01.2016.
4. Sh. Sanjeev Mathur has been promoted to the next higher grade i.e. Assistant Chief Technical Officer w.e.f. 02.01.2017.
5. Dr. Vikas Vohra has been promoted to the post of Principal Scientist on 02.04.2017 under Career Advancement Scheme (CAS).
6. Dr. Karan Veer Singh has been promoted to the next higher grade of Senior Scientist w.e.f. 07.02.2013 under CAS.

Joinings/Transfers

1. Sh. H.R. Arya, Administrative Officer, IARI Regional Station Karnal joined the NBAGR on the post Administrative Officer w.e.f. 01.04.2017.
2. Sh. Yoginder has been appointed to the post of Assistant Section officer at Election commission of India, New Delhi on deputation basis on 20.12.2017.
3. Sh. H.R. Arya has been promoted to the post of Senior Administrative Officer at NDRI Karnal and relieved from NBAGR on 27.12.2017.
4. Sh. Raj Kumar joined NBAGR on 26.12.2017 (FN) as Administrative Officer.

Superannuation

1. Sh. Ashok Kumar, Technical Officer superannuated on 31.03.2018.

* * *

हिन्दी खण्ड

- निदेशक की कलम से ...
- कार्यकारी सारांश
- राजभाषा प्रकोष्ठ की गतिविधियाँ


34वाँ स्थापना दिवस एवं राजभाषा पुरस्कार वितरण समारोह
34वाँ स्थापना दिवस एवं पुरस्कार वितरण समारोह
आपका हार्दिक अभिनंदन
पशुधन प्रकाश
डॉ. रणजीत सिंह कटारिया
श्री उमेश कुमार शर्मा
डॉ. के.एम.एल. पाठक
डॉ. आर.एस. गाँधी

हिन्दी खण्ड

निदेशक की कलम से ...

मैं निदेशक के रूप में, राष्ट्रीय एवं अंतर्राष्ट्रीय ख्याति प्राप्त प्रतिष्ठित संस्थान भाकृअनुप – राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो, करनाल के द्वारा अनुसंधान, प्रशिक्षण, विस्तार, शिक्षा एवं तकनीकी विस्तार आदि के क्षेत्रों में किये गए कार्यों एवं प्राप्त उपलब्धियों को, वार्षिक प्रतिवेदन जो कि वर्ष 2017–18 की उपलब्धियों का लेखा–जोखा है: को आपसे साझा करते हुए अपने आपको गौरवान्वित महसूस कर रहा हूँ।

अपने स्थापना दिवस 21 सितम्बर 1984 से यह यह संस्थान अविरल रूप से भारतीय पशु आनुवंशिक संसाधनों के महत्व के बारे में पशुपालकों में जागरूकता लाने हेतु प्रयत्नशील है। यह देश का एकमात्र संस्थान है जोकि देशी पशु आनुवंशिक संसाधनों के महत्व, पहचान, संरक्षण, उपयोग एवं उनके सतत उपयोग हेतु प्रयासरत है. अपनी स्थापना से अबतक की इस गौरवमयी यात्रा के दौरान संस्थान द्वारा 41 गाय, 13 भैंस, 28 बकरी, 42 भेंड़, 7 घोड़े एवं टट्टू, 9 ऊँट, 18 मुर्गी, 7 शूकर, 1 याक, 1 बत्तख़ , 1 गीज़ एवं 1 खच्चर की नस्लों का पंजीकरण किया गया है। संस्थान की वर्ष 2017–18 की गौरवमयी समग्र उपलब्धियों को इस रिपोर्ट के माध्यम से प्रस्तुत किया गया है।

वर्ष के दौरान केरल एवं तमिलनाडु के अवूणत गोवंशी पशुओं, उड़ीसा की मानदा भैंस, पंजाब एवं राजस्थान की चितरंगी भेंड़, दुम्बा भेंड़, कर्नाटक की बीदरी एवं नन्दीदुर्गा बकरी और लद्दाख के याक समूह का प्रारूपिक एवं आनुवंशिक रूप से सर्वेक्षण के माध्यम से अध्ययन किया गया. इसके अलावा गाय, भैंस, भेंड़, बकरी एवं अन्य पालतू प्रजातियों की कम ज्ञात नस्लों / समूहों के अध्ययन हेतु अन्य परियोजनाएं भी शुरू की गयी हैं। इस दौरान स्वदेशी मवेशियों में ए1 ए2 अलील्स और उनकी आनुवंशिक रूपरेखा का भी अध्ययन किया गया है, इससे भविष्य में देशी गायों एवं भैंसों की नस्लों का राष्ट्रीय एवं अंतर्राष्ट्रीय स्तर पर महत्व बढ़ेगा। मांडया भेंड़ की उत्तम माँस गुणवत्ता एवं ऊँचाई पर पाले जा रहे जन्स्कार टट्टुओं में सहनशीलता एवं उनकी मजबूती संबंधी लक्षणों के लिए कंडीडेट जीन की पहचान एवं उनके क्रियाविधि का अध्ययन भी किया गया है।

नस्ल संरक्षण राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो का एक महत्वपूर्ण अधिदेश है इसके तहत गोशालाओं के माध्यम से साहिवाल एवं हरियाणा नस्ल के संरक्षण के कार्य प्रगति पर है एवं इस परियोजना में कुल 46 बच्चो का जन्म हो चुका है जिनमें 5 साहिवाल एवं 41 हरियाणा नस्ल के बच्चे हैं। एक्स– सीटू संरक्षण कार्यक्रम के तहत मणिपुरी घोड़े एवं कच्छी ऊंटों की फाईब्रोब्लास्ट सेल लाईन बनाई गयी है। संस्थान के राष्ट्रीय जीन बैंक में गोवंशी नस्लों डांगी, राठी, खिल्लार एवं नागोरी के वीर्य डोज का समावेश किया गया है।

पशु आनुवंशिक संसाधन नेटवर्क परियोजना के अंतर्गत 10 नए पशु समूहों का समावेश, उनके लक्षनीकरण करने हेतु किया गया है। जिससे आने वाले समय में पंजीकृत नस्लों में वृद्धि होगी एवं अवूणत पशुओं की संख्या में कमी आयेगी। हमारा संस्थान भारत सरकार की नीति के तहत, देशभर के विभिन्न संस्थाओं में प्रयोग हो रहे प्रजनक नरों की सायटोजेनेटिक स्क्रीलनग और विभिन्न रोग परीक्षण हेतु परामर्श सेवा भी प्रदान कर रहा है, जिसका उद्देश्य प्रजनक नरों के आनुवंशिक दोषों का पता लगाना है जिससे उन्हें आगे बढ़ने से रोका जा सके।

संस्थान अनुसंधान समिति की बैठकें समय पर आयोजित हो रही हैं जिसमें वर्ष के दौरान पूर्ण हुई परियोजनाओं की अंतिम प्रगति रिपोर्ट, कार्यरत परियोजनाओं की की समीक्षा की गयी एवं नई परियोजनाओं को मंजूरी प्रदान की गयी। पिछले वर्ष कुल 7 अनुसंधान परियोजनाएं पूर्ण हुई एवं वर्तमान में 26 अनुसंधान परियोजनाओं पर कार्य जारी है जिसमें 5 बाह्य वित्त पोषित और एक नेशनल फेलो परियोजना शामिल है। इस दौरान 33 शोध पत्र एवं 12 तकनीकी लेख/लोकप्रिय लेख विभिन्न राष्ट्रीय एवं अंतर्राष्ट्रीय ख्यातिप्राप्त जर्नल एवं शोध पत्रिकओं में प्रकाशित हुए। इसके अतिरिक्त 5 किताबें, 5 मोनोग्राफ एवं 24 पुस्तक अध्याय भी संस्थान के वैज्ञानिकों द्वारा प्रकाशित किये गए। संस्थान पशु पालन शिक्षा, अनुसंधान, चिकित्सा एवं प्रसार कार्यक्रमों में संलग्न लोगों में क्षमता विकास के लिए भी योगदान कर रहा है जिसके तहत इस दौरान 5 प्रशिक्षण कार्यक्रम आयोजित किये गए। ब्यूरो के वैज्ञानिकों की विशेषज्ञता एवं उनके द्वारा किये गए कार्यों को विभिन्न राष्ट्रीय एवं अंतर्राष्ट्रीय मचों पर भी पहचान मिली है जहाँ पर इन्होंने अपने कार्यों को प्रस्तुत किया।

देश के विभिन्न राष्ट्रीय कार्यक्रमों जैसे कि मेरा गांव मेरा गौरव, जय किसान जय विज्ञान, एवं राष्ट्रीय स्वच्छता अभियान अदि में संस्थान के वैज्ञानिकों, अधिकारियों एवं कर्मचारियों ने सक्रिय रूप से भाग लिया। संस्थान द्वारा पांच प्रदर्शनियों का आयोजन देश के विभिन्न हिस्सों में संस्थान की गतिविधियों को बताने एवं देशी पशुओं के महत्व के बारे में जागरूकता फैलाने हेतु किया गया जिसमें लोगों ने काफी रुचि ली। पिछले वर्ष डॉ टी महापात्रा, सचिव (कृषि अनुसंधान एवं शिक्षा विभाग/डेयर) एवं महानिदेशक, भारतीय कृषि अनुसंधान परिषद्, नई दिल्ली एवं डॉ जे के जेना, उप– महानिदेशक (मत्स्य विज्ञान एवं पशु विज्ञान) ने संस्थान का दौरा किया एवं ब्यूरो के कार्यों की सराहना की। ब्यूरो परिवार द्वारा गणतंत्र दिवस, स्वतंत्रता दिवस, संस्थान स्थापना दिवस, अंतर्राष्ट्रीय जैव विविधता दिवस, सतर्कता सप्ताह एवं हिंदी पखवाड़ा पूर्ण उत्साह के साथ मनाया गया। वर्तमान वर्ष से ही प्रथम बार संस्थान ने देशी पंजीकृत पशु नस्लों के संरक्षण में संलग्न व्यक्तियों, संस्थाओं एवं समुदायों के लिए "नस्ल संरक्षण पुरस्कार" भी शरू किया है।

मैं, डॉ. टी महापात्रा, सचिव (कृषि अनुसंधान एवं शिक्षा विभाग/डेयर) एवं महानिदेशक, भारतीय कृषि अनुसंधान परिषद् नई दिल्ली एवं डॉ. जे के जेना, उप– महानिदेशक (मत्स्य विज्ञान एवं पशु विज्ञान), डॉ. आर एस गांधी, सहायक– महानिदेशक (पशु उत्पादन एवं प्रजनन) एवं डॉ विनीत भसीन, प्रधान वैज्ञानिक, भारतीय कृषि अनुसंधान परिषद्, नई दिल्ली का संस्थान के समग्र विकास हेतु मार्गदर्शन हेतु हृदय से आभारी हूँ। अनुसंधान सलाहकार समिति से प्राप्त सलाह एवं मार्गदर्शन हेतु मैं कृतज्ञता ज्ञापित करता हूँ। मैं संस्थान के सभी वैज्ञानिकों, अधिकारियों एवं कर्मचारियों को संस्थान की प्रगति में उनके योगदान के लिए, गर्व के साथ बधाई देता हूँ। साथ ही साथ मैं, वार्षिक प्रतिवेदन के सम्पादक मंडल के सदस्यों को भी धन्यवाद करता हूँ जिनके परिश्रम से यह दस्तावेज़ ब्यूरो की उपलब्धियों के आकार में आपके सम्मुख प्रस्तुत है। हम हमेशा ही सुधार के लिए आपके सुझाव और आलोचनाओं का स्वागत करते हैं।

(आर्जव शर्मा)
निदेशक

कार्यकारी सारांश

भा.कृ.अनु.प.–राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो पशुओं और कुक्कुट विशेष रूप से देश में स्वदेशी नस्लों के लाभ और उत्थान के लिए काम कर रहा मुख्य संस्थान है। संस्थान का व्यापक अधिदेश है कि 1) देश के पशुधन और कुक्कुट आनुवंशिक संसाधनों की पहचान, मूल्यांकन, लक्षण, संरक्षण और उपयोग और 2) पशु आनुवंशिक संसाधन प्रबंधन और नीतिगत मुद्दों में समन्वय और क्षमता निर्माण। संस्थान के अधिदेश को प्राप्त करने के लिए संस्थान में तीन विभाग– 1) पशु आनुवंशिक संसाधन 2) पशु आनुवंशिकी, और 3) पशु जैव प्रौद्योगिकी 2013 में बनाये गए हैं: इसके अलावा, दो इकाइयां– पशुधन सूचना और प्रबंधन और नेटवर्क परियोजना संस्थान की गतिविधियों का समर्थन करने के लिए भी काम कर रही हैं।

वित्तीय वर्ष 2017–18 के दौरान विभिन्न मदों (पूंजी, राजस्व और पेंशन और सेवानिवृत्ति लाभ) के तहत रु.1335.3 लाख की कुल प्राप्ति में रु.1318.49 लाख का कुल व्यय हुआ। नेटवर्क परियोजना के तहत, रु.77.0 लाख की कुल प्राप्ति से रु.76.6 लाख का कुल व्यय हुआ। वित्तीय वर्ष 2017–18 में रु.35.66 लाख राजस्व के रूप में प्राप्त किये गए।

भा.कृ.अनु.प.– राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो द्वारा स्वदेशी पशुधन और कुक्कुट की नौ नई नस्ल– गोवंश की एक, बकरी की दो और प्रति एक घोड़ा, सुअर, याक, हंस, बत्तख और चिकन पंजीकृत की गयी। पांच नस्लें देश के पूर्वोत्तर क्षेत्र से थी। संस्थान ने पहली बार याक, बतख और हंस की स्वदेशी नस्लों को पंजीकृत किया। इस तरह पंजीकृत स्वदेशी नस्लों की कुल संख्या 169 तक पहुंच गई है।

हरियाणा और पंजाब में पशु आनुवंशिक संसाधन के प्रबंधन के लिए पशुधन नीतियों और कार्यक्रमों के मूल्यांकन के लिए अध्ययन इस साल शुरू किया गया। पशुपालन की गतिविधियों पर प्रश्नावली आधारित जानकारी किसानों / पशुधन रखने वालों और अन्य हितधारकों से एकत्र की गई ।

भारत की आठ स्वदेशी भेड़ नस्लों को विभेदक कार्यात्मक विश्लेषण (डीएॅफ़ए), और अनुमानी – कृत्रिम तंत्रिका नेटवर्क (एएनएन) और समर्थन वेक्टर मशीन (एसवीएम) तरीके का उपयोग कर सात मोर्फोमेट्रिक लक्षण के आधार पर वगह्वकृत किया गया। द्विआधारी विभाजन 1–से–1 और 1–से–अन्य में, एसवीएम् मश्वडल ने अन्य तरीकों से सर्वश्रेष्ठ प्रदर्शन किया।

ओडिशा राज्य में मंदा और संभलपुरी भैंसों का सर्वेक्षण किया गया। मंदा ओडिशा के कोरापुट जिले में पाई जाती है। मंदा छोटे कद और सुगढ़ काठी की होती है। शरीर का रंग हल्का काला–भूरा है। सल्ग लंबे और भारी होते हैं। कठोर लेटेराइट मिट्टी में खेती के लिए ये उत्कृष्ट पशु होते हैं। दूध उत्पादन 2 से 4 किग्रा प्रति दिन तक होता है। संभलपुरी भैंस उड़ीसा के सम्भलपुर जिले और आसपास के छत्तीसगढ़ के जिलों में पाई जाती है। देशी इलाके में संभलपुरी भैंसों की घटती आबादी ल्चता का कारण बन रही है। भेद विश्लेषण द्वारा विभिन्न बश्वयोमीट्रिक लक्षण ओडिशा भैंसों को अलग–अलग समूहों में प्रकट करते हैं।

कर्नाटक में नंदीदुर्ग और बिदरी बकरियों की विशेषता के लिए सर्वेक्षण किया गया ।नंदीदुर्ग बकरी, चित्रदुर्ग, तुमकुर और दावणगेरे में वितरित हैं, जबकि बिदरी कर्नाटक के बीदर और कलबुगह्व जिलों में वितरित है। नंदीदुर्ग सफेद होती है, जबकि, पलकें भूरे या काले रंग की होते हैं। कान पत्तेदार और लटके हुए होते हैं। बिदरी बकरियों में, कोट रंग, थूथन और पलकें काले रंग की होते हैं। कान लटके हुए होतें हैं। दोनों बकरियों को केवल मांस के उद्देश्य के लिए रखा जाता है।

जम्मू–कश्मीर के नुबरा–लद्दाख क्षेत्र में सर्वेक्षण के दौरान, स्थानीय याक आबादी को लक्षणीकृत किया गया। उन्हें बौद्ध समुदाय द्वारा दूध, मांस, खाद, बाल फाइबर और परिवहन के लिए पाला जाता है। नुबरा के याक मध्यम आकार के होते हैं। रंग गहरा कत्थई या काला होता है। सींग ऊपर और पीछे की ओर घुमावदार होतें हैं। कान छोटे होतें हैं। श्रोणि कंधे क्षेत्र से बड़ा होता है। अधिकांश याक को घुमन्तु (पेस्टोरलिज्म) के तहत रखा जाता है। इस क्षेत्र में हाइब्रिड (गाय × याक) की प्राथमिकता याक संख्या में गिरावट का एक महत्वपूर्ण कारण थी।

जम्मू–कश्मीर के लद्दाख क्षेत्र में मूल गधे की आबादी को लक्षणीकृत किया गया। बौद्ध समुदायों द्वारा लद्दाखी गधे का पालन परिवहन और खाद के लिए किया जाता है। पशु

मध्यम आकार और शांत होते हैं। रंग हल्के से गहरा भूरे, कत्थई और पेट पर हल्के रंग या सफेद होते है। जानवर रात में भी आसानी से ट्रेक करने में सक्षम हैं। उपयोगिता में कमी के कारण गधे की आबादी काफी हद तक गिरावट आई है।

राजस्थान के श्रीगंगानगर, पंजाब के मुक्तसर, फ़ज़िलका में चितरंगी भेड़ का सर्वेक्षण किया गया। यह एक कालीन ऊन प्रकार की भेड़ है। चितरंगी आकार में मध्यम से बड़े होती हैं। कोट रंग सफेद होता है, आंखों, थूथन और कान पर गहरा पैच होता है, कान के दूरस्थ छोर पर विभिन्न आकार के सीरेशन होते हैं। वार्षिक चिकना ऊन उत्पादन 1.5 से 2 किलोग्राम है।

दुम्बा भेड़ के वितरण और विशेषता के लिए सर्वेक्षण किया गया। यह मुख्य रूप से राजस्थान के जयपुर, नागौर और अजमेर जिलों में पायी जाता है। अधिकतर कोट का रंग सफेद और भूरा होता है। कान आकार में बड़े, लटकनदार होते हैं। पूंछ में वसा के जमाव दुम्बा की विशेषता है। इसका मुख्य रूप से अनुष्ठानों (कुरबानी) के लिए पालन किया जाता है।

तेलंगाना राज्य के कम ज्ञात पशु आबादी (वंदारवी, जरी और कम्मा) के लक्षण वर्णन के लिए सर्वेक्षण किया गया। वारंगल जिले का वंदारवी सफेद रंग है। चेहरा लंबा और अवतल होता है। सल्ग लंबे और घुमावदार होते हैं। कृषि कार्यों के लिए बैलों का उपयोग किया जाता है। दैनिक दूध 1.0 से 2.5 किलो तक होता है। झारी अधिकतर भूरे होते हैं। शरीर छोटा और बेलनाकार होता है। भेद के लिए मुख्य चेहरा मुख्य होता है। शरीर ओंगोल गोवंश से छोटा होता है। बैल में कूबड़ मध्यम और गायों में छोटा होता है।

राष्ट्रीय पशु आनुवंशिक संसाधन ब्यूरो के राष्ट्रीय जीन बैंक में जर्मप्लास्म को विविध रूप (वीर्य, भ्रूण, डीएनए, अधिवृषणी शुक्राणुओं और दैहिक कोशिकाओं) में संरक्षण से मजबूत किया जा रहा है। कुल 8 पशु नस्लों की 23,975 वीर्य खुराक और कच्छी ऊंट और मारवाड़ी घोड़े से 400–400 दैहिक कोशिका की खुराक क्रायोप्रिजर्वेशन के लिए जोड़ी गयी।

दैहिक कोशिका बैंलकग के लिए मणिपुरी घोड़े और कच्छी ऊंट की फाइब्रोब्लास्ट कोशिका लाइन त्वचा से उत्पन्न की गई। मणिपुरी घोड़े और कच्छी ऊंट के कान ऊतकों का उपयोग अटैचमेंट सेल कल्चर विधि से सेल लाइनों की स्थापना के लिए किया गया। प्राथमिक कल्चर फाइब्रोब्लास्ट विशिष्ट मीडिया का उपयोग कर एक्सपेलान्ट कल्चर तकनीक से स्थापित की गई । कोशिकाओं को क्रायोप्रिजर्वेशन किया गया।

गौशालाओं में स्वदेशी गायों के संरक्षण के साथ–साथ सतत सुधार के मॉडल के विकास के लिए एक परियोजना के अन्तर्गत हरियाणा की तीन गोशालाएँ हरियाणा और साहिवाल गायों के अनुवांशिक सुधार और संरक्षण के लिए चुनी गयी। कुल 52 हरियाणा और 4 साहिवाल को कृत्रिम गर्भाधान किया गया। कुल 46 बछड़े पैदा हुए। साहिवाल में दैनिक दूध 4.0 से 9.0 किग्रा, जबकि हरियाणा में 1.0 से 4.0 किलोग्राम तक प्राप्त हुआ। दो स्वास्थ्य शिविर भी आयोजित किए गए।

आनुवांशिक विश्लेषण के दौरान कर्नाटक के नंदीदुर्ग और बिद्री बकरियों में सभी मार्कर पॉलिमॉर्फिक में पाए गए। दोनों आबादी में विविधता के पर्याप्त स्तर की पुष्टि हुई। कोई भी बड़ी या हालिया अनुवांशिक बाधा अनुपस्थित थी। 2 डी समन्वय विश्लेषण में दोनों बकरियों को अलग पाया गया ।

पांच ओडिशा भैंस आबादी के डेटा विश्लेषण के आधार पर माइक्रोसाइटेबल मार्करों ने संकेत दिया कि मंदा भैंस सभी से बहुत अलग थी। संरचना विश्लेषण से पता चला कि मंदा और मुर्राह सबसे विशिष्ट हैं। परलखमुंडी में कालाहांडी भैंस का मिश्रण पाया गया। मेडियन नेटवर्क से चिल्का और दलदल भैंसों का साझाकरण का संकेत मिलता है। चिलिका में नस्ल विशिष्ट हैप्लोटाइप की संख्या अधिक थी।

चितरंगी और दुम्बा भेड़ का 24 मार्करों से आनुवंशिक निरूपण किया गया एवं क्रमशः 237 और 243 विशिष्ट एलीलों की पहचान की गई। औसत एफआईएस (इनब्रिलडग अनुमान) क्रमशः 0.096 और 0.043 थी, जो हेटरोज्यगोट्स की संख्या में कमी दर्शाती है।

बांडूर और कर्नाटक की स्थानीय भेड़ की कंकाल मांसपेशियों का ट्रांसक्रिप्टोमिक प्रोफाइल पता किया गया जिससे कुल 20568 अलग–अलग व्यक्त ट्रांस्क्रिप्ट का पता चला। इनमें से बांडूर में 1236 उच्च विनियमित और 602 निम्न विनियमित थे। सभी विभिन्न व्यक्त जीनों को 132 जीन ओंटोलॉजी जैविक प्रक्रिया, 146 सेलुलर घटकों और 117 आणविक कार्यों के लिए वगह्नकृत किया

जा सका । मांस की गुणवत्ता के लिए प्रासंगिक प्रमुख मार्गों का पता चला।

संकर पशु प्रजनन क्षमता में मिथाइलीकरण की भूमिका पता करने के लिए, सहिवाल, एचएफ और एचएफ संकर (फ्रिजवाल) के शुक्राणु में अर्धसूत्रीविभाजन के विशिष्ट जीन के मिथाइलेशन प्रोफ़ाइल का आकलन किया गया। खराब शुक्राणु गतिशीलता के साथ फ्रिजवाल के डीएजेडएल, बीवीएच और पीआईवीआईएल1 जीन में उच्च डीएनए मिथाइलेशन पाया गया। कार्यात्मक अभिव्यक्ति का आकलन करने के लिए, निम्न वीर्य गतिशीलता वाले फ्रिजवाल की तुलना में बाउल, डी ए जी एल और बी वी एच जीन की अभिव्यक्ति एचएफ, सहिवाल और उत्तम गतिशीलता वाले संकर सांडों में काफी अधिक पाई गयी।

जीनोम विस्तृत एस एन पी और इन्डेल्स चार याक आबादी –अरुणाचली, हिमाचली, लद्दाखी और सिक्किमी में पहचान की गई। आरडी 10 में पहचाने गए कुल एसएनपी क्रमशः 256051, 241934, 312518 और 150425 थे। कुल मिलाकर, 5797575 एसएनपी 9.42] के कवरेज के साथ उच्च गुणवत्ता वाले थे। लद्दाखी और सिक्किमी याक आबादी अलग–अलग पाए गए।

जंस्कारी घोड़ों की उच्च ऊंचाई पर सहनशीलता परीक्षण के दौरान व्यक्त जीनों की पहचान करने के लिए पी बी एम् सी का ट्रांस्क्रिप्टोम विश्लेषण अभ्यास से पहले और अभ्यास के दौरान उत्पन्न किया गया। अभ्यास के दौरान जंस्कारी घोड़ों में कुल 646 जीन अलग–अलग व्यक्त हुए।

चोकला, मगरा, मारवाड़ी और मद्रास रेड भेड़ में एचएसपी जीन की कार्यात्मक प्रोफ़ाइल का मूल्यांकन सामान्य और तनावग्रस्त स्थिति के तहत किया गया। एसएनपी के लिए 5 चयनित लोकस की जीनोटाइलपग के दौरान गई सहिष्णुता के लिए चुलनदा लाभ प्राप्त करने के लिए पाया गया। इन भेड़ों में टी 3 हार्मोन की सांद्रता को प्रभावित करने वाले 2 लोकस पर जीनोटाइप पाए गए। एचएसपी की जीन अभिव्यक्ति मद्रास रेड में सबसे ज्यादा और मारवाड़ी में कम से कम पाई गयी।

बीटा केसिन के 13 ज्ञात रूपों के लिए एलिलिक और जीनोटाइपिक प्रोफाइल भारतीय मूल, विदेशी और क्रॉसब्रेड गोवंश का अनुमान लगाया गया। ए 1 / ए 2 के अलावा 13 ज्ञात रूपों में से केवल बी संस्करण तीनों गोवंश में पाया गया। करणफ्रीज के दूध में बीटा केसिन का अभिव्यक्ति विश्लेषण भी किया गया। चूहे (मधुमेह प्रगति) में बीसीएम7 और बीसीएम9 के प्रभाव का पता लगाने के परीक्षणों को पूरा किया गया और नमूने आगे विश्लेषण के लिए एकत्र किए गए।

17 भैंस नस्ल /आबादी के 625 जानवरों में उत्पन्न सीक्वेंलसग (जीबीएस) डेटा द्वारा जेनोटाइलपग का उपयोग ललकेज डिसक्वीलिब्रियम का अनुमान लगाने के लिए किया गया। कुल 23,306 एसएनपी जीनोटाइप किए गए । 0.2 से अधिक आर 2 मानते हुए, नदी के भैंसों के लिए 20–25 केबी और दलदल भैंसों के लिए 25–50 केबी की जेनेटिक दूरी ब्लॉक पाई गयी। एसएनपी की संख्या– नदी के लिए 1,50,000 और दलदल भैंसों के लिए 1,20,000 एसोसिएशन मानचित्रण के लिए आवश्यक मिले ।

17 भैंस नस्लों / आबादी के बीच मिश्रण की पहचान के लिए कुल 23,306 एसएनपी का विश्लेषण किया गया। चिलिका, मेहसाणा, तोडा, असम और मणिपुरी को छोड़कर देश की अधिकांश भैंस आबादी के लिए उच्च स्तर की मिश्रण थी। स्थानिक अनुवांशिक विश्लेषण ने सभी आबादी के समूह को ग्यारह समूहों में, मुख्य रूप से क्षेत्रवार द्वारा अनुमति दी।

जीनोम वाइड एसोसिएशन अध्ययन 12 सांडों की 1763 भैंस संतानों के एसएनपी मार्करों और दूध के लक्षणों पर फेनोमिक डेटा के आधार पर की गयी। मैनहट्टन प्लश्वट से पता चला कि आसपास के जीनोमिक क्षेत्र में दूध उपज गुण के साथ मजबूती से जुड़े थे। एसएनपी प्रभावों के आधार पर दुग्ध गुणों के लिए ब्लप और ब्लू का अनुमान लगाया गया। एसएनपी प्रभाव की उपलब्धता के बाद, अनुमानित मूल्य का अनुमान लगाया जा सकता है।

भैंसों के दुग्धकाल के विभिन्न चरणों के लिए ट्रांस्क्रिप्टोम उत्पन्न किया गया । दुग्धकाल के विभिन्न चरणों में उच्च विनियमित जीन एम् ऐ पी के संकेतन मार्ग (III बनाम I), कॢडएक में कैल्शियम विनियमन (III बनाम II), बी डी एन ऍफ़ संकेतन मार्ग (II बनाम I) और व्यायाम प्रेरित सर्केडियन विनियमन (II बनाम I) थे। भैंस प्रतिलेखों की डी नोवो असेंबली भी की गई ।

जर्सी हैप्लोटाइप (जेएच1), होल्स्टीन हैप्लोटाइप –एचएच3 और एचएच4, होल्स्टीन कोलेस्ट्रॉल की कमी

सहित विभिन्न घातक आनुवांशिक रोगों के लोकस को भारतीय गोवंशों में निरूपित किया गया। दो उत्परिवतह्न एलील – जेएच1 और एचएच4 हेटेरोजाइगस स्थिति में क्रमशः जर्सी और होल्स्टीन अनुवांशिक समूहों में पता चले। पीसीआर आधारित प्रोटोकश्वल गोवंशों में जेएच1 और एचएच3 की स्क्रीलनग के लिए विकसित किए गए।

संस्थान विभिन्न सरकारी एजेंसियां को क्रोमोसोमल दोषों एवं अनुवांशिक बीमारियों के पता लगाने के लिए सेवाएं प्रदान करता है। गत वर्ष क्रोमोसोमल दोषों के लिए कुल 344 नर स्क्रीन किए गए। अनुवांशिक बीमारियों के लिए कुल 142 नर स्क्रीन किए गए। एक नर में गुणसूत्र दोष पाया गया। इस सेवा के द्वारा संस्थान को रु. 8,30,500/– राजस्व के रूप में प्राप्त हुए।

नेटवर्क प्रोजेक्ट के तहत, लक्षणीकरण के लिए 9 नई आबादी चुनी गयी और 2 नस्लों को उनके आवास में संरक्षित किया जा रहा है।

पिछले साल कुल 7 शोध परियोजनाएं पूरी की गई। वर्तमान में संस्थान में चल रहे पांच बाहरी वित्त पोषित और एक राष्ट्रीय फेलो परियोजनाओं सहित 22 शोध परियोजनाएं हैं।

राष्ट्रीय और अंतर्राष्ट्रीय पत्रिकाओं में कुल 33 शोध पत्र प्रकाशित किए गए। 12 तकनीकी / लोकप्रिय लेख प्रकाशित किए गए। संस्थान द्वारा पांच पुस्तकें और मोनोग्राफ भी प्रकाशित किए गए ।

वैज्ञानिक और अकादमिक कर्मचारियों के लिए शॉर्ट कोर्स और मॉडल ट्रेलनग कोर्स का प्रशिक्षण आयोजित किया गया। आईसीएआर संस्थानों के प्रशासनिक, तकनीकी और सहायक कर्मचारियों के कौशल को बढ़ाने के लिए दो प्रशिक्षण कार्यक्रम आयोजित किए गए।

ब्यूरो के वैज्ञानिकों ने मेरा गांव मेरा गौरव में भाग लिया और विभिन्न गांवों का दौरा किया और किसानों के बीच जागरूकता पैदा। संस्थान की गतिविधियों को प्रदृशत करने और स्वदेशी जानवरों के लाभों के बारे में किसानों को संवेदनशील बनाने के लिए विभिन्न स्थानों पर सात प्रदर्शनी आयोजित की गईं। संस्थान ने अलग अलग अवसर जैसे की ब्यूरो का स्थापना दिवस, जैव विविधता दिन, गणतंत्र दिवस और स्वतंत्रता दिवस, जय किसान जय विज्ञान, राष्ट्रीय स्वच्छता अभियान, सतर्कता सप्ताह, अंतर्राष्ट्रीय योग दिन, कृषि शिक्षा दिवस, लहदी पखवाड़ा इत्यादि मनाये।

ब्यूरो पुस्तकालय में, विभिन्न पत्रिकाओं में 23 विदेशी और भारतीय पत्रिकाएं शामिल की गई।

संस्थान अनुसंधान समिति (आईआरएसी) और अनुसंधान सलाहकार समिति समय पर आयोजित की गई और अनुसंधान परियोजनाओं की प्रगति की समीक्षा की गई।

संस्थान के 22 कर्मचारियों के एक दल ने आईसीएआर (उत्तरी क्षेत्र) खेलों में भाग लिया। बास्केटबॉल और वश्वलीबश्वल स्मैलशग टीम सेमीफाइनल दौर तक पहुँची। ब्यूरो के कर्मचारियों ने गणतंत्र दिवस के अवसर पर आयोजित वाृषक खेल प्रतियोगिता – 2018 के विभिन्न खेलों में भाग लिया।

सचिव डेयर व महानिदेशक, आईसीएआर तथा उपमहानिदेशक (प.वि.), आईसीएआर सहित कई प्रतिष्ठित व्यक्तियों ने संस्थान का दौरा किया।

वैज्ञानिकों ने देश के भीतर प्रशिक्षण कार्यक्रमों और कार्यशालाओं, संगोष्ठी, सम्मेलनों में भाग लिया ।

ब्यूरो के वैज्ञानिकों को भा.कृ.अनु.प.––नेशनल डेयरी अनुसन्धान संस्थान के पशु आनुवंशिकी और प्रजनन, एनिमल बायोटेक्नोलॉजी और पशु जैव रसायन की स्नातकोत्तर संकाय में शामिल किया गया है और इन डिवीजनों में विभिन्न पाठ्यक्रमों को पढ़ाने का कार्य करते हैं। वैज्ञानिक नियमित रूप से विभिन्न संस्थानों और विश्वविद्यालयों के छात्रों को मार्गदर्शन कर रहे हैं, जिनमें मास्टर्स और पीएचडी डिग्री के लिए नेशनल डेयरी अनुसन्धान संस्थान भी शामिल है।

वर्तमान में संस्थान में 29 वैज्ञानिक, 16 तकनीकी, 17 प्रशासनिक और 4 कुशल कर्मचारी हैं। दो वैज्ञानिकों और चार तकनीकी कर्मचारियों को अपने अगले उच्च ग्रेड में पदोन्नति प्राप्त हुई। दो कर्मचारी संस्थान में शामिल, दो स्थानांतरित और एक सेवानिवृत हुए।

◆

राजभाषा प्रकोष्ठ की गतिविधियाँ

संस्थान राजभाषा कार्यान्वयन समिति की बैठकें

संस्थान में राजभाषा कार्यान्वयन समिति की बैठकें निरंतर की जाती हैं। इन बैठकों में लिए गए निर्णयों पर क्रियान्वयन व अनुपालन किया जाता है। प्रत्येक तिमाही में निष्पादित कार्रवाई पर चर्चा करके पुष्टि की जाती है। इस अवधि के दौरान अभी तक, दो बैठकें 2.5.2017, 29.7.2017 19.1.2018 तथा 26.3.2018 को आयोजित की गई हैं।

संस्थान राजभाषा सलाहकार समिति की बैठकों का आयोजन

संस्थान में समय–समय पर संस्थान राजभाषा सलाहकार समिति की बैठकों का आयोजन भी किया जाता है जिसमे संस्थान की वार्षिक हिंदी पत्रिका "पशुधन प्रकाश" के प्रकाशन से संबंधित, हिंदी चेतना माह अथवा पखवाड़ा के आयोजन संबंधित विषयों पर चर्चा करके कार्यक्रमों की रूप–रेखा बना जाती है। राजभाषा सलाहकार समिति की बैठक का आयोजन 27.7.2017 तथा 08.8.2017 को किया गया।

संस्थान में हिंदी व्याख्यान/कार्यशालाओं का आयोजन

संस्थान में राजभाषा हिंदी के प्रचार–प्रसार तथा इसके दैनिक राजकीय कार्यों में अधिकाधिक प्रयोग को प्रगति देने हेतु हिंदी व्याख्यानों/कार्यशालाओं का आयोजन किया जाता है. इसी प्रक्रिया में 14.9.2018 तथा 15.2.2018 को आयोजित की गई हैं।

हिंदी पखवाड़ा के आयोजन का संक्षिप्त विवरण

ब्यूरो में प्रत्येक वर्ष की भांति इस वर्ष भी 6–21 सितम्बर, 2017 तक हिंदी पखवाड़े का आयोजन किया गया। निदेशक महोदय द्वारा गठित हिंदी पखवाड़ा आयोजन समिति जिसके अध्यक्ष डॉ. एन. के. वर्मा, प्रधान वैज्ञानिक तथा सदस्यगण डॉ. अनिल मिश्र, डॉ. सोनिका अहलावत, डॉ. करणवीर सिंह और सदस्य सचिव श्री सतपाल, राजभाषा अधिकारी ने ब्यूरो स्टाफ के लिए लिखित व मौखिक प्रतियोगिताओं का संचालन किया।

हिंदी लेखन प्रतियोगिताओं के अंतर्गत हिंदी निबंध प्रतियोगिता का आयोजन किया गया। निबंध लेखन का विषय गो संरक्षण में गोचरण का महत्व रखा गया था। इसके अतिरिक्त हिंदी पत्र लेखन प्रतियोगिता, टिप्पणी/मसोदा लेखन प्रतियोगिता एवं शब्दार्थ व अनुवाद प्रतियोगिता, आशु भाषण, भाषण प्रतियोगिता जिसका विषय "नकदी रहित भारत" था, का आयोजन किया गया। दिनांक 14.9.2017 को हिंदी दिवस के शुभ अवसर पर विशेष रूप से तीन हिंदी शब्द ज्ञान प्रतियोगिता/कार्यशाला का आयोजन किया गया. संस्थान में हिंदी उत्कृष्ट कार्मिक के चयन हेतु 2016–17 के दौरान किये गये राजकीय कार्यों में से हिंदी में किये गए कार्यों का मूल्यांकन गठित समिति द्वारा करके विजेताओं को पुरस्कृत किया गया।

ब्यूरो के वैज्ञानिकों/तकनीकी अधिकारियों/शोधवेत्ताओं हेतु दिनांक 12.9.2017 को "मेरा गांव मेरा गोरव"

विषय पर हिंदी लेख पोस्टर–प्रदर्शन प्रतियोगिता का आयोजन किया गया तथा दिनांक 13.9.2017 को हिंदी में शौध–पत्र प्रस्तुतीकरण प्रतियोगिता का आयोजन किया गया।

पुरस्कार वितरण समारोह

दिनांक 21.9.2017 को संस्थान ने अपना 34वां स्थापना दिवस तथा हिंदी पुरस्कार वितरण समारोह आयोजित किया। समारोह के दौरान ही मुख्य अतिथि डॉ. के.एम.एल. पाठक, कुलपति, पंडित दीनदयाल उपाध्याय पशु विज्ञान एवम् गो अनुसन्धान विश्वविद्यालय, मेरठ ने हिंदी प्रतियोगिताओं के विजेताओं को पुरस्कार प्रदान किये। इसी शुभ अवसर पर ब्यूरो की वार्षिक हिंदी पत्रिका "पशुधन प्रकाश" के सप्तम अंक (वर्ष 2016) में प्रकाशित लेखों के मूल्याँकन के आधार पर तीन श्रेष्ठ लेखों को भी पुरस्कार प्रदान किये गए।

वार्षिक हिंदी पत्रिका पशुधन प्रकाश के अष्टम अंक का विमोचन

पुरस्कार वितरण समारोह के दौरान मुख्य अतिथि डॉ. के.एम.एल. पाठक, कुलपति, पंडित दीनदयाल उपाध्याय पशु विज्ञान एवम् गो अनुसन्धान विश्वविद्यालय, मेरठ ने ब्यूरो की वार्षिक हिंदी पत्रिका पशुधन प्रकाश के अष्टम अंक (वर्ष 2017) का विमोचन भी किया।

विशेष उपलब्धि

नगर राजभाषा कार्यान्वयन समिति द्वारा दिए जाने वाले राजभाषा पुरस्कारों के अंतर्गत वर्ष 2016–17 का द्वितीय पुरस्कार दिनांक 09.6.2017 को नराकास की छमाही बैठक के दौरान हमारे संस्थान को मिला, जिसमे संस्थान के लिए एक ट्राफी तथा प्रशस्ति पत्र प्राप्त हुआ।

* * *

भाकृअनुप
ICAR

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

Agrisearch with a human touch

ICAR-NATIONAL BUREAU OF ANIMAL GENETIC RESOURCES

(An ISO 9001:2008 Certified Institute)

G.T. Road By-Pass, Near Basant Vihar, Karnal-132 001 (Haryana) India
Phone: 0184-2267918 (O), Fax: 0184-2267654
E-mail: director.nbagr@icar.gov.in; directornbagr@gmail.com
Website: www.nbagr.res.in

intech Design-n-Print 093541 01541