



NBAGR



Newsletter

Volume-9 No. 1

DEDICATED TO ANIMAL GENETIC RESOURCES OF INDIA

January-June, 2012

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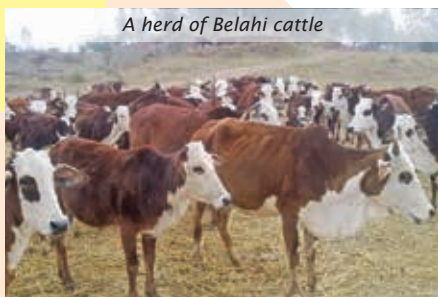
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From Director's Desk...

The fast pace of loss in domestic animal diversity and increasing genetic erosion of farm animal breeds are the emerging prime concerns globally. Livestock biodiversity in most of the developing and under developed countries has become more vulnerable due to increasing pressure of rearing livestock more under intensive and commercial animal production systems. India is not an exception for that which is a globally acknowledged mega biodiversity center with the repository of huge and diverse livestock populations distributed in a large range of geographical, ecological and climatic regions. Therefore, NBAGR, as a nodal agency in the country has huge onus to protect, preserve and sustainably utilize the vast and varied farm animal biodiversity. During its 28 years old journey, NBAGR has immensely contributed by having characterized almost all well-known indigenous livestock breeds and developed breed descriptors and databases on phenotypic and genetic characterization of AnGR. Now, our focus and commitment is to characterize the lesser known farm animal populations which are in plenty but studied inadequately. A number of such new populations of cattle, buffalo, sheep and goat were identified during recent years and are in process of characterization. Continuing with this, the Institute has registered nine more native farm animal breeds during the reported period. This included Kosali, Malnad Gidda and Pulikulam cattle breeds, Kalahandi buffalo breed, Konkan Kanyal and Berari goat breeds, Ghoongroo and Niang Megha pig breeds and Spiti breed of donkey. Total number of registered indigenous breeds in the country will now be 144, which include 37 cattle, 13 buffalo, 23 goat, 39 sheep, 6 horses & ponies, 8 camel, 2 pig, 1 donkey and 15 chicken breeds. In Bureau, a large number of data on genomic resources pertaining to buffalo, cattle, camel and goat has been generated. A number of candidate genes of economic importance and environmental adaptation traits such as animal product quantity and quality traits, disease resistance and thermo regulatory traits have been characterized. A large number of SNPs were identified and added in genetic database. For farm animal breed conservation programme, institute has been working in collaboration with other ICAR institutes, state agricultural universities and non-governmental organization for conservation of Tharparkar and Krishna valley cattle and Kilakarsal sheep. National Gene Bank at NBAGR is being enriched under *ex-situ* conservation programme with germplasm of livestock breeds at risk. During the reported period, the semen doses of Ongole, Rathi, Vechur cattle and Nili Ravi, Surti, Bhadawari buffaloes breeds have been added for long term storage. The bureau has organized one international workshop and two training programmes successfully. It was a moment of great honour for the institute to receive Taradevi Modi Rashtra Utthan Award 2011-12 recognising our tremendous efforts and contribution to the conservation of cattle genetic resources in the country. I feel immensely pleased to put forth this issue of NBAGR News letter which has a glimpse of all such on-going research and development activities and look forward to the suggestions and constructive feedback from our valuable readers for further spearheading our campaign on conservation and sustainable management of farm AnGR of India.



B.K. Joshi
(B K Joshi)



A herd of Belahi cattle

"The greatness of a nation and its moral progress can be judged by the way its animals are treated."

- Mahatma Gandhi

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RESEARCH ACCOMPLISHMENTS

The salient research findings, emerged from different research projects completed during the reported period are:

Characterization of Nukra horses for variations in KIT gene:

The white coat colour phenotypes, which are classified as Nukra horse may arise from the cremello or the dominant white genotypes. The expression of these genotypes looks quite similar in adult horses except minor differences like the cremello horses have green eyes whereas the dominant white horses have the brown eyes. The dominant white type of coat colour arises due to the altered or impaired function of the KIT gene which leads to impairment of normal development and distribution of melanocytes arising from upper neural crest leading to white coat colour and skin. Since, the pigment cells of the eyes do not descend from the upper neural crest the dominant white horses have normal pigmentation in the eyes. In field, it was observed that though most of the horses described as Nukra horses by the owners/breeders had the cremello genotype some of the Nukra horses (about 10%) had the dominant white type of the genotype. Till now seventeen variations leading to altered or truncated function of KIT gene, named W1-W17 have been identified and associated with the dominant white coat colour across various horse breeds. These mutations are distributed across the Kit gene. Initially, regions covering intron-2, exons 4 (W3), (W7), 5 (W6), 7 (W10, W16), 10 (W15), 12 (W4, W9, W17), 13 (W2), 15 (W5, W8), 17/intron17 (W13, W14), 19 (W11) were selected and the primers were designed and synthesized. In exon-7, GAAC deletion with respect to wild type sequence was found which has been reported earlier as W10 variation in other horse breeds. It is concluded that the dominant white type animals may not be selected for propagation considering pleiotropic effects associated with dominant white coat colour.

Genetic structuring of important native cattle (Bos indicus) breeds from different agro-climatic regions of India:

A total of 838 animals from 20 Indian cattle breeds adapted to diverse agro-climatic regions of the country were genotyped utilizing 25 microsatellite/SSR markers. Majority of the breeds from North and north-western region grouped separately from that of breeds from Southern region. The analysis also indicated discrete breed structuring for Kangayam, Ongole, Umblachery, Red Kandhari and Malvi cattle. The mitochondrial D-loop based analysis revealed southern, draft purpose and grey coat colored breeds to be comparatively more

SECTORAL NEWS

FAO Guidelines for Phenotypic characterization of animal genetic resources

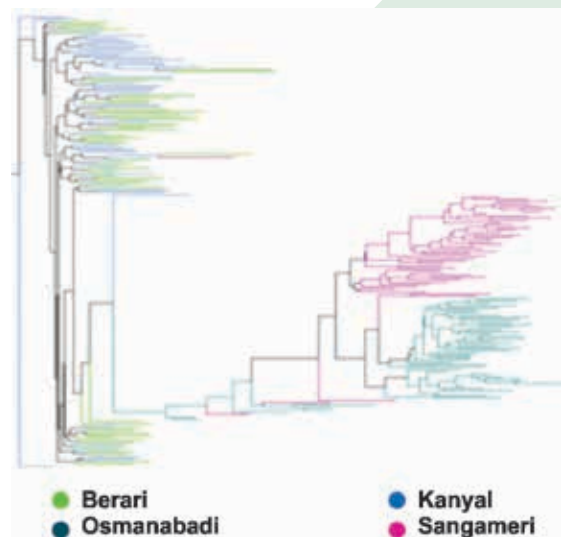
As part of its Animal Production and Health Guidelines, FAO has recently published a series of guidelines to support countries in their implementation of the Global Plan of Action for Animal Genetic Resources. It has been endorsed by the Commission on Genetic Resources for Food and Agriculture. It addresses Strategic Priority Area 1 of the Global Plan of Action – “Characterization, inventory and monitoring of trends and associated risks” and complements the recently published guidelines on molecular genetic characterization and on surveying and monitoring of animal genetic resources. The objective is to provide advice on how to conduct a well-targeted and cost-effective phenotypic characterization study that contributes to the improvement of animal genetic resources management. An overview of the concepts and approaches that underpin phenotypic characterization is followed by practical guidance on planning and implementing field work, data management and data analysis. The annexes include lists of phenotypic variables for major livestock species, as well as a framework for recording data on breeds’ production environments.

diverse. The phylo-geography and network analysis revealed southern breeds to be primitive in comparison to northern cattle breeds. Network analysis indicated distinct dichotomy and independent domestication events for Indian zebu cattle and taurine cattle.

The candidate gene analysis across the breeding bulls utilized in AI revealed that except at Beta-casein locus (A2 allele), the frequency of functionally important alleles is low at other analyzed loci, suggesting the need for screening of the breeding bulls before selection. Genes belonging to casein cluster, whey proteins and Toll like receptors were sequence characterized in a large set of Indian cattle breeds. Sequence analysis revealed a total of 116 variants within 5'flanking region of casein and whey protein genes with respect to *Bos taurus* sequence, of which 50 were novel to Indian cattle breeds. Across the TLR1-6-10 gene cluster, a total of 106 SNPs, of which 38, 52 were non-synonymous and novel respectively, were identified, indicating substantial variation which could further be exploited for association with disease resistance.

Genetic diversity among goat breeds of Maharashtra state

Microsatellite based genetic diversity investigated in Konkan Kanyal, Berari, Sangamneri and Osmanabadi goat populations of Maharashtra state revealed a total of 479 alleles (192 in Sangamneri, 153 in Osmanabadi, 294 in Berari and 255 in Konkan Kanyal). Mean number of alleles per locus was 7.68, 6.12, 11.76 and 10.20 and mean observed heterozygosity were 0.53, 0.42, 0.67 and 0.67 for Sangamneri, Osmanabadi, Berari and Kanyal goat populations respectively. The fixation coefficients of subpopulations within the total population, measured as F_{st} varied from 0.04 (OarHH64) to 0.68 (OarJMP29) with a mean of 0.17 ($P < 0.05$) which implied that 83% of the total genetic variation corresponded to the differences among individuals within populations. The bottleneck test showed that there was significant deficiency of heterozygosity but the suspected genetic bottleneck was found to be absent as the mode-shift curve is a typical "L" shape. The genetic distances between four breeds / populations indicated the distinctness of Berari and Konkan Kanyal from Sangamneri and Osmanabadi. The Nei's genetic distance observed between breeds are 0.472 (Sangamneri & Osmanabadi), 0.667 (Sangamneri and Berari), 0.819 (Sangamneri and Konkan Kanyal), 0.797 (Osmanabadi and Berari), 0.994 (Osmanabadi and Konkan Kanyal) and 0.092 (Berari and Konkan Kanyal). Konkan Kanyal is genetically more distant from Osmanabadi and Sangamneri than Berari. Sangamneri and Osmanabadi goat breeds were assigned to cluster -3 where the proportion of membership for each breed is 0.975 (Sangamneri) and 0.992 (Osmanabadi). Kanyal and Berari goat populations were assigned to another cluster (Cluster 4). The proportion for their membership was 0.923 (Konkan Kanyal) and 0.869 (Berari). Based on the phenotype and geographical locations of breeding tracts, Konkan Kanyal and Berari also forms distinct populations and can be considered as separate breeds.



Phylogenetic tree showing relationship between four goat populations

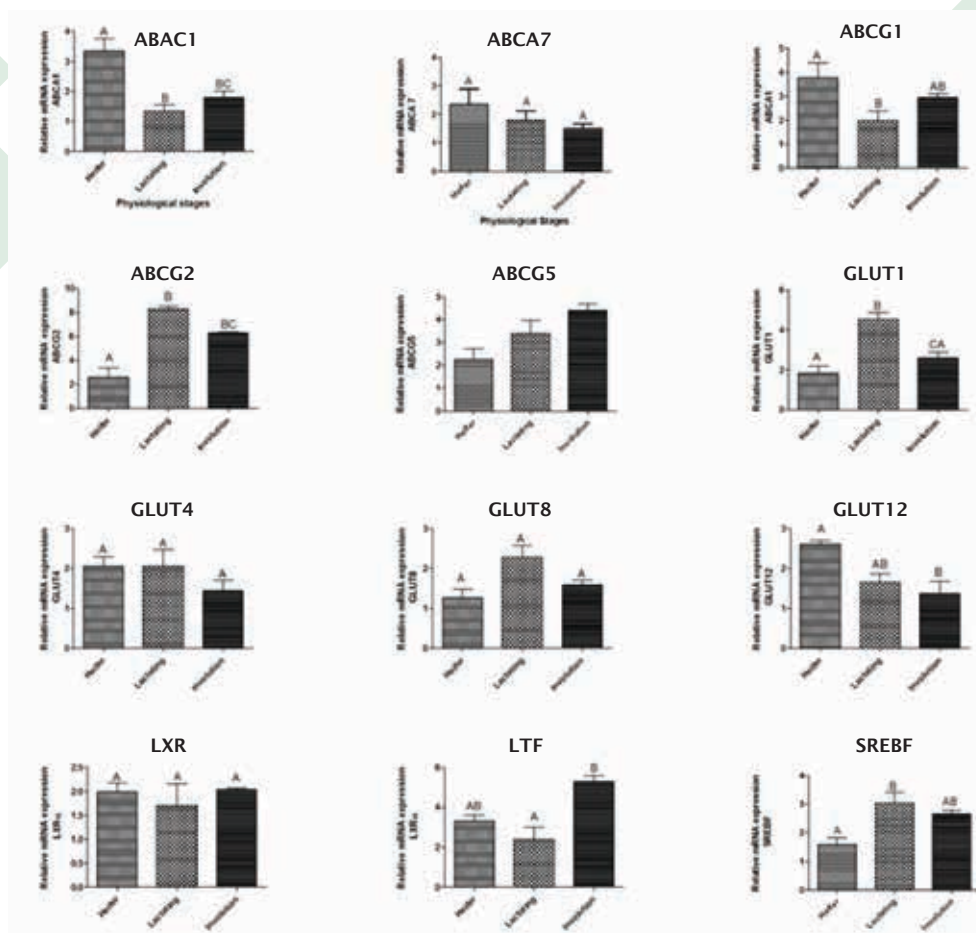
Nucleotide diversity in candidate genes for mutton quality traits in Indian sheep

The exon 3 and 3'UTR region of ovine Growth differentiation factor 8 (GDF8) gene was PCR amplified and sequenced across 45 sheep samples belonging to different sheep breeds (Muzzafarnagri, Malpura, Magra, Nali, Chokla from Northwestern arid and semi arid region, Deccani, Madgyal, Bandur from Southern peninsular region and Ganjam, Garole sheep from eastern region of India). Sequence alignments and comparisons were

carried out using DNAMAN (Version 5.0, Lynnon BioSoft, Vaudreuil, Canada) software programme which revealed that the consensus sequence in Indian sheep shared >90% homology with the reference sequence (DQ530260). Several singletons but no SNPs could be detected in the investigated region of exon 3. The study was also conducted to search for the G to A transition reported in exotic sheep in the 3'UTR, which creates a recognition motif for miRNAs, which in turn suppresses the translation of the gene resulting in increased muscularity. It was observed that in all the samples of Indian sheep investigated the normal G allele was present in the homozygous state.

Stage specific expression of Lipid and Glucose transporters and their regulatory genes in buffalo mammary tissue

In the present study, expression level of various candidate genes associated with cholesterol transport including ABAC1, ABCG1, ABCA7, ABCG5, ABCG2; their regulators, different SREBF1, LXR- α and glucose transporters viz., GLUT 1, GLUT8, GLUT4 and GLUT12 was compared across different physiological stages of buffalo mammary gland (lactation vs involution; lactation vs heifer; heifer vs involution). The importance of the study stems from the fact that till date no information is available about the expression kinetics of these important transporters in riverine buffalo mammary gland. The differential expression of ABCA1, ABCG1, ABCA7 and ABCG5 genes



Relative mRNA abundance of ABC and glucose transporters and their regulators during different physiological stages of buffalo mammary gland. Each bar represents the mean calculated from 4 animals assessed in duplicate \pm S.E.M. (n = 8). Means with different letters are significantly different (P<0.05)

suggested their distinct functional roles during different physiological stages of buffalo mammary gland. On the other hand, significant ($p < 0.05$) induction of ABCG2 gene in lactating mammary tissue in comparison to involution and heifer stages indicated its role during lactation. Few recent studies have associated ABCG2 as candidate gene with important functional role in regulating milk yield, fat and protein concentration in bovines. This strongly supports the conserved aspect of its role in mammary gland physiology in large ruminants.

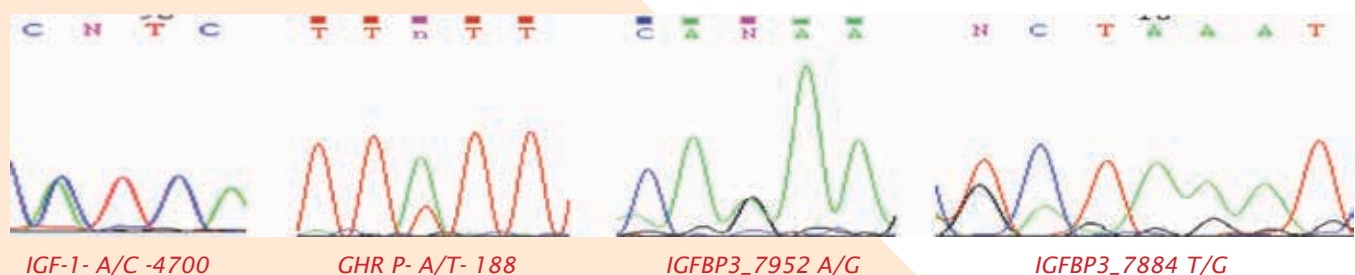
The expression of LXR- α and SREBF1- key regulators of ABCA1 and ABCA7 genes, respectively were also analyzed. The expression pattern of LXR- α gene reflected the fact that ABCA1 and other ABC cholesterol transporters are regulated to a certain extent by LXR- α gene. Similarly, SREBF1 expression indicated its role in regulation of ABCA7 gene. Lactoferrin (LTF) which was included as control gene and major marker for involution, showed significantly higher expression during involution in comparison to lactating stage of buffalo mammary gland. Amongst the various glucose transporters, GLUT1 and GLUT8 appeared to be major glucose transporters in buffalo mammary gland as their expression was higher during lactation in comparison to involution and heifer stages. On the other hand, GLUT4 & GLUT12 mRNA expression was greater during heifer stage in comparison to involution and lactating tissue. The present result has helped to unravel distinct expression pattern and functional role of individual transporters genes in buffalo mammary gland during different physiological states.

Characterization of candidate genes regulating muscle growth and meat quality in buffalo

Characterization by sequencing of thyroglobulin, calpain, calpastatin, insulin-like growth factor-1, stanniocalcin, fatty acid synthase, myogenic factor-5, leptin and fatty acid binding protein-3 genes involved in muscle growth and meat quality indicated several unique nucleotide changes in buffalo thyroglobulin compared to that of cattle. Polymorphism analysis and genotyping of insulin-like growth factor-1, leptin, fatty acid binding protein, fatty acid synthase, calpain and calpastatin genes in buffalo revealed some unique nucleotide variations between buffalo and cattle. Sequence analysis of thioestrane region and 3'UTR of buffalo fatty acid synthase helped in identification of polymorphism in buffalo as well as unique variations in 3'UTR of riverine and swamp buffaloes. Expression analysis of selected genes- stanniocalcin, leptin, fatty acid synthase and IGF receptor carried out in adipose, skeletal muscle and liver tissues of young (heifer stage) and aged (spent) buffaloes, revealed differential expression of only leptin gene in two groups compared.

Relationships of Insulin-like growth factor-1, Growth hormone receptor (GHR) and Insulin-like growth factor binding protein-3 (IGFBP-3) gene polymorphisms with growth traits in Sirohi breed of Indian goats

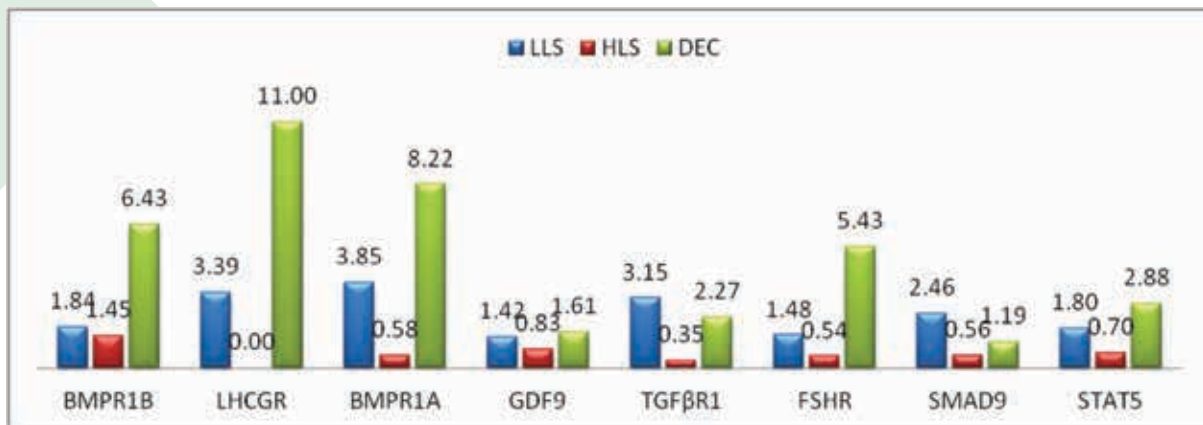
Gene polymorphism at IGF1, GHR and IGFBP-3 genes and their effects on growth traits in Sirohi breed of Indian goats were detected using direct gene sequencing method in 169 Sirohi goats. The single nucleotide polymorphisms at locus 4700 detected in Intron1 of IGF1 gene had three genotypes and observed significantly associated with body weights at birth, 3, 6 and 9 month of age. The SNP at the locus 188 in promoter region



of GHR gene had three genotypes and observed significantly associated with body weight, body heights, body lengths at birth. SNP at locus 7884 observed in exon-2 of IGFBP-3 gene had three genotypes and were non-significant source of variation in body weights studied but significantly influenced the body heights, body lengths and body girth at 9 month of age. The SNP at the locus 7952 in exon-2 of IGFBP-3 gene had three genotypes and observed significantly associated with body weight at 3 month of age. The studied SNPs, thus, may be helpful in marker-assisted selection in the Sirohi breed of Indian goats.

Gene expression profiling in *FecB* carrier and non-carrier ewes under high and low planes of nutrition

To study the effect of nutrition on fecundity under DBT funded project, three different groups of ewes selected- *FecB* non-carrier Deccani, high and low litter size *FecB* carrier animals. Three ewes in each group were kept under normal routine of grazing and feeding and three ewes offered additional 100 gm cotton seed cake and 50 gm maize daily for four months. After estrous synchronization, ovarian status of each animal recorded and cyclic ovaries and follicles collected in *RNA Later* by laparoscopy. RNA was extracted and Sybr-Green quantitative real-time PCR performed to assess the expression of eight different genes regulating ovulation. Ovarian status of animals under different nutritional planes indicated significant differences in low litter size animals only (Av. no. of follicles 1.7 in low plane of nutrition Vs 2.8 in high plane of nutrition). Moderate level of expression differences across all the genes studied in low litter size BB ewes resulted in significantly higher number of follicles developed in animals under higher plane of nutrition. Among ewes kept under different planes of nutrition, Deccani showed higher expression of *BMPRIA*, *BMPRIB*, *FSHR* and *LHCGR* genes in higher plane of nutrition without any significant effect on follicular development.



*Fold change in expression of different fecundity related genes in ewes under high plane of nutrition in low litter size (LLS) *FecB* carrier, high litter size (HLS) *FecB* carrier and Deccani (DEC) *FecB* non-carrier, compared to ewes under low plane of nutrition.*

Identification of polymorphism in *CAST* gene of indigenous goats

Calpastatin (*CAST*) is a protein inhibitor of the ubiquitous calcium-dependent proteases- μ -calpain and m -calpain. The relative levels of the components of the calpain-calpastatin system determine the extent of meat tenderization during postmortem storage. Present study identified polymorphisms in *CAST* gene in Indian goat breeds differing in phenotype (weight and size) and geographical distribution. As complete caprine gene sequence is not yet available, bovine *CAST* gene in the GenBank database (NW_001495281.2) was utilized for analysis of regions of *CAST* gene in goats. 3126 bp of relevant DNA was sequenced in seven Indian goat

breeds that include 222 bp of three exons (exon 3, 7 and 8), 2529bp of intronic region (Intron 3, 5, 6, 7, 8 and 12) and 375 bp of 3'UTR. Sequence data from these samples were entered in the NCBI GenBank database under the following accession numbers: exons 3, 7, 8 and intron 5 (JQ073718), Intron 12 (JQ739234) and 3'UTR (JQ073719).

One hundred forty two variations were identified in investigated sequences of indigenous goat as compared to cattle. Using comparative sequencing ten novel SNPs have been identified of which, only one was in the transcribed region. The SNP in exon 3 is a non-synonymous transition (g82263A>G), which changes amino acid (Lys>Arg) at position 21 of 22 amino acid conceptualized protein sequence. Majority of observed SNPs (9) were in non-coding region of CAST gene. Two novel SNPs g84659T>C and g84661G>A have been identified in intron 5, six in intron 7 and one in intron 8. Twenty variations were observed as compared to cattle in the 3'UTR which has gained attention due to its importance in regulation of gene functions. CAST gene sequences of indigenous goats were subjected to basic local alignment search to know the sequence homology with the corresponding gene of other species. The BLAST result revealed that similarity with *Bos taurus* of exonic regions (exon 3, 7, 8), intron 5 and 3'UTR was 98%, 93% and 94% respectively. Since sequence for intron 12 is available for cattle and sheep, it was compared with both. Intron 12 of caprine CAST gene showed higher homology with *Ovis aries* (98%) than with *Bos taurus* (93%). Three PCR-RFLP loci have been established for novel SNPs that will help in further analysis of genetic polymorphism in indigenous goats.

Polymorphism in CAST gene of Indian goat

Region	Nucleotide position	SNP
Exon 3	82263	A/G
Intron 5	84659	T/C
	84661	G/A
Intron 7	90105	G/C
	90144	T/C
	90149	A/G
	90255	A/G
	90283	G/A
Intron 8	90306	C/T
	90413	A/G

FARM ANIMAL BREED REGISTRATION

Breed registration Committee in its meeting on 14th May, 2012 at New Delhi approved registration of nine breeds of livestock species which include three breeds of cattle, one of buffalo, two of goat, two of pig and one breed of donkey. The accession numbers have been assigned to these registered breeds. With this, total number of registered indigenous livestock breeds in the country has reached 144, which included 37 of cattle, 13 of buffalo, 23 of goat, 39 of sheep, 6 of horses & ponies, 8 of camel, 2 of pig, 1 of donkey and 15 of chicken.

Kalahandi buffalo (INDIA_BUFFALO_1500_KALAHANDI_01013)

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



Pulikulam cattle (INDIA_CATTLE_1800_PULIKULAM_03035)

Pulikulam cattle are maintained in large migratory herds in Madurai and nearby region of Tamilnadu. Utility is draught and manure. These cattle are used in games like bull riding (Jallikattu) in local area. Breed is more resistance to communicable and parasitic diseases as compared to crossbreds under hot and wet conditions.



Kosali cattle (INDIA_CATTLE_2600_KOSALI_03036)

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



Malnad Gidda cattle (INDIA_CATTLE_0800_MALNADGIDDA_03037)

Malnad Gidda is a short statured cattle breed from Western Ghat of Karnataka. Breed is reared for milk and manure purpose. Animals have excellent endurance power and resistance to diseases.



Konkan Kanyal goat (INDIA_GOAT_1100_KONKAN KANYAL_06022)

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



Berari goat (INDIA_GOAT_1100_BERARI_06023)

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



Ghoongroo pig (INDIA_PIG_2100_GHOONGROO_09001)

Ghoongroo pig is reared for pork and manure purpose in Darjeeling and nearby Tarai area of West Bengal. These pigs are black coloured and have upwardly curved snout and large heart shaped ears.



Niang Megha pig (INDIA_PIG_1300_NIANGMEGHA_09002)

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



Spiti donkey (INDIA_DONKEY__0600_SPITI_05001)

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



IMPORTANT MEETINGS

Institute Research Committee (IRC): Institute Research Committee meeting was held on 20th, 21st & 24th April, 2012 under the Chairmanship of Dr. B.K. Joshi, Director, NBAGR. Final reports of nine completed projects and proposals of eight new research projects were discussed and approved.

Research Advisory Committee: The first meeting of newly constituted Research Advisory Committee was held on 11th January, 2012 under the chairmanship of Dr. R Prabhakaran, Vice Chancellor, TANVASU, Chennai.

TRAININGS/HRD

- ◆ NBAGR jointly with NDRI, Karnal organized an International workshop on “Transcriptomics, Proteomics and Structural Biology held at NBAGR from Feb 27-29, 2012 under NAIP subproject on “Analysis of mammary gland transcriptome and proteome during lactation and involution in indigenous cattle and buffalo for identification of probable mammary biomarkers”. More than 100 researchers from all over the country participated in the workshop.
- ◆ A subject matter training on “Advances in Animal Bioinformatics” was organized from Feb. to 21st to March 3rd, 2012 under NAIP subproject ‘Establishment of National Agricultural Bioinformatics Grid (NABG) in ICAR.
- ◆ A summer short course on “Genomic and phenomic tools for the analysis of livestock genome” sponsored by Education Division, Indian Council of Agricultural Research was conducted from June 14th to June 23rd, 2012. Twenty one participants from various universities attended the course.



Overseas Deputation

1. Dr. R.A.K. Aggarwal, Principal Scientist awarded DBT Crest Award for six months at Washington State University, USA from August, 2011 to February, 2012.
2. Dr. R.K. Vijh, Dr. M.S. Tantia and Dr. R.S. Kataria attended Plant Animal Genome XX Conference held at a San Diego, USA during 14-18 January, 2012.

Fairs/ Exhibitions: For bringing awareness among farmers, livestock keepers and other stake holders about conservation and sustainable management of native farm livestock, the exhibitions were installed at different places on different occasions:

- ◆ An exhibition during Dairy Mela on 24th-26th Feb., 2012, at NDRI.
- ◆ An exhibition on occasion of seminar on cow science and “Tara Devi Modi Rashtra Uttahan Puraskar 2011-12” on January 24, 2012 at New Delhi.
- ◆ An exhibition on occasion of “Seminar on Indigenous Cattle”, on March 18, 2012 at Sangrur Gaushala, Sangrur (Punjab).

CELEBRATIONS

International Biodiversity Day

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



Republic Day

The Bureau staff and families celebrated the 63rd Republic day at the Bureau campus. Dr. BK Joshi, Director, NBAGR hoisted the tricolor and addressed the gathering. Children presented the cultural programmes to mark the occasion.

National Science Day

National Science Day was celebrated on 28th February, 2012 at the Institute campus. The students and teachers of various schools of the city participated in this celebration. To mark the event of Science day, an exhibition was displayed at NBAGR museum and an essay writing competition was organized for students of different age groups. The winners were given prizes.

SPORTS

The institute Volley ball fetched Winners trophy in Volley ball (Smashing) and Runners up trophy in Volley ball (Shooting) during ICAR Inter-institutional sports meet (North Zone) held at National Dairy Research Institute, Karnal from April 25-28, 2012.



PUBLICATIONS/ AWARDS

Research papers

1. Behl J, Verma NK, Tyagi N, Mishra, P, Behl R, and Joshi BK. (2012). The major Histocompatibility Complex in Bovines: A Review. ISRN Veterinary science, doi:10.5402/2012/872710.
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3. Dubey PK, Aggarwal J, Goyal S, Gahlawat SK, Kathiravan P, Mishra BP and Kataria RS. (2012). Sequence and topological characterization of Toll-like receptor 8 gene of Indian riverine buffalo (*Bubalus bubalis*). Tropical Animal Health and Production. DOI: 10.1007/s11250-012-0178-1.
4. Dubey PK, Goyal S, Aggarwal J, Gahlawat SK, Kathiravan P, Mishra BP and Kataria RS. (2012). Development of tetra primers ARMS-PCR assay for the detection of A1551G polymorphism in TLR8 gene of riverine buffalo. Journal of Applied Animal Research 40: 17-19.

5. Dubey PK, Goyal S, Kathiravan P, Mishra BP, Gahlawat SK and Kataria RS. (2012). Sequence characterization of river buffalo Toll-like receptor (TLR) genes 1-10 reveals distinct relationship with cattle and sheep. *International Journal of Immunogenetics*. DOI: 10.1111/j.1744-313X.2012.01135.x.
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7. Gong H, Zhou H, McKenzie GW, Yu Z, Clerens S, Dyer JM, Plowman JE, Wright MW, Arora R, Bawden CS, Chen Y, Li Ji, Hickford JGH. (2012). An Updated Nomenclature for Keratin-Associated Proteins (KAPs). *International Journal of Biological Sciences* 8(2):258-264.
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9. Kathiravan P, Kataria RS and Mishra BP. (2012). Power of exclusion of 19 microsatellite markers for parentage testing in river buffalo (*Bubalus bubalis*). *Molecular Biology Reports*. DOI 10.1007/s11033-012-1669-x.
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Monographs/Bulletin

1. Banni- A Unique Germplasm of Western India by BP Mishra, KP Singh, RS Kataria, DK Sadana P Kathiravan and BK Joshi. Monograph # 68, 2012.
2. Toda- The Unique Hill Buffalo of Tamil Nadu by P Kathiravan, SMK Karthickeyan, R Venkataramanan, M Iyue, BP Mishra, RS Kataria and BK Joshi. Monograph # 72, 2012.
3. Buffalo Genetic Resources of India-Marathwadi by RS Kataria, P Kathiravan, BP Mishra, DK Sadana, BV Gujar, V Vohra and BK Joshi. Monograph # 73, 2012.
4. Berari-An important goat germplasm of Vidarbha by NK Verma, SV Kuralkar, RAK Aggarwal, SP Dixit, Priyanka Mishra, Prajakta Kuralkar, PS Dangi, and BK Joshi. Monograph# 76, 2012.

Awards/Rewards/Recognition

Received Best poster award for the following research presentations at National Symposium on “Role of Indigenous animal genetic resources in rural food security vis-à-vis climate change” and IX annual convention of society for conservation of domestic animal biodiversity (SOCDAB) held on 24-25th February, 2012 at BAIF Pune campus, Pune.

- ♦ “Extensive Polymorphism in Toll-Like Receptor (TLR)2, 6, 1 and 10 Genes in tropically adapted Indian Cattle” by Monika Sodhi, Amit Kishore, Divya Ray, Ankita Sharma, BP Mishra, Neha Kapila and M Mukesh. Pp81.
- ♦ “Mammary epithelial cells of riverine buffalo reveals coordinated transcriptional adaptation to thermal stress” by Neha Kapila, Monika Sodhi, Amit Kishore, Ankita Sharma, AK Mohanty and M Mukesh. Pp150
- ♦ “Early transcriptomic response of buffalo mammary tissue explant to heat stress unravel enrichment of gene networks and pathways associated with cell cycle, apoptosis, heat shock proteins and interleukin signaling” by M Mukesh, Meenu Chopra, Avijit Poddar, Amit Kishore, Neha Kapila, and Monika Sodhi. Pp161.
- ♦ “Domestic Animal products GI constraints and issues: Chilika curd a typical case study” by Dhiraj Kumar Nanda, Rameshwar Singh, S K Tomar, S K Dash, Jayakumar S, Dilip K Arora, Reeti Chaudhary and Dinesh Kumar.

Best Paper Award for “Lesser known cattle populations of Bihar region: Genetic structure and differentiation” by Rekha Sharma, PK Singh, A Maitra, A K Pandey, S R Singh and Birender Singh in X UGC sponsored National Seminar on “Transfer of biotechnology for sustainable development & environment protection” on 21st & 22nd Jan., 2012 at Govt. College, Aron, Dist. Guna (MP).

DISTINGUISHED VISITORS

1. A group of Kerala State Progressive Farmers visited on 24th Jan. 2012
2. Dr. Juan J. Loo, Associate Professor, Mammalian Nutri-Physio-Genomics Lab, Department of Animal Science, University of Illinois, Urbana Champaign, IL, USA visited on 28th Feb. 2012.
3. Dr.Md.Nure Alam Siddiky, Program Officer (Livestock), SAARC Agriculture Centre, Bangladesh visited on 16th April 2012.
4. A delegation comprising of 7 senior officers from Royal Govt. of Bhutan, Ministry of Agriculture and Forests, Bhutan visited on 14th May 2012.
5. A team of 12 farmers from Barnala visited on 29th May 2012.
6. A delegation from FAO led by Dr.Venkateswarlu Dasyam visited on 30th May 2012.

PERSONNEL

Appointments/Joining/Transfers

1. Dr. Karan Vir Singh, Scientist (SS) joined on transfer from NBFGR Lucknow to NBAGR, Karnal on 16.01.2012.
2. Sh. Jagtar Singh, Administrative Officer joined on transfer from ICAR Research Complex for Goa to NBAGR, Karnal on 14.05.2012.
3. Dr. Dinesh Kumar, Sr. Scientist (Biotechnology) transferred from NBAGR to IASRI on 18.05.2012.
4. Sh. Yoginder, Assistant joined on 29.06.2012.

Superannuation

1. Dr. (Ms.) S. Bhatia, Principle Scientist superannuated on 29.02.2012.
2. Sh. C. K. Thakral, Finance & Accounts Officer superannuated on 31.03.2012.

Promotions

1. Smt. Neerja Kaul, SSS promoted to the post of Lower Divisional Clerk w.e.f 13.03.2012.
2. Sh. Naresh Kumar, SSS promoted to the post of Lower Divisional Clerk w.e.f 17.03.2012.
3. Sh. Babu Ram, SSS promoted to the post of Lower Divisional Clerk w.e.f 17.03.2012.