



4. Genetic Resources

CROPS

Germplasm augmentation, conservation and use:

Explored and collected 2,203 cultivated and wild germplasm from 21 states of the country, and added 1,021 specimens (herbaria, seeds and other economic products) to the National Herbarium of Cultivated Plants at the NBPGR, New Delhi. Germplasm conserved for long-term has increased in the National Gene Bank; *orthodox seed samples* - 16,299 accessions, *non-orthodox cryopreserved samples* - 455, and *in-vitro tissue cultures* - 57. Germplasm exchange included import of international nursery trial entries and transgenics. Promising germplasm introductions include rust and powdery mildew resistant *Triticum aestivum* (EC 592591) from China; anthracnose and bacterial wilt resistant *Cicer arietinum* (EC 589469), and *Lycopersicon esculentum* (EC 589472-84) with multiple resistance from Taiwan; lodging resistant upright bushy type *Phaseolus vulgaris* (EC 589468) with mid-season maturity, resistance to viruses and tolerance to rust; powdery mildew resistant *Cucumis melo* (EC 589374), and high-yielding



Maize accessions collected from Nagaland

Perilla frutescens (EC 592842-59) with high-oil content from the USA. Introduced transgenics include drought-tolerant *Gossypium* (EC 589424-27), containing *rolB* gene of *Agrobacterium rhizogenes*, and glyphosate herbicide and lepidopteran pest infestation tolerant cotton from China and the USA (EC 589428-34), containing *CP4 EPSPS*, *cry 1 Ac* and *cry 2 Ab* genes. Characterized and evaluated 25,181 germplasm accessions that are maintained at the NBPGR. Conducted 190 experiments including germplasm evaluation (63), breeding trials (87), agronomic (32) and quality traits (8) in different agroclimatic zones. Supplied 49,184 germplasm samples for research use and crop improvement in the country.

A total of 29 germplasm accessions of mango were collected, added to the field gene bank and maintained. In clonal selection, a total of seven clones, viz. two of Alphonso and five of Bangalora, were collected. Among the collections, Dudhiya Malda gave the highest yield followed by Dholikothi Maldah. The maximum fruit yield (125.75 kg/tree) was obtained from Bangalore Goa followed by Zafrani Gola. The evaluation of seedling germplasm revealed that the maximum number of fruits and yield were recorded in Peddapur 16. Collection No.7/80 was the highest yielder followed by collection No. 10/80. Clone Rati Banganpalli was found promising for cluster-bearing habit; Early Baneshan for early maturity; Pedda Baneshan and Allahabad Baneshan for bigger sized fruits. Bangalora clones Salem and Javori, recorded bigger sized fruits weighing 300–500 g and export quality. Mallika recorded maximum fruit yield, average fruit weight, high TSS, and low acidity. In guava, morphological characterization was carried out for 12 genotypes following IPGRI now descriptors. Out of 18 accessions tested, 10 were able to withstand salinity up to 6.0 dS/m with minimum damage to plant growth. In



Monitoring Global Plan of Action (GPA)

The FAO-funded Project *Establishment of Information Sharing Mechanisms for Monitoring the Implementation of GPA* has yielded two publications, including Indian experience of National Information Sharing Mechanisms (NISM). This experience of a large and elaborate National Agricultural Research System (NARS) has set exemplary tone for developing NISM by other countries.

banana, eight accessions were added in field gene bank. RAPD analysis corroborated genetic variability discovered by isozyme analysis between *Fusarium* wilt resistant Silk banana cultivar and Martman and other susceptible members of the group. Manjeri Nendran-II banana continued to be superior for yield and tolerance to Sigatoka leaf spot. Among the already identified Kanthali clones at Mohanpur, clone-I and clone-II have been observed to be more potential.

The citrus genetic resources are being maintained and evaluated for a set of descriptors at different centres. A total of 19 accessions were added to citrus germplasm collection. Acid lime selections, viz. RHR-L 122 and RHR-L 124, confirmed their superiority for yield, summer cropping and tolerance to canker. Kagzi lime clone, PDKV lime, was found promising for yield and has been released. Mandarin orange selection 5 outyielded at Akola, while Khasi mandarin selection CRS 4 consistently recorded high yield at Tinsukia. In litchi, 52 accessions were maintained in the field gene bank. Longan (*Dimocarpus longan*), a related species of litchi, maturing in August, was found to be promising. In sapota, seven accessions were added to the germplasm collection. In pomegranate, 119 germplasm accessions were collected. Four accessions of jackfruit were added to the genetic resources. The jackfruit accession NJ 1 was found superior for growth parameters.

In arid zone fruits, a total of 311 genotypes/strains of *Ziziphus*, 154 of pomegranate, 48 of date palm, 50 of aonla, 18 of bael, 65 of *Cordia*, 9 of *khejri* and 2 of mulberry collected from different parts of the country were maintained in the national germplasm repository. At Godhra, 1,882 germplasm/strains of different arid fruits and vegetable crops were maintained.

In vegetable crops, a total of 6,000 germplasm accessions have been maintained. This includes 1,200 in tomato, 600 in brinjal, 307 in chilli and sweet pepper, 760 in okra, 95 in cauliflower, 425 in pea, 181 in cowpea, 115 in dolichos, 275 in French bean and 2,042 in cucurbits. During the reported period, 2,000 germplasm lines in different vegetables were collected. The promising lines

identified for different traits were F7028 for high lycopene, F6061 for high carotenoid, H 88-78-4 for resistance to TyLCV in tomato; SA 90 for high carotenoid in pumpkin; VR 315 for resistance to YVMV in okra and BS 35 for resistance to leaf curl virus in chilli. A total of 4,350 accessions of different tuber crops have been collected and being maintained.

Plant quarantine: Out of 30,739 exotic germplasm processed for quarantine clearance, 17.71% were found infested/infected with insects and mites, nematodes, fungi, bacteria or viruses; 96.64% of the infected/infested accessions have been salvaged. Important interceptions include **insects**- *Bruchophagus roddi*, *Bruchus dentipes*, *B. lentis*, *B. rufimanus*, *Rhizopertha dominica*, *Sitophilus oryzae*, *S. zeamais*, *Sitotroga cereallela*, *Tribolium castaneum*; **mites** - *Oligonychus* sp.; **nematodes** - *Aphelenchoides besseyi*, *Helicotylenchus pseudorobustus*, *Pratylenchus penetrans* and *Xiphinema diversicaudatum*; **fungi and bacteria** - *Alternaria brassicae*, *A. helianthi*, *A. padwickii*, *Botrytis cinerea*, *Colletotrichum capsici*, *C. dematium*, *Cercospora kikuchii*, *Diplodia maydis*, *Drechslera maydis*, *D. oryzae*, *Fusarium moniliforme*, *F. oxysporum*, *F. solani*, *Peronospora manshurica*, *Pseudomonas syringae*, *Puccinia helianthi*, *Rhizoctonia solani*, *Sclerotium oryzae* and *Xanthomonas campestris* pv. *campestris*; **viruses** - Alfalfa mosaic virus, bean common mosaic virus, broad bean stain virus, cucumber mosaic virus, grape wine fan leaf virus, pea seed-borne mosaic virus and tomato black ring virus.

DNA fingerprinting: Okra species *Abelmoschus moschatus*, *A. ficulneus* and *A. esculentus* have been found closely related, and *A. tuberculatus*, a distant relative, when analysed by sequencing Internal Transcribed Spacers (*ITS-1*, *ITS-2*) from nrDNA and three intergenic spacers (*trnC-trnD*, *trnE-trnF* and *trnH-psbA*) from cpDNA.

Genetic diversity analysis: Forty-five rice landraces from Kerala and adjacent regions have been characterized using 25 STMS markers and



Pongamia pinnata (VNK-P 113), unique accession with high seeds/pod from Vizianagaram district, Andhra Pradesh



Indigenous *Bacillus thuringiensis* strains isolated

Bacillus thuringiensis isolates (PDBC-BT1 and PDBC-BNG-BT1) have shown 100% mortality of *Plutella xylostella* and *Helicoverpa armigera* larvae. PDBC-BTI also gave 100% mortality of first instar larvae of *Chilo partellus* and *Sesamia inferens*.

clustered into groups based on the geographical locations. Seventeen of the 179 alleles detected (9.49%) were unique to specific landraces. The results indicate substantial exchange of pollen between populations, and moderate genetic differentiation among sub-populations.

AGRICULTURALLY IMPORTANT MICROORGANISMS

Germplasm augmentation, conservation and use:

Filamentous fungi, bacteria, actinomycetes and yeasts cultures 2,517 from soil, plants and insects have been isolated and maintained in the NBAIM repository. Gene sequences of partial ITS-1 region, complete 5.8S rDNA and partial ITS-2 region have been submitted to GenBank. Two species-specific primers and an oligo-nucleotide probe from conserved sequence of ITS region have been designed for identification of *Macrophomina phaseolina*. Growth of soil-borne pathogenic fungi *in vitro* could be suppressed using strains belonging to *Pseudomonas fluorescens*, *P. aeuriginosa*, *Bacillus subtilis*, *B. brevis*, *Fusarium oxysporum*, *Hypocrella discoidea*, *Metarrhizium anisopliae*, *Trichoderma harzianum*, *T. koningii* and *Verticillium lecanii*. Diagnostic probes have been developed for *Fusarium udum*; following a simple procedure based on the sequencing of only a small fragment of 16S rRNA for identification of *Bacillus* genus, and also for species-level identification.

Twenty different groups of *Bacillus* in Indo-Gangetic plains have been identified based on 16S rDNA-RFLP analysis. More than 200 isolates of actinomycetes have been isolated; six isolates belonging to *Streptomyces* species were good producers of protease. Temperature tolerant cellulase and xylanase producing bacteria have been identified which appeared promising for biomass degradation. And bacterial inoculants that can alleviate harmful effects of salinity and improve growth of wheat in salt-affected soil have been developed. These are capable of producing IAA and solubilize phosphorus at a salt concentration of 8%.

PESTS AND NATURAL ENEMIES

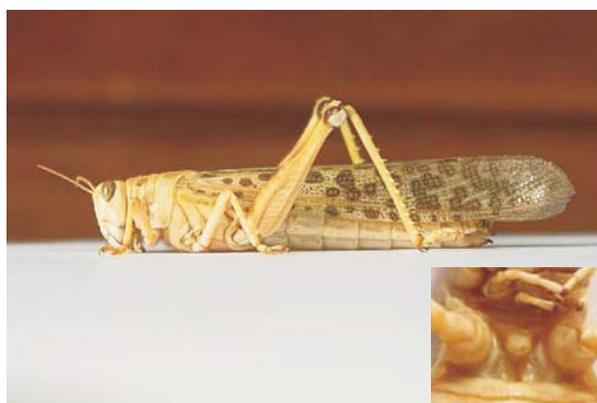
Biosystematics: Agriculturally Important Insect

Biodiversity (AIIB) was explored through field surveys in 27 states/union territories in 165 districts which led to maintenance of 319,877 insects and mites. Among the insects collected Hymenoptera, Coleoptera, Diptera, Hemiptera, Lepidoptera and Coleoptera were most abundant. More than 65 crops in their various stages of growth from sowing to post-harvesting stages were covered. Towards the objective of identification and morphological characterization, 14 different insects/mite groups were focussed upon and 15,830 species were studied. The detailed studies were focussed on 225 species of pests, and their defenders, namely parasitoids and predators. Nineteen diagnostic keys for identification of taxa at various levels, namely families, genera and species, have been developed, of which most significant are families of Lepidoptera and Hymenoptera, genera and species of leafhoppers, plant-hoppers and fruit flies. Detailed taxonomic studies have led to description of a new species of *Trichogrammatoidea*. The faunistics, diversity and taxonomy of different insect groups, viz. Hymenoptera, Hemiptera and Coleoptera have been published.

There was an epidemic of an invasive pest, gall wasp in eucalyptus that is used commercially for production of pulp and other raw materials for paper industry in different parts of India. This



Symptoms of damage of *Leptocybe invasa*



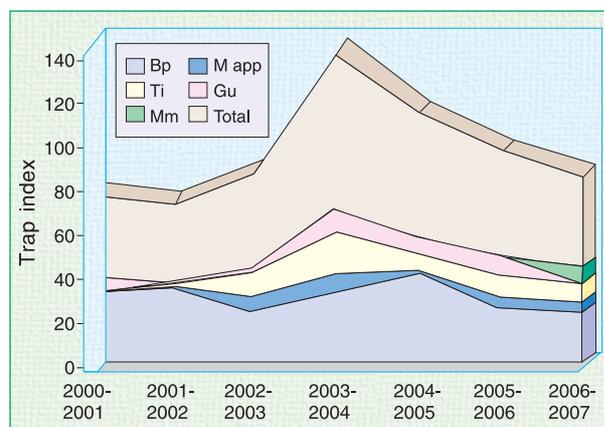
Schistocerca gregaria; with prosternal tubercle (inset)



invasive pest on eucalyptus nurseries and plantations in Andhra Pradesh, Karnataka and Tamil Nadu, Delhi, Uttar Pradesh, Haryana, Rajasthan and Madhya Pradesh has been identified as *Leptocybe invasa* (Eulophidae: Hymenoptera) details of its ecology and bionomics have been worked out. Due to the outbreak of desert locust, *Schistocerca gregaria* in six villages of Jalore district of western Rajasthan and adjoining localities in Gujarat during *kharif* 81 hectares and 129 farmers had been affected in villages Partappur, Paladsar, Luniasar, Barsam and Mekhpura in Sanchore tehsil and Vanse in Bilmal tehsil. The technical support provided by the project aided diagnostics of locust, paved way for clearing confusion regarding its similarity with migratory locust, *Locusta migratoria migratorioides*, which occurred in epidemic in Leh of Ladakh in Jammu and Kashmir in 2006–07.

Molecular characterization of parasitoids and predators: The ITS-2 region of DNA of *Trichogramma chilonis* (DQ 220703), *T. brassicae* (DQ314611), *T. mwanzai* (DQ381279), *T. evanescens* (DQ381280), *Trichogramma brasiliense* (DQ381281), *T. dendrolimi* (DQ344045), *T. embryophagum* (DQ344044), *T. japonicum* (DQ 471294) and *T. pretiosum* (DQ 525178) have been sequenced and deposited with Genbank.

Rodent diversity: In rice-rice-pulses cropping system in coastal Andhra Pradesh only *Bandicota bengalensis* (> 80%) and *Mus booduga* were found. In lower Brahmaputra zone in Asom, four species *B. bengalensis* (49%), *R. nitidus* (27%), *R. sikkimensis* (17%) and *M. booduga* (7%) occurred. In Karnataka, *B. bengalensis*, *Millardia meltada*, *M. booduga* and *Tatera indica* were found in rice-ragi-soybean, sugarcane fields in varying proportions with predominance of lesser bandicoots. Seven species (3 rats, 1 gerbil and 3 mouse species) *Bandicota bengalensis*, *Tatera indica*, *Mus musculus*, *Golunda ellioti*, *M. meltada*, *M. booduga* and *Millardia platythrix* were reported in Punjab.



Year-wise abundance of different rodent species in crop fields in Punjab

In Asom, *Rattus rattus* (32%), *B. bengalensis* (29%), *M. musculus* (21%), *R. sikkimensis* (4.5%) and *R. norvegicus* (12.8%) were reported inhabiting in urban stores and *R. rattus* (41%), *B. bengalensis* (25%), *M. musculus* (25%) and *R. sikkimensis* (9%) in rural storage. Commensalization of a field rodent *Tatera indica* was seen in grain mandis situated in outstations of Jodhpur town. In Punjab, similarly *Rattus rattus* was trapped from inside the stores and *Bandicota bengalensis* from outside in the vicinity of stores. Studies of recently introduced *Bandicota bengalensis* in Jodhpur revealed very heavy infestation of bandicoots in the city area. Their population remained almost constant throughout the year. Maximum body weight of bandicoots was recorded in January, followed by March.

ANIMALS

Phenotypic characterization

Red Sindhi cattle: Red Sindhi cattle coat is red but under body parts are whitish/gray colour. Body is large, compact and straight. The average body length, height at wither, heart girth, paunch girth, face length, face width, horn length, ear length, tail length without switch and teat length



Red Sindhi cattle needs immediate attention for conservation

were recorded. Body weights of calves at 3, 6 and 12 months of age and of adult animals were 41, 58 and 110, 450 kg in males; and 40, 55.0, 95 and 320 kg in females respectively. The average age at first fertile service, age at first calving, lactation milk yield, lactation length, gestation period, dry period, service period and inter-calving period were 1,215±53 and 1,577±56 days, 1,532±88 kg, 291±5, 291±3, 195±14, 192±14 and 485±13 days respectively. The population status indicated that the breed is threatened in the country and needs immediate attention for conservation.

Krishna Valley cattle: The breed is distributed around Krishna River in Karnataka state, hence named as Krishna Valley. The animals are of



medium size. The coat colour varies from grey to white with darker shades. The average measurements of body length, height at wither, chest girth, paunch girth, face length, ear length, horn length, horn circumference, tail length are 129, 119, 157.62, 153.12, 46.87, 19.75, 21.87, 20.87, 73.25 cm, respectively, in bulls and 106.25, 110.5, 155.5, 163.25, 41.25, 22, 36, 18, 67.25 cm in females. The breed is utilized for draught purpose. The average daily milk yield ranges from 3 to 5 kg. Age at first calving is 3–4 years and inter-calving period varied from 1.5 to 2 years.

Madras Red sheep: Madras Red sheep is distributed in Chennai, Kancheepuram, Tiruvellore, Villupuram, Vellore, Cuddalore and Thiruvannamalai districts of Tamil Nadu. They are of medium size, well built with a broad and deep chest and straight top line. Average adult body weight is 31.8 ± 1.05 kg in rams and 24.5 ± 0.35 kg in ewes. The skin is fine and soft with short hair. The coat colour is light to dark red/brown/tan. Age at first breeding is about 12 months in rams with an average breeding life of about 4 years. Lambing season is October-January. Age at first lambing ranges between 18 and 24 months. An ewe produces about 5–7 lambs in its lifetime.



Madras Red sheep—age at first lambing is between 18 and 24 months; ewe produces 5–7 lambs in its lifetime

Tiruchy Black sheep: Tiruchy Black sheep are found in the native habitat in Pannagaram, Nallampalli, Dharmapuri, Palakodu, Kairimangalam, Krishnagiri of Dharmapuri district of Tamil Nadu. The animals are medium to small in size. Average body weight is 35.5 ± 0.9 kg in rams and 29.6 ± 0.3 kg in ewes. Body is completely black. Fleece is extremely coarse, hairy and open. Age at first breeding is 12–18 months in rams with a breeding life of 4–5 years. In ewes age at first lambing is 12–18 months. Lambing per cent is 70–80 with a lambing interval of about 10–12 months. An ewe produces 5 to 6 lambs in its lifetime.



Tiruchy Black sheep—average body weight in rams 35–37 kg and in ewes 29–30 kg

Magra sheep: Magra sheep prevails in Bikaner district of Rajasthan. The animals are medium to large in size. Face is white with brown circular patches around the eyes, which is a characteristic of this breed and hence also named as *Rata Chakria/chakria*. Age at first breeding in males is 18–24 months. In ewes, age at first lambing is 18–24 months. The average body weight at birth, 3, 6, and 12 months of age are 2.2, 15.9, 21.5 and 29.1 kg in males, and 2.4, 14.7, 19.4 and



Magra sheep—known for lustrous, carpet quality wool; average greasy wool production is 1.5 – 2.0 kg/annum

25.6 kg in females respectively. The breed is known for lustrous and carpet quality wool production. Animals are shorn thrice a year in March, July and November. Average greasy wool production is 1.5 to 2.5 kg/annum in three clips.

Gohilwadi goat: Gohilwadi breed of goat has derived its name from Gohilwad, which was a part of the Kathiawar region. The animals are spread mainly in Junagadh, Amreli and Bhavnagar districts. The Gohilwadi goats are of medium to large size having the average measurements of 81.04, 79.78, 79.23 and 82.70 cm for height at withers, body length, heart girth and paunch girth respectively. The coat colour is uniformly black





Gohilwadi goat—milk yield of 3 litres/day was recorded in some elite goats

covered with long coarse hair. Face is proportionate to the body measuring 20.93 cm. Both sexes have wattles. Some of the elite milch goats yield about 3.0 litres milk per day.

Daothigir chicken: The Daothigir chicken is found in districts of Kokrajhar, Chirang, Udalguri and Baska of Assam. Plumage color is mostly black interspersed with white feathers. Comb is red, single, erect and large in size. Average weight of cock is 1.79 ± 0.13 kg and that of hen 1.63 ± 0.13 kg. The annual egg production ranges from 60 to 70. Average egg weight is 44.42 ± 1.35 g.

Tellichery chicken: Tellichery birds are found mainly in Calicut district but are also available in surrounding areas in Kannur and Malappuram districts of Kerala, and adjoining Mahe of Pondicherry. Plumage color is black with shining bluish tinge on hackle, back and tail feathers. Comb is red, single and large in size. Average weight of cock is 1.62 ± 0.16 kg and of hen 1.24 ± 0.10 kg. Eggs are tinted and their annual production ranges from 60 to 80; and average egg weight is 40.02 ± 0.94 g.

Genetic characterization

Cattle: Within breed diversity was estimated for Dangi cattle of Maharashtra. The comparison of allelic diversity and heterozygosity values of Dangi cattle with Tharparkar, Rathi, Gir, Kankrej, Mewati, Nagori, Rathi, Khillar provided the relative genetic variability that existed in these Indian cattle breeds. The average inbreeding coefficient (F_{IS}) in Dangi cattle was 0.102 while this was lowest in Kankrej cattle which did not show any heterozygote deficiency. The interbreed differentiation — F_{ST} — between Dangi and other cattle populations reflected moderate level of genetic divergence between different pairs of cattle breeds; maximum divergence of Dangi cattle is with Tharparkar and minimum with Kankrej cattle. The mean differentiation value indicated that majority of the breed differences corresponded to differen-

tiation among individuals.

The comparative microsatellite analysis of cattle breeds Ponwar, Gangatiri, Kherigarh and Kenkatha, and Siri cattle were completed. The genetic relationship tree based on genetic distances showed that 4 breeds of Uttar Pradesh are divided into 2 branches where Ponwar and Kherigarh clustered together and were clearly differentiated from Gangatiri and Kenkatha that formed the second branch. The pattern of population differentiation revealed the comparative close relationship of Ponwar and Kherigarh breeds and of Gangatiri and Kenkatha breeds. The breeding tract of Ponwar and Kherigarh are adjacent to each other, whereas that of Gangatiri and Kenkatha are distant from these two and also from each other.

Buffalo: *Karyotypic feature of Chilika buffalo.* Distinctive karyotypic features of swamp and river buffaloes were exploited to explicitly ascertain whether Chilika buffaloes belong to the riverine or swamp category. The chromosomal constitution and karyotypic characteristics of Chilika buffaloes investigated were identical to those of typical riverine type buffaloes standardized internationally (CSKBB 1994). Cytogenetic analyses thus confirm the riverine status of Chilika buffaloes of Orissa. This assumes special significance in the light of general belief and swamp type behaviour of Chilika buffaloes and the fact that another type of buffaloes (Paralakhemundi buffaloes) found in the vicinity of breeding tract of Chilika in the same state of Orissa has been cytogenetically authenticated to be swamp type.

Molecular characterization of buffaloes. Full length cDNA of serum lysozyme gene of riverine buffalo was cloned and characterized. DRB3 exon 2 was found highly polymorphic in Umblacherry cattle. Based on sequencing results, the *Rsa* I-*v* seems to be a new genotype. Single strand conformation polymorphisms (SSCP) in two different fragments of serum lysozyme gene were identified in Murrah, Surti, Mehsana and Bhadawari buffaloes. cDNA encoding entire coding sequences of Toll-like receptor, MIP1-alpha and TNF- α were cloned and characterized in buffalo. Significant association of ITGB2/*Msp*I genotypes with the per cent neutrophil and lymphocyte was observed in buffalo. cDNA of uterine milk protein (UTMP) and genomic sequence (>4 kb) of ghrelin gene of buffalo was cloned and characterized.

Buffalo phenotype and milk yield relationship. Specific breed characters of Murrah, viz. coat colour, type of head and face, tail and tail switch, etc. showed significant relationship with milk production. Buffaloes of docile temperament, having fine skin, more capacious udder and cylindrical teats produced more milk. However, type of horns was not associated with milk production.



Identification of molecular markers associated with production and reproduction performance for early germplasm selection. For characterization of buffalo growth hormone (GH) gene, DNA prepared from low and high producing buffalo subgroups and progeny tested sires, revealed a >760 bp size amplicon, whose Msp restriction patterns showed more number of restriction sites than cattle GH gene.

Goats: *Changthangi goat.* The estimates of effective number of alleles and gene diversity revealed substantial genetic variation at 25 loci. The average observed and expected heterozygosity values were 0.599 and 0.740 respectively. The mean polymorphic information content (PIC) value further reflected high level of polymorphism across the loci. The analysis of data showed a normal L-shaped distribution representing likelihood that Changthangi population has not experienced a recent reduction of their effective population size.

Sheep: *Jalauni sheep.* The genetic variability was examined at 25 microsatellite loci covering 19 chromosomes. Allele frequencies loci ranged from 0.022 to 0.863. A total of 148 alleles were identified with an allele diversity of 5.92. The effective allele number (3.71) was lower than the allele diversity. The mean observed heterozygosity (0.589) and gene diversity (0.681) estimates elucidated substantial genetic diversity within Jalauni breed. The breed exhibited high genetic polymorphism. The typical L-like distribution implied the absence a recent genetic bottleneck in this indigenous breed of sheep.

Chhotanagpuri sheep. Genetic diversity in Chhotanagpuri sheep was estimated in terms of allele frequency, observed number of alleles, effective number of alleles, observed heterozygosity, expected heterozygosity and within breed heterozygosity deficit. Distinct alleles (141) were detected across the analyzed microsatellite loci. A normal L-shaped curve suggested that the population has not experienced a genetic bottleneck. Within population inbreeding estimate (F_{IS}) ranged from 0.01 (CSSM31) to 0.68 (OaeAE129) with an average positive value of 0.24.

Mithun: *Nagami.* The genetic characterization was carried out using 28 cattle primers. The number of alleles observed varied from 3 to 9 with a mean of 5.11 ± 1.57 , whereas average effective number ranged from 1.317 to 4.842. The overall mean of Shannon index and PIC values were 1.020 ± 0.407 and 0.482 ± 0.186 respectively. Nagami mithun population showed heterozygotic deficiency at 12 of the 25 loci but has not suffered with the population bottleneck in the recent past. Decreasing heterozygosity suggests that immediate attention is required to increase the outbred population.

Yak: *Paternally inherited species specific ssp1-*

PCR-RFLP assay for hybridization analysis in yak-cattle hybrid populations. Species hybridization between yak and cattle is commonly practised in yak tracts in India to utilize hybrid vigour. Hybrid females are sterile while males including backcross males are sterile. F_1 hybrid females (Dzomo) are backcrossed to bulls from either of the parental species. Using backcrossing, a number of generations (up to F_5/F_6) of hybrids is produced. It is difficult to identify the sire in F_2 and a further generation as mating generally takes place while they are in herds in vast grazing land. SRY gene is the only single copy Y-chromosomal gene without a X-chromosomal homologue. A simple reliable Ssp1-PCR-RFLP assay to identify male mediated introgression based on mutation in SRY gene was developed for identification of paternal origin of hybrids between yak and cattle. This assay could be used to identify the paternal species in yak and cattle hybrids of different filial generations.

Association of polymorphism of defensin genes with milk somatic cell count in yaks and zebu cattle. Defensins have antimicrobial role in various tissues including mammary gland. Defensin/*TaqI* PCR-RFLP studies showed polymorphic patterns in yaks, and their hybrids, cattle, mithun. The defensin genotypes have significant effect on somatic cell count (SCC) in hill cattle and yaks. B_2 type individuals either in homozygous or in heterozygous conditions had lower somatic cell count. Defensin genotypes showed an effect on SCC in milk of yak and cattle.

Poultry: *Molecular characterization of layer and broiler germplasm.* Six different genetic groups of a diallel cross of chicken were analyzed with five microsatellite markers, viz. MCW007, ADL020, ADL023, ADL102 and ADL176. ADL176 was the highest polymorphic marker, depicting the availability of six alleles in the crossbred populations. Genotypic proportion was found distributed from low to moderate and the allelic frequency of all microsatellites, except ADL176, varied. In ADL176, some alleles were rare with the existence of only 3 to 4% in the population. These alleles may be in the path of extinction from the population and are mostly present in heterozygotic condition.

The genotypes of MCW007, ADL 176, and ADL020 microsatellite were found associated with body weight. The ADL023 microsatellite was associated with egg production. Microsatellites MCW007, ADL020, ADL023 and ADL176 were found associated with age at sexual maturity.

Identification of genetic polymorphism in genes regulating appetite in chicken. Genes — ghrelin and melanocortin-4 receptor — controlling appetite and energy balance in poultry were studied to



identify the single nucleotide polymorphism (SNP). Dahlem Red birds and control broilers (CB) populations were screened for polymorphism. Different alleles A, B and C were identified in CB line and alleles A and B were seen in NB lines with varying allele frequencies. The 336 bp fragment in MC4R gene was amplified in chicken, duck, emu, ostrich, quail and turkey, sequenced, and compared. The sequences have been submitted to the NCBI gene bank. In the coding region, there were 2–5 substitutions across the species.

Genetic characterization of native ducks. Indian Runner Native duck was characterized using RAPD-PCR technique and also 14 microsatellite loci. The RAPD-PCR analysis resolved 66.67% polymorphic bands.

Conservation: During the period, *in-situ* conservation units for Beetal goat; Surti goat; and Kilakarsel sheep, and *ex-situ* conservation units for Krishna Valley cattle and Jaffarabadi buffalo; Kherigarh and Ponwar cattle were continued.

DNA repository of Ganjam, Kendrapara, Deccani, Nellore, Nali, Magra, Chokla, Garole, Patanwari, Marwari, Kheri, Malpura, Muzaffarnagri, Jaisalmeri and Sonadi has been created. *FecB* gene in Garole, Garole × Malpura, and backcross progeny, Ganjam, Kendrapara and Deccani sheep has been identified. In genetic improvement for resistance to *Haemonchus contortus* in sheep, preliminary study revealed that mortality rate was 6.06 in R-line while in S-line it was 12.90%.

Genetic diversity and population structure of Jamunapari goats. Allelic richness, gene diversity, linkage disequilibrium, effective population size were analysed, and bottleneck analysis was carried out. Despite the smallest population size, the amount of variability both in terms of allelic richness and gene diversity observed in Jamunapari goats is higher. No recent bottleneck was observed in the population. There was no sign of recent reductions in N_e in Jamunapari population. The base line information on genetic diversity, bottleneck analysis and mismatch analysis was obtained to assist the conservation decision management of the breed.

Marwari breed conservation at farmer's door. The Marwari breed of equines is threatened due to non-availability of true-to-breed stallions and indiscriminate breeding practices. To conserve the true-to-breed Marwari germplasm, the population in the field was characterized phenotypically and genotypically. The semen was collected and cryopreserved from selected stallions at farmers' door using mobile semen laboratory, first ever thought activity in the country and probably globally in any other domestic livestock. This semen was used for artificial insemination (AI)



Marwari—artificial insemination was carried out in Marwari mares to produce superior offsprings

of 10 Marwari mares at the centre to produce superior offspring.

FISH

Development of a resource mapping population and a new set of microsatellite markers in rohu:

A backcross family with about 50 individuals was generated by crossing *Labeo rohita* female with *L. calbasu* male. Microsatellites (40) were characterized from rohu genome, and PCR amplification of these microsatellite loci in kalbasu showed more than 15 loci to be cross amplifying. This indicated that about 80% of the rohu markers can be mapped using the current inter-species mapping panel.

Molecular characterization of backcross population of Indian major carps (*Labeo rohita* and *Catla catla*):

Random RAPD primers (10 mer oligonucleotides) from 3 complete sets, viz. OPA, OPG and OPQ series, and some other arbitrary primers tested already like OPC-13, OPE-7, OPF-14, OPK-02, OPK-12, OPK-17, OPY-20 were used, mounting to a total of 19 primers. Out of them, 11 primers (OPA-02, OPA-04, OPA-05, OPA-07, OPC-13, OPG-02, OPG-03, OPG-18, OPK-12, OPK-17 and OPY-20) were found satisfactory with respect to amplification and band clarity. Analysis of 314 bands from four combinations of template DNA samples having catla, rohu, F_1 hybrids, B_1 backcross, B_1R backcross and BC_1F_2 backcross in a formatted loading of progeny's DNA along with parental DNA side by side showed quite a good number of catla type bands, rohu type bands as well as few typical bands. Parentage catla bands showed the sharing of 20–100% in various progenies, whereas rohu bands showed 40–100% in various progenies.



Genomic library of *Pangasius pangasius*: Microsatellite enriched genomic library was constructed for the riverine catfishes, *Pangasius pangasius* to identify sequences containing microsatellite repeat regions. Of the 28 sequences found to contain microsatellite repeats, primers were designed for these loci and tested for

amplification of microsatellite loci. The 15 pairs of primers gave amplified products with 42 individuals collected from rivers, Brahmaputra and Mahanadi. This genotyping provided 9 polymorphic loci while four were monomorphic. These microsatellite markers are useful for population genetic structuring in *P. pangasius*. □

