

# Genetic Resources

## CROPS

### Plant exploration and germplasm collection:

Explorations (33) were undertaken, and 2,203 accessions were collected including 784 of wild species. In the National Herbarium of Cultivated Plants (NHCP), 371 herbarium specimens, 121 seed samples and 21 economic products were added; and the total reaches to 19,688 specimens.

Diverse crops accessions (25,456) including international trial materials (7,485) were introduced from various countries. About 15,000 accessions including ICRISAT germplasm were exported to 19 countries. Nearly 15,500 samples of crops and

their wild relatives were supplied to Indian researchers.

A total of 13,850 accessions of orthodox-seed species were added to the National Genebank for long-term storage at  $-18^{\circ}\text{C}$ .

Accessions of fruit crops (20), bulb and tuber crops (17), medicinal and aromatic plants (5) and spices (3) were added to *in-vitro* Genebank. In all, 1,991 accessions (nearly 32,000 cultures) belonging to 52 genera and 158 species of vegetatively propagated crops, medicinal and aromatic plants and threatened species were conserved. Accessions of fruits and nuts (214), spices (9), industrial crops (136) and medicinal and aromatic plants (72) were preserved.

### Introductions of germplasm from other countries

Country	Species	Registration No.
Serbia	Winter wheat <i>Triticum aestivum</i>	EC 609394–9413 631734
USA	<i>T. aestivum</i> translocation line with grain softness gene	-
Kenya	<i>Oryza sativa</i> inbred and thermosensitive genetic male sterile lines	EC 609524–47
USA	<i>Hordeum vulgare</i> spring lines with low phytate and good quality grain	EC 607790
USA	<i>Hordeum vulgare</i> cv. Lentah with good yield	EC 631731
USA	<i>Lens esculenta</i> cv. Morton with winter hardiness	EC 608175
Taiwan	<i>Lycopersicon esculentum</i> resistant to bacterial wilt, <i>Fusarium</i> wilt, gemini virus, grey leaf spot pathogen, tomato mosaic virus	EC 606703–04
Taiwan	<i>Capsicum</i> sp. resistant to chilli veinal mottled virus, poty virus Y and bacterial wilt	EC 628903–08
USA	Apple, pear, peach and apricot cultivars	EC 616557–63

### Wild sugarcane from Gujarat



*Saccharum spontaneum* in Gujarat riverbeds

A total of 32 accessions of *Saccharum spontaneum* were collected from different districts. Another related wild species *Erianthus bengalensis* was found on the field bunds in north Gujarat.

**Plant quarantine:** Ten phytosanitary certificates were issued for export of 873 samples. Over 25,000 accessions were processed for quarantine clearance. About 540 samples were found infested/infected with different pests; out of which 526 were salvaged. Important interceptions include **insects:** *Araecerus fasciculatus*, *Bruchus lentis*, *Callosobruchus subinnotatus*, *Chrysomphalus dictyospermi*, *Pectinophora gossypiella*, *Rhizopertha dominica*, *Tribolium castaneum*, *Sitophilus oryzae*, *S. zeamais*, *Sitotroga cerealella*; **nematodes:** *Aphelenchoides besseyi*; **fungi and bacteria:** *Alternaria brassicae*, *A. brassicicola*, *Botrytis cinerea*, *Colletotrichum dematium*, *C. graminicola*, *Drechslera maydis*, *Fusarium solani*, *Peronospora manshurica*, *Puccinia helianthi*, *Xanthomonas campestris* pv. *campestris* and *Xanthomonas vesicatoria*; **viruses:** Alfalfa mosaic virus, Bean common mosaic virus, Bean yellow mosaic virus, Cowpea mottle virus, Pea enation mosaic virus and Raspberry ring spot virus.

**DNA fingerprinting:** In watermelon, 232 simple sequence repeats (SSRs) were identified, and primers for the amplification of the sequences were designed and tested using selected cultivars.

PCR-based detection protocols were worked out for detection of late-blight resistant *RB* gene in genetically modified potato (with *RB* gene up to a limit of detection of 0.01%); *cryIAC* gene in *Bt* okra up to a limit of detection of 0.01%; multiplex PCR-based detection of *amaI* gene, 35S promoter, *nos* terminator and *nptII* marker genes in genetically modified potato with *amaI* gene; and *cryIAC* gene, endogenous  $\alpha$ -*tubulin* (*TubA*) gene and *nos* terminator/*nptII* marker gene in *Bt* rice. Qualitative detection procedures using Real Time PCR were developed for *cryIAC* gene in *Bt* brinjal. PCR-based diagnostic kits were developed and released for detection of endogenous genes, specific transgenes and 35S promoter sequence in genetically modified cotton (*cryIAC*, *cry2Ab* genes), brinjal (*cryIAC* gene), cauliflower (*cryIAC* gene), mustard (*barnase* and *barstar* genes) and tomato (*osmotin* gene).

## AGRICULTURALLY IMPORTANT MICROORGANISMS

**Isolation, characterization and documentation:** In the northern Indo-Gangetic plains, based on sequencing of 16S rDNA, isolates from the effluent-treated soils are *Bacillus humi*, *B. drentensis*, *B. asahii*, *B. cohnii*, *B. pumilus*, *B. niacini*, *B. djibelloresis*, *B. fumarioli*, *B. senequalensis*, *B. oleronius* and *B. sporothemodurans*. Functional diversity with regard to production of IAA and siderophore and p-solubilization has revealed that

over the years there has been enrichment of species of *Bacillus* and *Pseudomonas* that have lost plant-growth promoting traits.

**Microbial consortia to alleviate salinity:** Bacterial inoculants developed to alleviate harmful effects of salinity for enhanced growth and yield of wheat, identified through sequencing of 16S rDNA, are *Bacillus pumilus* EU 927407, *B. aquimaris* EU 927408, *B. arsenicus* EU 927409, *Arthrobacter* sp. EU 927410, *Bacillus cereus* EU 927411, *Pseudomonas medicona* EU 927412, *Bacillus subtilis* EU 927413, *Bacillus pumilus* EU 927414 and *Bacillus aquimaris* EU 927415. These were submitted to NCBI Gene bank and accession numbers were obtained.

**Potent biocontrol agent against *Fusarium*:** Of the 23 isolates of *Trichoderma* obtained from the Uttarakhand soil samples, 10 showed more than 40% inhibition in all the assays against *Fusarium melonis*, *F. cucumerinum* and *F. lycopersici*. PCR amplification using primers, internal transcribed spacers, ITS-1 and ITS-4, followed by RFLP analysis with restriction endonuclease *Hind III*, could cluster 10 isolates into 8 groups. RAPD analysis with oligonucleotide primer OPV 14 revealed significant level of polymorphism among the isolates.

**Microbial shift in soils:** The community-level physiological profiling of soil microbes using BIOLOG showed significant shift in C utilization pattern of the effluent-irrigated soils over the control soils.

Fast-growing actinomycetes strains isolated from the effluent-contaminated sites were characterized at the molecular level and their 16S rDNA and PCR-RFLP analysis using restriction endonucleases *MboI* and *TaqI*, grouped these 45 isolates into 12 clusters, of which 6 clusters were unique isolates from the effluent-irrigated soils, and 2 were unique isolates from the control soils. These isolates were able to produce xylanase and cellulase at 85-290 and 28-70 IU/ml/min.

**Bacteria and fungi identified:** From salt lake of Sambhar, Rajasthan, bacteria capable of growing at 20% NaCl and at pH of 12 were isolated. Molecular diversity clustered bacteria into 29 groups- and sequencing of 16S rDNA led to identification of *Halomonas* sp., *Marinobacter alkaliphilus*, *Marinobacter hydrocarbonoelasticus*, *Halomonas variabilis*, *Alteromonadales*, *Nitrinicola laxisaponensis*, *Bacillus thuringiensis*, *Chromohalobacter salexigens*, *Marinobacter aquaeolei*. From Leh region, psychrophilic fungi growing at 4° C or lower temperature were isolated and identified as *Asordaria sicutii*, *Gemocyces* sp., *Penicillium* sp., *Ulocladium consortiale*, *Thelebolaceae* sp. and *Ulocladium* sp.

## PESTS AND NATURAL ENEMIES

**Biosystematics:** Field surveys in 20 states/union territories led to collection of 98,122 insects and mites belonging to economically important group. Taxonomic keys have been developed for the genera and the species of Largidae, Pyrocoridae and Cercopidae. Two new species of Eriophyiidae have been identified and described.

### Eucalyptus pest identified

There was an epidemic of an invasive pest, gall wasp, in eucalyptus that is used commercially for pulp production and for other raw materials for paper industry in the different parts of India. This pest was found to be occurring as a regular and serious pest in eucalyptus nurseries and plantations not only in Andhra Pradesh, Karnataka and Tamil Nadu, but also in Delhi, Uttar Pradesh, Haryana, Rajasthan and Madhya Pradesh. This has now been identified as *Leptocybe invasa* (Eulophidae: Hymenoptera), and details of its ecology and bionomics have been worked out.

### Genetic diversity of Trichogrammatids:

Internal transcribed spacer, ITS-2, and RFLP analysis enabled molecular differentiation of 12 species of trichogrammatid egg parasitoids. Microbial symbionts that influence sex ratio of these egg parasitoids provide clue on the influence of *Trichogramma* female.

**Rodent surveys:** In Punjab dominance of *Bandicota bengalensis* was noticed, followed by *Tatera indica*, *Mus* spp. and *Golunda ellioti*.

**Distribution pattern of rodent-pest complexes in crop fields in Karnataka**

Crops	Pest species complex	Live-burrow density/ha
Irrigated rice	<i>B. bengalensis</i> > <i>Mus booduga</i>	73
Ragi	<i>T. indica</i> > <i>B. bengalensis</i> > <i>M. booduga</i>	40–50
Maize	<i>B. bengalensis</i> > <i>T. indica</i> > <i>M. booduga</i>	6–20
Pearl millet	<i>B. bengalensis</i>	8–10
Wheat	<i>B. bengalensis</i>	26–30
Pigeonpea	<i>T. indica</i> > <i>B. bengalensis</i> > <i>M. booduga</i>	20–25
Cowpea and mungbean	<i>T. indica</i> > <i>B. bengalensis</i> > <i>M. booduga</i>	8–30
Soybean	<i>B. bengalensis</i> > <i>T. indica</i> > <i>M. booduga</i>	24–29
Sunflower	<i>T. indica</i> , <i>M. booduga</i> and <i>Mus platythrix</i>	12–30
Sugarcane	<i>B. bengalensis</i> > <i>M. booduga</i>	10–25
Tuberose (a flower crop)	<i>B. bengalensis</i> > <i>M. booduga</i> > <i>Milardia meltada</i>	47

### Mitigating desert locust outbreak in Rajasthan and Gujarat

There was an outbreak of the desert locust in six villages of Jalore district of western Rajasthan and adjoining localities in Gujarat during *kharif*. In all, 81 hectares and 129 farmers had been affected in the villages Partappur, Paladsar, Luniasar, Barsam and Mekhpura in Sanchore tehsil and Vanse in Bilmal tehsil. The project aided diagnostics of the locust, and paved way for clearing the confusion of whether it is the same migratory locust, which occurred in epidemic in Leh of Ladakh in Jammu and Kashmir in 2006. Taxonomic studies confirmed it to be the desert locust *Schistocerca gregaria*; characterized by the presence of prosternal tubercle. This facilitated quick and timely management of the locust by the plant-protection agencies.

Highest trap index of *B. bengalensis* was 56.25 from fodder crops in October. In Andhra Pradesh, the rodent population in terms of active live-burrows was high in rice-sugarcane cropping system compared to rice-rice-pulse or rice-rice cropping systems. In rice-rice cropping system, burrow infestation was low to medium in *kharif* and low in *rabi*. In arid Rajasthan, a complex of two gerbils, *Tatera indica* and *Meriones hurrianae*, was predominant in *bajra*-mungbean-mothbean in *kharif*.

**Lesser bandicoot rat in the arid region:** In recent years, lesser bandicoot rat *B. bengalensis* population remained almost constant throughout the year in Jodhpur with a trap index up to 14.0. Average daily intake of pearl millet grains by *B. bengalensis* was 13.57 g/day as compared to 6.19 and 5.24 g/day by *Rattus rattus* and *Tatera indica*, indicating more than two times higher potential losses to stored grains, besides other damages and contaminations caused to stored commodities.

## HORTICULTURE

**Mango:** Mango accessions, 11 at RFRS, Vengurle, 15 at Periyakulam, 10 at FRS, Sangareddy and 4 at AES, Paria were added. Two clones of Alphonso and one of Bangalora were added in the germplasm. Bangalora was the highest-yielding cultivar followed by Dholikothi Maldah at RAC, Sabour Campus, while Mallika gave higher fruit yield at Pantnagar. Seedling selection, Peddapur 16 and Pargi 16, recorded the maximum yield at FRS, Sangareddy, while seedling No.7/80 and 10/85 at Sabour and Latif Aliwala, Surkhroo 1 and Surkhroo 2 at Pantnagar. Clone Rati Banganpalli showed cluster-bearing habit while Benishan early maturity; Pedda Benishan and Allahabad Benishan with bigger-size fruits than Benishan. At FRS, Rewa, a clone of Chausa

(Chausa No. 2) was found promising.

**Guava:** Six new accessions of guava three each at FRS, Sangareddy and FRS, Rewa were collected. Cultivar Sardar gave the highest yield followed by Pant Prabhat at Pantnagar, while Guthneewala, Safeda (J 2) and Portugal gave higher yield at FRS, Rewa. At FRS, Sangareddy, cv. Kohir Safeda performed better followed by Allahabad Safeda, while Sardar, MPUA&T- S 1 and MPUA&T-S 2 at RCA, Udaipur and Allahabad Safeda and Safed Jam at BAC, Sabour.

**Litchi:** Two clones of Bombai litchi were collected by BCKV, Mohanpur. Litchi cultivar Rose Scented outyielded at Pantnagar, Shahi and Late Bedana at RAU, Pusa and Bombai and Muzaffarpur at BCKV, Mohanpur.

**Tropical fruits:** Under All-India Co-ordinated Research Project on Tropical Fruits, genetic resources of varieties/species of tropical fruits were maintained and evaluated at different centres. Nine sweet orange clones, 21 accessions in banana, 1 in sapota and 2 in jackfruit were added to the germplasm collection. At Kannara, two introduced hybrids (TMB 5295-1 and SH 3640) are under multilocational trial. Acid lime selections 2 and 5 and mandarin selections 5 and 4 continue to record higher yield under Akola conditions. An elite clone of acid lime has been identified from Vaigai Dam, Tamil Nadu. In banana, Acc. No. 73 - 9 has been identified as a promising genotype. At Coimbatore, a field tolerant papaya genotype against PRSV was identified which is under multiplication.

**Citrus:** Two clones, one early maturing (N2) and another less seeded (N4) (less than 3 seeds/fruit) were identified. Under clonal selection programme, 49 exotic germplasm comprising 31 Scion (14 mandarin, 9 sweet orange, 7 grapefruit and pummelo from USA, France, Japan), 19 rootstock (mostly from USA, a few from Australia) and 532 indigenous collection have been collected and maintained at NRCC, Nagpur. Besides, 55 superior clones of Nagpur mandarin, 13 of acid lime and 13 of Mosambi were also collected. More than 215 genotypes/accessions of pomegranate were collected from Jammu and Kashmir, Uttarakhand, Himachal Pradesh, Maharashtra and Karnataka. At present, over 160 germplasm accessions were maintained.

**Arid fruits:** Tikadi, Khavaspura and Sanaur 5 cultivars of ber were found tolerant to low temperature (-1 °C), while Sanaur 1, Jogia and Kathaphal were moderately tolerant. Early doka stage was observed in cultivars, Khuneizi, Muscat and Tayer of date palm. Two new germplasm of wood apple have been added. Promising genotypes of aonla, Narendra Aonla 27, Narendra Aonla 28 and Narendra Aonla 29 were identified.

Pomegranate anardana types (05) were collected from Shimla. Out of 16 different types of Bhagawa in Maharashtra, Sel 4 was found superior in yield and quality parameters. In bael, two genotypes, viz. a Narendra Bael 19 and Narendra Bael 20, were significant. Higher fruit yield/plant was recorded in Singapur seedling and Red tamarind. Custard apple accession AS 1(APK (Ca)1 showed yield of 12.50 kg/ tree. At Rahuri, evaluation of germplasm of Bullock Heart (*Annona atemoya*), Island Gem (*Annona atemoya*) and Annona Hy. No. 2 (*Annona squamosa* × *Annona cherimoya*) indicated superiority for fruit quality.

**Cashew:** Four germplasm accessions were added to National Cashew Field Gene Bank (NCFGB), raising the total germplasm to 513. At various Regional Cashew Field Gene Banks (RCFGBs) at different AICRP-Cashew Centres, 1,272 accessions have been conserved.

**Vegetable crops:** Out of 161 germplasm lines in chilli, GP 276 for high capsaicin content (0.581%), GP 89 for high oleoresin content (14.51) and GP299 for high capsanthin (53375EOA); okra (IIVR 402 for resistance to YVMV); early cauliflower (Kuwari 23/42 for earliness and heat tolerance); late cauliflower (RSK 1301 for resistance to downy mildew; cabbage (Ac 208 for bluish green colour and resistance to black rot); lablab bean (IS 21 for earliness) and ivy gourd (CG 84 for resistance to mosaic) were found promising.

**Mushroom:** About 302 wild mushrooms of *Termitomyces*, *Lepista*, *Chlorophyllum*, *Agrocybe*, *Leucocoprinus* and *Mycena* spp. were collected. The DNA sequence from *Tricholomella constricta* has been deposited. This is second DNA sequence data from the world and first of this species from India. DNA sequence of two new *Volvariella* spp. has also been deposited. Two new species of *Volvariella* were identified. Genomic DNA from 12 strains of *A. bisporus* and *C. indica* were isolated and purified. DNA fingerprints were developed using 4 random primers. Seven new strains/SSI of paddy straw mushroom (*Volvariella volvacea*) were evaluated for their mushroom yield and quality. Strain bbsr-007 gave highest mushroom yield of 31% on a 1:1 mixture of paddy straw + cotton waste in 2 weeks of cropping. A total of 130 specimens of wild fleshy fungi were collected from the forest areas of different regions. The important collected species were *Ganoderma* spp., *Agaricus bisporus*, *Schizophyllum commune*, *Polyporus* spp., *Termitomyces* spp., *Auricularia polytricha*, *Rassula* spp., *Cantharellus* spp., *Calocybe* spp., *Pleurotus* spp., *Phellorinia inguinans*, *Podaxis pistillaris*, *Daldania concentrica*, *Ramaria* spp., *Tricholoma* spp., *Hericium erinaceum*, *Lapiota procera*, *Lycoperdon*

spp., *Mycena* spp. and *Volvariella volvacea*.

**Oil palm:** Seeds of 12 promising oil palms, viz. Baratang (2 nos.), Theni (5 nos.), Nellore, (4 nos.), Sulia, Mangalore (5 nos of Nigerian source), were collected from commercial plantations of Little Andaman. One high-yielding virescence dura, was collected. One dwarf Surinam palm was identified at Palode. One more dwarf Nigerian sterile pisifera was identified in OPIL estate. Two high-yielding virescence type dwarf palms were identified at PCKL, Athirapalli. One dwarf tenera of Costarican origin was collected from a plantation in Andhra Pradesh.

**Spices:** A total of 585 black pepper germplasm have been maintained under different AICRPS centres. The characterization resulted in identification of high-yielding accessions, viz. Karimunda II with a maximum green berry yield of 5.60 kg/vine followed by Valiyaramundi (3.45 kg/vine) and TMB IV (1.80 kg/vine). In cardamom, 305 germplasm have been maintained. Ginger (660 accessions) and turmeric (1,280 accessions) have been maintained under AICRPS centres. Out of the 265 turmeric germplasm accessions screened for resistance against leaf spot and leaf blotch diseases, the turmeric germplasm accessions, viz. CL 1, CL 2, CL 3, CL 6, CL 14, CL 22, CL 25, CL 31, CL 32, CL 33, CL 53, CL 54, CL 148, CL 153 and CL 230 were resistant to leaf spot (8 – 10 PDI) and leaf blotch. In tree spices, a total of 37 clove, 119 nutmeg, 39 cinnamon and 6 cassia accessions have been maintained. In coriander 1,809, in cumin 623, in fennel 670 and in fenugreek 976 accessions were maintained.

**Flowers:** At Bhubaneswar, five new cultivars of rose were added to the existing germplasm of 324 cultivars including 201 HT, 73 floribunda, 42 miniature and 8 climbing roses.

**Orchids:** A total of 3,130 orchid accessions maintained at NRC for Orchids, Pakyang, Sikkim. Two orchid species, Euranthes and Ione, have been collected and enriched germplasm collection.

**Betelvine:** The cultivar, Vasanaa Kapoori, performed better than others in respect to leaf yield, 20% more than the control. GN 1 hybrid (Ghodi Bangla × Kapoori Nasik) exhibited normal vigour. Even in GN hybrid, yield was much below than the local check variety. The hybrids could not establish at BCKV centre.

**Tuber crops:** In tuber crops, four early-maturing hybrids and 12 others suitable for table purpose were identified. The 164 SSR marker-tested cassava mosaic resistant clones received from CIAT were evaluated. Flour clones, viz. CR 43-11, CR 43-7, CR 54A-3 and CR 59-8, had high yield (>40 tonnes/ha) coupled with CMD resistance. Out of 1,820 first clonal hybrids evaluated for identifying TLB tolerant clones, 12 were symptom-free and

being evaluated along with Mukhtakeshi. Also hybrid seeds were generated incorporating TLB-free wild taro as one of the parents (seven crosses) to produce TLB-resistant taro hybrids. Fifteen high-yielding hybrids were identified from the replicated trial and being evaluated to confirm the performance. About 118 hybrids were evaluated for isolation of high-yielding good cooking types.

In cassava, ME 833 gave higher yield at Yethapur and CM 9905 at Thiruvananthapuram. H 740/92 recorded significantly higher yield at Yethapur and Peddapuram. Three clonal selections, PDP 5, PDP 6 and PDP 7, obtained from crosses Ambakadan × Sree Prabha (TCH 2) and Ambakadan × H 165 showed high degree of resistance to cassava mosaic virus with high yield potential.

In sweet potato, two selections, viz. CARI – SP1 and CARI-SP2, from Port Blair with consistent higher yield under Island ecosystem were identified for Andaman and Nicobar Islands. IGSP 14, CO 3-4, SV 280, DOP 93-19 and ST 10 were identified as good yielders at different centres. Among orange fleshed sweet potato entries, Kamalasundari, 440038, CIPSWA 2, ST 14, IGSPC 15, 362-7 and SV 98 showed better performance in different states.

Yam bean RM 1, DPH 101, DPH 88 and DPH 70 were the maximum tuber yielders at different centres. Among the collection of *Colocasia*, *C. esculenta* var. *antiquorum*, taro collections, ML 1 and ML 9 were good yielders in Meghalaya. JCC 25, IG Col 4 and BCC 17 in taro were identified as good yielders for Asom, Chhattisgarh and West Bengal.

## ANIMALS

### Livestock information management

**Individual assignment using genetic algorithm:** A computational methodology based on genetic algorithm was developed to solve the individual assignment problem using microsatellite data. Its results were compared, and accuracy of assignment was also tested. Performance using genetic algorithm methodology is comparable with that of existing methods with the data generated from actual allelic frequency values of Red Kandhari, Deoni, Hariana and Sahiwal cattlebreeds.

### Phenotypic characterization

**Bargur cattle:** Bargur cows are distributed in and around Bargur hills in Bhavani Taluk of Erode district, and also in Kolathur Taluk of Salem district especially the regions adjoining the Bargur hills. Bargur village (34 hamlets) has 10,102 cattle of which 90% conform to breed characteristics of Bargur cattle. The animals are maintained in low

### Evaluation of indigenous pig germplasm

Indigenous pig herds of three strains, were established at the NRC Pig for genetic evaluation, improvement and conservation. Unrelated pigs of Nagaland, Meghalaya and Northern West Bengal (Ghungroo) were directly procured from farmers' field and the founder stock was established at the institute. The litter size at birth in indigenous pigs from north Bengal (Ghungroo) was on an average 12 piglets in comparison to seven in Meghalaya and five in Nagaland. The weaning weight is about 12 kg in Ghunguroo in comparison to Meghalaya local (5.25 kg) and Nagaland local (4.5 kg). Ghungroo has the potential to be developed as the Indian Meishan pig in the future.



Ghungroo pig with litter

input system by grazing animals in deep thick forests. *Patti* system is practiced, whereby herdsmen keep animals in *pattis* during night. Animals are small; brown colour with white patches. The average body length, height at wither, heart girth, paunch girth, face length, face width, horn length, ear length and tail length without switch in cows were 99, 108, 139, 144, 42, 14, 35, 17 and 62cm, respectively. The birth weight varied between 15 and 18 kg. Cows are poor milkers; average daily yield is 1.14 kg. Age at first calving varies from 36 to 60 months with an average of 48 months. Calving interval varies from 16 to 18 months, lactation length 180 days to 240 days, service period 120 to 180 days, and dry period from 150 to 210 days.

**Malnad Gidda cattle:** Malnad Gidda, a dwarf cattle is mainly distributed in Shimoga, Chickmagalur, North and South Kannada, and Belgaum districts of Karnataka. The breed population has declined especially in last two decades. The animals are kept under low input system of management. There are five major coat colours in the breed (black, brown, red, fawn, white and sometimes mixture of any two). The average body length and height at withers were 87.04±0.65 cm and 90.29±0.46 cm, respectively, for cows, and 86.53±1.93 cm and 91±1.47 cm, respectively, for adult males. The average chest girth and paunch girth were 118.36±0.67 and 121.39±0.82 cm for cows and 118.47±3.93 and 118.67±3.90 cm for adult males. Birth weight, weight at maturity, age at first calving, age at first service in males, calving interval, service period and number of services/conception were 8.56 ± 0.44 kg, 87.29±2.95 kg, 45.41± 1.22 months,

### Sex identification of meat

Method for identification of sex from meat was standardized. It involves PCR amplification of Amelogenin XY gene. In males amino acid coding region of the Amelogenin gene on the Y chromosome (AMELY) is shorter than its X chromosome counterpart i.e. it is having a deletion region. Hence PCR amplification of AMEL gene gives amplicons of two sizes (217, 280 bp) in male and only amplicon of single size (280 bp) in female DNA samples. Repeatability of the assay was confirmed by testing in different field samples.

38.06 ± 1.24 months, 17.02 ± 0.68 months, 8.38 months, and 1.48, respectively. About 15% cows are producing more than 2 kg milk/day. In elite cows, the lactation period, dry period, average daily milk yield, peak yield, lactation milk yield were estimated as 8.95 months, 7.17 months, 2.11 kg, 3.09 kg, 569.13 kg, respectively.

**Balangir sheep:** The Balangir sheep is distributed in Balangir, Kalahandi Baudh and Angul districts of Orissa. Animals are small; average body weight, body length, height at withers and chest girth were 23.0±0.74kg, 57.6±0.84cm, 62.1±0.74cm and 69.7±0.84cm in rams and 20.4±0.17kg, 55.6±0.22cm, 59.6±0.18cm and 67.2±0.22cm in ewes, respectively. Coat colour ranged from light to dark brown or patches of white and brown. Males are horned and females are polled. Body is covered with coarse, open and colour fleece. Face, belly and legs are devoid of wool. In males, age at first breeding was 8-12 months with a breeding life of 1-3 years. Lambing rate was 70-100%. Balangir sheep are primarily maintained for mutton.

**Surti goat:** Surti goats are found in Bharuch, Nambada, Navsari, Valsad and Vadodara districts of Gujarat. Animals are of medium size with varied colour patterns, viz. white, black tan, and grayish. Mottled animals are also found. Surti goats are good milch animals with well developed funnel/bowl shaped udder. The milk production ranged from 1.5 to 4 kg/day. Surti goats are good breeders showing first oestrous at an age of 6-8 months and kid at 13-14 months of age. Twins are born to majority of does (50-60%), and triplets are rare (5%). Males also show sexual maturity at the age of 6-7 months. The major breeding season is March-April and minor is October-November. The average body weight of adult male and female is 29.03 and 31.06 kg, respectively.

**Busra chicken:** Busra birds are found in Navapur taluk of Nandurbar and Sakri taluk of Dule districts of Maharashtra, and Songadh and Uchhal taluks of Surat district of Gujarat. These birds are reared for home consumption as well as for sale of live birds and eggs. Birds are kept in

the free range system. Flock size varied from 2 to 25 with an average of 8.6. Plumage is mostly white mixed with black feathers on neck, back, tail, and reddish brown feathers on shoulders and wings. Comb is red, single, small to medium in size, stands erect; beak yellow; wattles red, small to medium size; and shank, yellow. Weight of cock ranged from 0.85 to 1.25kg (average  $1.11 \pm 0.06$  kg) and of hen from 0.8 to 1.2 kg (average  $0.98 \pm 0.06$  kg). Age at first egg ranged from 5-7 months (average of about 6 months). Annual egg production ranged from 40 to 55. Hatchability on total egg basis ranged from 60 to 85%. Dressing percentage is about 65 – 70%. Eggs are small weighing about 28-38g (average  $31.56 \pm 1.40$ g). Shell colour is mostly light brown. Egg shell is mostly strong with an average thickness of  $37.73 \pm 1.47 \mu$ . Albumen index, yolk index and haugh unit were  $0.059 \pm 0.007$ ,  $0.352 \pm 0.012$  and  $73.66 \pm 4.04$ , respectively.



Busra birds are kept for home consumption and sale of live birds

## Genetic characterization

**Cytogenetic status of Assamese buffalo:** All the non-descript buffaloes found in Assam resemble swamp buffaloes in external features. They are of small body size, low milk yield and are classified as swamp buffaloes (Assamese swamp buffaloes). Distinctive karyotypic features of swamp and river buffaloes were exploited to explicitly ascertain their riverine or swamp status. Majority of the animals investigated—picked from different parts of Assam—were riverine type, which is in contradiction to the general classification of Assamese buffaloes as swamp type.

Only four animals had a diploid count of 49 chromosomes, with one large size metacentric chromosome characteristic of swamp buffaloes. These four animals were thus crosses of River × Swamp type indicating the presence of swamp type buffaloes also in the vicinity, probably of the wild type.

**Buffalo lactoferrin gene:** Lactoferrin is a potential candidate gene in dairy cattle breeding for increasing resistance against infections especially in mammary gland. Polymorphism in this gene was studied by analyzing the 5' flanking region of lactoferrin gene in Murrah, Jaffarabadi, Marathwada, Toda and Pandharpuri buffalo breeds. Ten distinct SSCP (single strand conformation polymorphism patterns) were observed, which further revealed 13 polymorphisms with 8 transitions, 4 trans-versions and one deletion mutation upon sequence analysis. Sequencing indicated homology with *Bos taurus* (96%), *Bos indicus* (95%), *Capra hircus* (91%), *Ovis aries* (92%), *Sus scrofa* (57%) and *Homo sapiens* (28%). Sequence analysis of SSCP variants revealed 34 nucleotide changes in bubaline lactoferrin gene from that of *Bos taurus* across

### Comparative Genetic resistance to H5N1

Genetic resistance of indigenous stock — Kadaknath and Aseel Peela vis a vis high yielding SDL-IC (Synthetic Dam Line-Immunocompetent)—broilers against induced infection of H5N1 was evaluated.

The birds were subjected to induced-infection intra-nasally with a dose of 1,000 EID 50 (determined by a prior experiment) of H5N1 (narapur/7972 strain). The overall survivability percentages were 8, 2 and 0% in SDL-IC broilers, Aseel and Kadaknath, respectively. The MDT (mean death time) was highest in SDL-IC (6.96 days) followed by Aseel (5.92 days) and Kadaknath (3.12 days). The day-wise and cumulative mortality percentages and MDT were significantly different among genetic groups. So far, no report is available in literature on survival of chicken after induced challenge of H5N1 whereas, for the first time, in present case 1 out of 50 Aseel and 4 out of 50 SDL-IC broilers survived for 10 days experimental period after H5N1 induced infection at higher dose than reported in literature. The four surviving SDL-IC broilers did not show any clinical sign and were apparently healthy whereas the Aseel was depressed.

The overall severity of clinical signs was less with delayed onset of symptoms in SDL-IC broilers as compared to other two genetic groups. The overall severity of gross PM lesions was less in Kadaknath followed by Aseel and SDL-IC broilers, which might be due to the least MDT in Kadaknath as compared to other genetic groups. During early as well as late phases of H5N1 infection, lungs were most severely affected followed by brain in all the 3 genetic groups.

The expression profiles of genes indicated better genetic resistance in SDL-IC broilers as compared to Aseel and Kadaknath against H5N1 infection, which was in agreement with results of challenge trial. Nucleotide analysis of differentially expressing genes also revealed variation (transitions, transversion and insertion/deletion) in both exon and intron regions among the three genetic groups.

different exonic regions. Analysis of different intronic regions revealed 38 nucleotide changes. Further, analysis of sequence data revealed five novel SNPs in intronic region and two SNPs in exonic region of bubaline lactoferrin gene. The SNPs identified in the lactoferrin promoter, exonic and intronic regions may serve as potential candidate marker(s) in buffaloes.

**Phylogenetic relationship among bovine species:** RAPD analysis on five bovine species under the genus *Bos* (Bovis), viz. yak (*Pheophagus grunniens*), mithun (*Bos frontalis*), *Bos indicus*, *Bos taurus* and buffalo (*Bubalus bubalis*) showed that yak shares highest genetic similarity with mithun (42%) followed by exotic cattle (27%), indigenous cattle (29%) and buffalo (16%). In comparison with yak, mithun was slightly closer to both the cattle species. Among the five species studied, buffalo seemed to be the most distinct from others. These results suggested that during the course of evolution, chromosomal rearrangement might have played little role in the diversification of bovines.

### Molecular genetic characterization

**Sheep and goat:** Microsatellite based genotyping of Patanwadi, Marwari and Dumba Sheep breeds revealed genetic distance of 0.033 between Patanwadi and Marwari, 0.049 between Patanwadi and Dumba, and 0.066 between Marwari and Dumba, indicating less genetic distance between Patanwadi and Marwari sheep breeds.

Microsatellite based genotyping was completed for Coimbatore sheep, Barghur cattle, Salem Black and Tellicherry goat at Core lab, TANVASU, Chennai, and diversity analysis for Bachaur cattle, Shahbadi and Ganjam sheep breeds at Core lab, NBAGR, Karnal. Diversity analysis indicated existence of substantial genetic variability and had no recent bottleneck in the populations investigated. Under trait-specific gene characterization, polymorphism at the *DGATI* locus was also investigated by PCR-SSCP assay in native goat breeds.

Calpastatin gene, responsible for meat tenderness, was genotyped in Deccani, Nellore, Sonadi, Malpura, Nali, Ganjam, Chokla and Garole sheep breeds. Nellore sheep revealed the highest polymorphism in the calpastatin gene. Nellore and Malpura sheep are closer in terms of meat tenderness.

**Layer and broiler germplasm:** Genetic diversity analysis of 6 genetic groups of a diallel cross was carried out by 14 microsatellite markers. The genotypes showed varied genetic identity/diversity. In a study using 14 microsatellite markers located on different chromosomes, the markers *ADL023*, *MCW041*, *ADL210* and *MCW110* were

significantly associated with egg production up to 28, 64 and 72 weeks of age. *MCW007*, *ADL020*, *ADL023* and *ADL176* microsatellites correlated significantly with age at sexual maturity. The genotypes of *MCW007* microsatellite were associated with body weight.

Genetic manipulation through introgression of major gene, transgenesis and reconstitution of poultry species: Two pure broiler strains (NNWP and NNCP) having specific introgressed naked neck gene, have undergone specialized selection programme over thirteen generations. The naked neck birds showed consistently relative superiority over normal for array of broiler traits. Presently, CARIBRO-Mritunjai is the only proven commercial (Naked Neck) broiler to perform exceedingly well in hot and humid conditions (tropical climate). To improve the general immunocompetence, the male and female progeny of NNCP population were selected for high 5-week body weight and high response to HI titre, and in NNWP population only male progeny was selected for high 5-week body weight and high response to HI titre.

**Role of apoptotic genes during forced moulting:** Apoptotic genes, viz. Caspase-1, Caspase-2, Caspase-3, Caspase-6, Caspase-8, Caspase-9, p53, Bcl-2 and Bcl-xL, were studied in the regressing reproductive tissue of force moulted White Leghorn hens. The mRNAs of all caspases under study except Caspase-6 were found in the regressing ovarian and oviduct (magnum and uterus) tissues. The involvement of apoptotic genes of intrinsic pathway (p53, bcl-2, bcl-xL) was also found in the ovary, magnum, and uterus of the moulted birds. The present investigation clearly indicated that apoptotic genes involved in both extrinsic and intrinsic pathways control reproductive regression in moulting birds.

**Isolation and molecular characterization of methanogenic archaea:** The methanogenic archaea

#### Genetic characterization of predominant *Salmonella* serovar in seafood

PCR ribotyping and band pattern analysis of *Salmonella* Weltevreden and *Salmonella* Rissen isolates, the most common isolates from different seafood revealed three ribotype profiles in *Salmonella* Rissen and four major ribotype patterns in *Salmonella* Weltevreden strains indicating distinct genetic diversity among them. Studies on the genetic variations among *Salmonella* Typhi isolates by PFGE and VNTR showed similar genetic homology among *Salmonella* Typhi strains isolated from different seafoods. These molecular fingerprinting techniques showed that there were intra-serovar genetic variations among predominant *Salmonella* serovars in seafood.

were isolated from the rumen of small and large ruminants. Uncultured archaeal sequences were also characterized from the metagenomic library constructed with rumen content. Archaeal isolates *Methanobrevibacter* and *Methanosarcina* were isolated. An organism with 94% sequence similarity with *Methaniculleus marisnigri* was recorded for the first time in India.

### Network Project on Animal Genetic Resources

**In-situ conservation:** At the *in-situ* Conservation Unit of Beetal goat, 173 Beetal does were registered and their performance data recorded. Male kids were selected, tagged and registered, and their body weights were recorded up to 12 months of age. The awareness for pure breeding of Beetal was created among the selected farmers, which resulted in an increase of flock size by 5-7. This was also attributed to the culling of non-Beetal goats and sheep in flocks. At Navsari, 150 Surti goats were registered in 11 villages of Bharuch, Surat and Navsari districts. The male kids were born with slightly higher birth weight than female kids. The daily weight gain up to the age of 3 months was approximately 75.88g for male and 74.11g for female kids.

At Kilakarsel sheep *in-situ* Conservation Unit, 358 animals of Kilakarsel (1.5%) were identified by surveying 23,621 sheep in five districts. The number of pure Kilakarsel sheep was very less, therefore it was categorized as a threatened breed. Purebred Kilakarsel sheep are being reared to produce 50 rams for distribution in field.

**Ex-situ conservation:** At BAIF, Pune, bull calves of Krishna Valley cattle were reared at germplasm unit in individual bull-pens. The bull calves, weighing at least 260 kg were used for semen collection, and 7,000 semen doses were stored. On an average 1,000 semen doses per Jaffarabadi bull were produced and stored. At the UPLDB Lucknow, 12 male calves of Ponwar cattle and 11 male calves of Kherigarh cattle are being trained for semen donation.

## FISH

**Coldwater fisheries:** The coldwater fish genetic stocks of the Kumaon region, Uttarakhand, were surveyed in river Kosi, Ramnagar, Gola and Chirapani stream and *Tor putitora*, *Schizothorax richardsonii*, *Barilius* species, *Garra* species and *Riama bola* were recorded. The cyprinid family fish species were assessed for their molecular systematics at subfamily level and the sequence was submitted to NCBI database with the accession numbers of AM778102 to 06 and AM950230.

They indicated the possible occurrence of subfamilies Schizothoracinae, Cyprininae and Rasborinae.

**Development of microsatellite markers in *Macrobrachium rosenbergii*:** With regard to development of microsatellite markers in giant freshwater prawn, *Macrobrachium rosenbergii*, over 3,000 colonies from a partial genomic library were screened. A total of 92 positive colonies were detected and 30 colonies were selected on the basis of signals strength of which 12 could be sequenced. Eight loci were polymorphic and all the loci except one were in the agreement with HWE. No significant pair-wise linkage disequilibrium was found among the loci. These markers may prove useful for characterization of natural population as well as brood stock management of this species.

**Genetic linkage mapping in Indian major carps:** Marker to marker linkage study was initiated in rohu, the first attempt of its kind in Indian fish species. Rohu and kalbasu (*Labeo calbasu*) have 25 pairs of chromosomes and produce viable F1 hybrids. Pair-wise recombination estimation using LINKMFEX software showed eight loci to be linked with a minimum LOD score of 3.0 forming three linkage group in male parent spanning 67.29 cM.

**Gene banking of Indian catfish *Horabagrus nigricollaris*:** *Horabagrus nigricollaris*, an endemic, cultivable yellow catfish, is found only in one river (Chalakkudy River, Kerala) originating from southern part of the biodiversity hotspot – the Western Ghats, South India. This species enjoys a good market value as a food and ornamental fish. The species was categorized as critically endangered due to its highly restricted distribution, loss of habitat, over exploitation, destructive fishing practices and trade. Hence, captive breeding and milt cryopreservation techniques were developed for the species.

**DNA barcoding of Indian fishes:** A comprehensive programme on DNA barcoding of fishes of India is being carried out at the NBFGR, Lucknow. The total DNA was isolated for 1,427 samples of 410 species and PCR amplification was done for 733 samples of 280 species. DNA sequencing was done in 540 samples of 182 species. DNA barcodes were prepared for 180 species. A total of 395 DNA sequences of 110 species were submitted to BOLD.

**Species-specific DNA - based diagnostic assay for *Gyrodactylus elegans*:** A standardized DNA based-diagnostic technique for species-specific identification of the trematode, *Gyrodactylus elegans* was developed. This is the first attempt in the country, towards molecular detection of fish parasites.