

5. Genetic Resources

Crops

Agro-biodiversity component of the plant genetic resources covers whole gamut of genetic resources (from advanced cultivars to primitive landraces, domesticates, semi-domesticates, wild and weedy relatives) and the diversity of ecosystems and agro-ecosystems within the landscapes. The resources include all agricultural crops and some of their wild relatives that possess valuable traits. Occasionally genes, DNA fragments and RNA fragments are included under the purview of the genetic resources, and these genomic resources are conserved in gene banks. Plant genetic diversity provides valuable traits needed for meeting the challenges for evolving crop varieties suitable for changing environment. The ICAR institutions are involved in the augmentation and conservation of genetic resources for developing new crop varieties.

Germplasm augmentation, conservation and use:

Thirty- three explorations were undertaken in 16 states, and 1,722 accessions, including 322 wild species were collected.



Sorghum-landrace diversity, collected from tribal pockets of Khammam district, Andhra Pradesh - *Dubba jonna*, *Tella jonna*, *Gaddi jonna*, *Konda jonna* and *Pachcha jonna*

A total of 266 specimens were added to the National Herbarium of Cultivated Plants. The National Gene Bank was enriched with 5,414 accessions of orthodox seed species and 120 of non-orthodox plant materials.

Forty-four thousand sixty-nine accessions imported from 42 countries included 10,295 accessions of international trial materials. Promising introductions are in wheat: alien disomic substitution genetic stock (EC758755) of durum, genetic stock with *ph1b* mutant allele in adapted Kansas winter wheat (EC 755279),

Promising wheat genotypes identified for quality components

Genotype	Traits
KLM 1005	Durum lines with bold grains (TGW*: 51g) and high protein (14% at 14% grain moisture)
WSM 24	Durum lines with bold grains (TGW: 53g) and high protein (13.5% at 14% grain moisture)
KLM 1008	Bread wheat lines with bold grains (TGW: 51g) and high protein (13.4% at 14% grain moisture)
BW 5872	Bread wheat line with good sedimentation volume (54 ml)

*TGW: Thousand Grain Weight

registered lines with genes from elite cultivars possessing alternate growth habit (EC762316-17) from the USA and Waagan (EC 759227) having drought tolerance from Australia; in paddy: resistant to sheath blight and blast diseases (EC758366-8) from the USA; in safflower with high oleic acid (EC755659-88) from Mexico; in snapmelon (EC 766817-33) with *Fusarium* wilt resistance and gummy stem blight resistance from the USA; in tomato: tolerant to heat and resistant to late blight, *Fusarium* wilt, tomato yellow leaf curl virus and tobacco mosaic virus (EC779308) from Taiwan, and wild tomato (EC 774472-3) from the USA; in chilli: CMS lines (EC 771549-54) and *Phytophthora*



Prunus mira (Behmi)– a cold hardy wild relative of peach and almond; used for edible purpose and as a source of oil locally, and as a rootstock



Germplasm Portal

A web-based portal has been developed to facilitate access to information on the PGR conserved at the National Gene Bank. The PGR Portal is a gateway to information on plant genetic resources conserved in the Indian National Gene bank, housed at the National Bureau of Plant Genetic Resources (NBPGR), New Delhi. The NBPGR is the nodal organization in India for acquisition and management of indigenous and exotic plant genetic resources for food and agriculture. The Indian National Gene bank conserved about 0.4 million accessions belonging to 1,812 species. The PGR Portal is an endeavour in this direction to facilitate easy availability of information about the conserved germplasm. The information provided through the PGR Portal is accessible to researchers, farmers, students and policy-makers. Users can either search for accession information (simple search) or for characterization and preliminary evaluation data (advanced search).

Jute and allied fibres germplasm from Tamil Nadu and Kerala

A total of 235 accessions of jute and allied fibres: 137 species of *Corchorus*, including *C. olitorius*, *C. pseudo-olitorius*, *C. aestuans*, *C. tridens*, *C. fascicularis*, *C. trilocularis*, *C. urticifolius*; 35 species of *Hibiscus*, including *H. sabdariffa*, *H. cannabinus*, *H. hirtus*, *H. surattensis*; 36 species of *Crotalaria*; 17 species of *Agave* and 10 species of *Urena* were collected. *H. sabdariffa* WHIN 61 with about 3-m height was collected from monolithic rock in Kerala and *C. aestuans* WCIN 302 with high yield, soft and white fibre was collected from farmer's field in Tamil Nadu. Some unique mutants of *tossa* jute (cv JRO 204, JRO 8432) with soft stem and undulated phenotypes, producing lesser fibres with low lignin content, have been identified. In addition, hard stem mutant with coarser fibre-producing ability, super dwarf mutant plant of 30- cm height (control 320 cm) and a twisted bark mutant in *tossa* jute have also been identified.

resistant lines (EC 771558-60) including core sets in chilli; lima bean and hyacinth bean from Taiwan. A total of 25,438 accessions were characterized and evaluated. These included wheat evaluated for terminal heat tolerance, tolerance to spot- blotch disease and rusts. In all, 7,770 accessions were supplied for research and crop improvement within the country.

A total of 141,191 imported plant materials, including seeds, vegetatively propagated materials and transgenics were processed for quarantine clearance. Out of 3,838 samples infested/ infected with different pests, 3,437 have been salvaged. Thirteen phytosanitary certificates were issued for export of 1,294 plant materials.

In Maize, five lines V 334, V 336, V 400, V410 and V 414 exhibited moderate tolerance/ resistance against *Helminthosporium turcicum* leaf blight, banded leaf and sheath blight and *H. maydis* leaf blight. These can directly be used as parental lines for hybrid development or as donors in maize-breeding programme.



Moderately resistant (V414, V 410, V 400, V 336, V 334) and highly susceptible (CM 212, CM 145) maize inbreds

In Groundnut, Spanish bunch types NRCG 14500 for high protein content (33%), NRCG 14430 for high shelling out-turn (73%), and Valencia types NRCG 14379 for high shelling (72%), NRCG 14448 for high protein content (31%) and M 13, M 548 and ICGS 76 for low oil and high sucrose content and with a desirable fatty-acid composition have been identified. Safflower accessions GMU 184 and EC 523368-2 were validated for resistance to aphids, while castor accessions RG 631 and RG 2469 showed resistance to leafhopper.

A large number of wild accessions of different pulse crops were characterized and utilized in breeding programmes for widening genetic base. Chickpea genotypes Katila, Avrodhi, Vaibhav, GCP 105 and JG 11 exhibited combined tolerance to heat and drought. Mungbean genotypes MH 2-15 and IPM 02-3 showed multiple resistance against most of the prevalent *kharif* diseases– mungbean yellow mosaic virus (MYMV), *Cercospora* leaf spot, anthracnose, leaf crinkle, leaf curl, stem necrosis and *Macrophomina* blight. IPM 02-15-4 was found resistant to MYMV in *rabi*. Urdbean genotype UH 7-13 showed multiple resistance against MYMV, *Cercospora* leaf spot, root-rot and leaf crinkle while IPU 10-17 exhibited broad spectrum of resistance against MYMV, urdbean leaf curl virus (ULCV) and anthracnose. Urdbean accession PGRU 95016, besides, accessions of *Vigna glabrescens* (IC 251372) and *V. umbellata* (IC 251442) exhibited photo-thermo-insensitivity that can facilitate development of widely adaptable genotype. Urdbean genotype Mash 114, DPU 88-31, Khairagarh Agra and AKU 15 showed resistance to root-knot nematode, *Meloidogyne javanica*.

Number of fieldpea genotypes showed multiple and multi-locational resistance against many diseases. These include Pant P 172 which was resistant to powdery mildew and rust; HFP 919 was resistant to downy mildew; and Pant P 184 was resistant to powdery mildew and *Ascochyta* blight, and Pant P 74 showed resistance to powdery mildew, downy mildew and rust.



Germplasm registration: Germplasm registered at the NBPGR comprise cereals (12), millets (4), grain-legumes (8), oilseeds (19), fibres and forages (13), spices (1), tuber crops (2), medicinal and aromatic plants (9) and commercial crops (7). Three pearl millet hybrids, Pusa 415 (MP 739), Pusa 605 (MH 564),

HHB 146 (MH 960), and one variety, Pusa Composite 334 (MP 334), were registered with PPV & FRA, New Delhi.

Vaidehi 95 (MSH 53), a dark-brown linted introgressed derivative of cotton, has been registered with the NBPGR, New Delhi (National Id: IC0584260

Important registered germplasm of crop-plants

Crop	National identity	Original identity	INGR No.	Unique features
Wheat	IC 0590875	UAS 320	13001	Resistant to flag smut disease
Wheat	IC 0595583	DBQW 1	13072	Good biscuit-making quality
Wheat	IC 0598203	HW 3601	13051	Carries gene for leaf rust resistance, <i>Lr 19</i> , and stem-rust resistance, <i>Sr 36</i>
Wheat	IC 0597682	UP 2672	13053	High protein content (14.1%)
Rice	IC 0594593	RPMRE 6	13073	Multiple resistance to gall midge, brown planthopper and white-backed planthopper
Rice	IC 0595533, IC 0595534	PANT CMS2A, CMS2B	13002	High panicle exertion (92.9%) and high out-crossing rate (41.30%)
Maize	IC 0594467	KDTML 82	13003	Drought tolerance
Maize	IC 0524594	MCM-11/01	13054	3-4 cobs / plant and early maturing
Maize	IC 0594369	DMR QPM 102	13074	Medium maturity, low ASI, high tryptophan, high protein
Sorghum	IC 0594687	BRJ 62	13005	Restorer on <i>Maldandi</i> source of male sterility
Sorghum	IC 0595529	PYPS 2	13006	Yellow grain, good <i>chapati</i> -making quality
Sorghum	IC 0597771	SSG 226	13055	Low hydrocyanic acid (66.6 ppm), high digestibility and high leaf-stem ratio
Pearl millet	IC 0283734	NSS 7809	13056	Popping trait
Greengram	IC 0546478	KSAS 06/105	13010	Photoinsensitive accession
Chickpea	IC 0595521, IC 0595522	GL 84100, GL 87045	13008, 13009	Resistant to <i>Ascochyta</i> blight and wilt
Pigeonpea	IC 0594374	IPA 9 F	13024	Resistant to <i>Fusarium</i> wilt
Groundnut	IC 0595257	TGM 167	13011	Gibberellin- insensitive dominant dwarf mutant
Groundnut	IC 0595258	NRCG 12431	13012	Low level of infection (7%) and free from colonization of <i>Aspergillus flavus</i> in kernels
Indian mustard	IC 0595268	NDUH-YJ6	13015	Low glucosinolate content in seed (≤ 10 μ moles/gram), high oil content ($\geq 45\%$), resistant to white rust, yellow-coloured seed-coat
Indian mustard	IC 0595525	BPR 549-9	13016	Salinity tolerant at juvenile stage, high water-use efficient
Indian mustard	IC 0593927	BPR 540-6	13027	Salinity, thermo- tolerant at juvenile stage
Soybean	IC 0595528	PK 515	13017	Resistant to yellow mosaic virus, moderately resistant to hairy caterpillar
Safflower	IC 0597598	Ole-9-P2-P1-P22	13066	High oleic acid (18.63%) and high oil (34%)
Cotton	IC 0594174	DDB 12	13029	Dark brown lint
Cotton	IC 0594175	DGC 78	13030	Green lint
Cotton	IC 0594176	DMB 225	13031	Medium brown lint
Cotton	IC 0584260	Vaidehi 95 (MSH 53)	13032	Dark brown lint
Cotton	IC 0584261	NISC 40	13033	Jassid tolerant
Cotton	IC 0584262	NISC 43	13034	Jassid tolerant
Cotton	IC 0584263	NISC 44	13035	Jassid tolerant
Cotton	IC 0597400	TCH 1728	13067	Leaf- hopper resistant, thick leaf, higher number of trichomes
Sugarcane	IC 0598218	SBI 1148-11-13-2-225	13071	Possessing high sucrose and red- rot resistance



Vaidehi 95 cotton

/Registration No: INGR13032). Three cultures, DTS 108, DTS 67 and DTS 44 have been identified as potential drought- tolerant cotton, based on their ability to withstand harsh summer.

Agriculturally important insects

Biosystematics and biodiversity: One new genus *Dvivarnus* Rajmohana & Veenakumari (Platygastridae) and 14 new species of insects and mites have been described from different parts of South India.

An undescribed species of *Montandioniola* (Anthocoridae) on *Butea monosperma* and a new genus and species of Anthocorini on *Ficus* sp. has been recorded.

A catalogue of Microgastrinae fauna of Reunion Island was published with a key for 34 species, belonging to 13 genera which include several species of Indian origin. *Blaptostethoides* sp. and *Xylocoris ater* are new records for India and *Carayonocoris affinis* has been recorded for the first time as a predator of

New Culture Storage and High Performance Computing Facilities

The National Agriculturally Important Microbial Culture Collection (NAIMCC) repository was enriched to house 4,500 microbial cultures. A set of lyophilized cultures and glycerol stocks are also being maintained for safety in the storage facility at the NBPGR, New Delhi. A high performance computing (HPC) infrastructure has been established at the NBAIM, Mau, to cater needs of high performance computing in the field of agricultural bioinformatics and computational biology under the National Agricultural Bioinformatics Grid (NABG). The facility along with number of computational biology and agricultural bioinformatics software databases at the IASRI, New Delhi, would provide seamless access to biological computing resources to researchers.

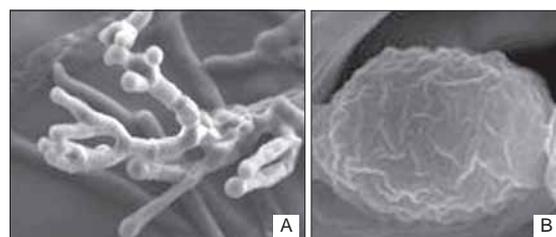
Hemiberlesia lataniae on agave. Three potential pests *Pleotrichophorus chrysanthemi* (Theobald) and *Reticulaphis foveolatae* (Takahashi) (Aphididae) and Jackbeardsley mealybug (*Pseudococcus jackbeardsleyi* Gimpel and Miller) (Pseudococcidae) have been recorded for the first time from India. The new invasive mealybug *Pseudococcus jackbeardsleyi* Gimpel and Miller that was not reported earlier in India was documented in Sathiyamangalam, Tamil Nadu, for the first time along with *P. marginatus* on papaya.

Diversity of plant- associated mites: For the first time in the country, DNA sequences of 15 species of economically important mites have been verified and deposited in the NCBI GenBank database with GenBank accession numbers; particularly of European red mite *Panonychus ulmi* (from Mashobra, Himachal Pradesh) and tea spidermite *Oligonychus coffeae* (from Jorhat, Asom).

Agriculturally important microorganisms

A new halophilic extremophile fungus: Mangrove is a highly productive marine ecosystem, where halophilic microbes are active in bio-mineralization and biotransformation of minerals.

A new halophilic extremophile fungus *Penicillioopsis clavariiformis* has been reported for the first time in India from Chora mangrove, Goa. The fungus tolerated extreme salinity up to 10 % (w/v) NaCl. Scanning electron micrographs revealed its unique morphology with biverticillate *Penicillium*, bearing masses of oval to ellipsoidal conidia.



Penicillioopsis clavariiformis AP SEM micrographs, showing biverticillate *Penicillium* (A) and conidia (B)

Image gallery of agriculturally important insects
(<http://www.nbaii.res.in/insectpests/index.php>)

An image gallery of the agriculturally important insects has been hosted on the NBAII's website, and currently it features 500 species with over 3,000 photographs. An interactive LucID Phoenix key to 28 known genera of Mymaridae of India has been prepared with fact sheets, diagnostics and illustrations. This will serve as an important herbarium for all stakeholders.





HORTICULTURE

Fruit crops

Trait specific germplasm were collected in mango (39), grape (38), pomegranate (92), rambutan (2), mangosteen (2), pulasan (1), jamun (32) and, bael and banana (2 each).

In mango, Safed Mulgoa had maximum fruit weight (1,813 g), Narayana Sheni and Ruswani had maximum TSS (24°Brix), while Appemidi (pickle mango) had unique sap flavour. These pickle mangoes have high terpenoids and a completely different combination of monoterpenes for their typical aroma. They contain more α -Phellandrene, β -Phellandrene, α -Pinene, β -Caryophyllene and Limonene. Of the 39 unique



Cluster bearing accession

accessions of mango from Andaman and Nicobar Islands, nine were observed polyembryonic and one showed cluster-bearing. In banana, Formosona (AAA) was high-yielding and resistant to *Fusarium* wilt (race - 4), while *Maia popuolu* had unique round, plump and starchy fruits. A banana introduction (*Pisang Awak* subgroup) was dwarf and promising for annual production with 15-18 kg bunch, 80-100 fruits and high TSS (30-32°Brix).

In citrus, 212 accessions were characterized and deposited in cryobank at NBPGR, New Delhi, for long-term conservation.

Of the 232 accessions of grape screened, nine were free from berry scarring and cracking.

In jamun, CISH J-37 and CISH-J-42, were identified and registered for their high pulp and TSS content.

Plantation crops

A new collection in cashew was made and the total holding in National Cashew Field Gene Bank (NCFGB) was increased to 528. Four hundred ten germplasm accessions of coconut (132 exotic), 164 of arecanut (23 exotic) and 301 of cocoa were maintained. Ten oil palm *dura* germplasm were evaluated at Mohitnagar, West Bengal and accession CA-17 was identified for maximum number (8.2palm/year), yield (108.4 kg) and weight (13.2 kg) of bunches.

Vegetable crops

In vegetables, 428 germplasm accessions consisting of round gourd (1) from USDA and hyacinth bean (35), amaranth (33), Indian spinach (23), capsicum (81), tomato (103), brinjal (117), ridge gourd (8) and chilli (27) from AVRDC were introduced. In addition, 23 lines of teasel gourd (*Momordica subangulata* subsp. *renigera*) were collected from parts of the country.

Cucumber accession, VRCU-58, for powdery mildew resistance, ash gourd accession, VRAG-12-02, for wax-less fruits, pumpkin accession, VRPK-05-01, for ultra-small fruits and pointed gourd accession, VRPG-105, for cluster-bearing; EC-528380, VRT 101-A, VRT 102 and EC-620419 tomato lines for heat tolerance and Co-3, D-3-2, I-4-4, Kashmiriya, G-4-5, EC-528380, VRT 101-A and EC-620419 for drought tolerance; brinjal lines, CIAH-1, CIAH-2, CIAH-12, CIAH-16, CIAH-21, CIAH-22 and CIAH-67, for earliness and more yield at high temperature; ridge gourd genotypes, AHRG-29 and AHRG-41, which set fruits at high temperature during May-June; and cowpea accessions, EC 472283, EC 30590, EC 15296, and EC 390241, for drought tolerance were identified.

Okra, accession IIHR-296-22-10-11-598, IIHR-291-14-11-585, IIHR-294-1-10-1-595, IIHR-285-6-10-11-138, VROB-178 and 307-10-1, showed field resistance to yellow vein mosaic virus with a yield potential of 6.7 – 8.1 kg / 2.4 m² plot.

Cowpea, IIHR 310, recorded maximum pod yield while IIHR-317 was early (45 days) for pod maturity and accession IC 471955 showed resistance to aphid-borne mosaic virus.

In teasel gourd (*Momordica subangulata* subsp. *renigera*), considerable variability for vine pubescence (scarcely pubescent to pubescent), leaf margin (entire to dentate), leaf pubescence (sparse to dense), leaf colour (light to dark green), leaf lobing (unlobed to lobed), leaf tip (acute/acuminate/ovate/obovate), extent of marginal dentations (close to spaced), female flower bract size (minute to large), female flower bract position (near axis to just below gynoeceum), fruit blossom end rostration (faint to appreciable length) and calyx persistence (semi-persistent to persistent) was observed. However, all the accessions were uniform in the shape of stem nodal region (quadrangular) and fruit surface echination (densely echinate). A wide range of variation was observed for fruit weight (20.43–71.33g), fruit length (4.27–9.93 cm), fruit diameter (2.55–4.27cm), fruit stalk length (6.43–17.00cm), inter-node length (4.22–11.70 cm), leaf length (7.44–13.22 cm), leaf width (6.66–12.04 cm) and petiole length (2.48–7.52 cm).



Variability in teasel gourd accessions



Inventory of 2,677 accessions of cultivated types and 408 wild relatives of different vegetables was prepared and IVGRIS (Indian Vegetable Genetic Resource Information System) database developed.

A highly pungent chilli accession, IC 553688, was registered with NBPGR and 140 germplasm in cherry tomato, *Luffa cylindrica*, *Capsicum annuum*, brinjal and tomato were shared through Material Transfer Agreement.

Muskmelon varieties/genotypes evaluated for fruit fly resistance indicated that AHMM/BR-1, RM-50 and AHMM/BR-8 were highly resistant.

Tuber crops

In tuber crops, 15 cassava, 4 sweet potato, 7 greater yam, 2 *Dioscorea*, 2 tannia, one *Curcuma* sp. and 7 taro germplasm were collected. A large accession of cassava (1,923), sweet potato (1,472), yams (1,151), taro (921), elephant-foot yam (277), tannia (28), yam bean (212), Chinese potato (130) and minor tuber crops (37) were maintained in field gene bank.

The short duration triploid cassava accession was most suitable for rainfed tracts of Andhra Pradesh. A new promising clone (CMR-100) suitable for chips making was identified along with cassava mosaic disease (CMD) resistance, middle branching, uniform tuber shape (cylindrical), light yellow flesh, non-bitter and high dry matter (43%).

Sweet potato genotypes with high extractable starch (ST-10), high carotene (ST-14) and high anthocyanin (ST-13) content were registered at NBPGR, New Delhi.

Anthocyanin rich ST-13, carotene rich CIPSWA-2, and high-yielding greater yam Da-25, were recommended for release. Promising greater yam accession (Da-331) with purple flesh and high yield; tall white yam hybrid (Dr-657) with high yield, good tuber shape and better cooking quality; dwarf white yam hybrids (Drd-1068, Drd-1157) with higher yield (25 t/ha) and good culinary property were identified for release.

Medicinal and aromatic plants

Six elite germplasm, one each of Madhunashini (DGS-22-INGR 13041), kalmegh (DMAPR AP3-INGR-13042), Aloe (DMAPR AB1(INGR-13043) Ashwagandha (DWS-6-INGR-13047), and two of guggal (NRC CW2-INGR-13044 and NRC CW1-INGR-13045) were identified and registered with NBPGR, New Delhi.

In Aswagandha, eight lines with more than 8q/ha dry root yield (control 5.2 q/ha) and more than 0.3 % of total withanolides content were identified. The lines, IIHR-WS-3 and IIHR-WS-48, had more than 0.3% total withanolides up to 300 days after planting. In addition, 29 lines with higher dry root yield (15g/plant) and withanolides in F₄ generation were advanced for further evaluation.

In Jatamansi (*Nardostachys grandiflorum*), a cross-pollinated, genomic hexaploid (2n=78) was observed.

Spices

In black pepper, three unique collections, a drought tolerant type, another farmer-bred line with profuse spikes (Ponmani) and; a third one with a spike length up to 27.3 cm were added to the germplasm.

In seed spices, 208 germplasm lines comprising coriander (133), cumin (68), fennel (54), fenugreek (208 indigenous and 54 exotic), ajowain (94), nigella (12), dill (14), anise (18) and celery (36) were evaluated.

Mushroom

In mushrooms, 178 specimens comprising mainly of *Morchella*, *Auricularia*, *Lentinula*, *Pleurotus*, *Leucocoprinus* and *Isaria* genera were collected from Rajasthan, Gujarat, Maharashtra, Haryana and Himachal Pradesh. Of these, 173 were identified up to genus level and 83 cultures deposited in DMR Gene Bank.

Livestock

Phenotypic characterization and conservation of farm animal genetic resources

Mizoram cattle: The native tracts of Mizoram cattle are Champhai and Kolasib districts of Mizoram. Phenotypic characters are: cylindrical body and strong legs; varying body colour, viz. brown (85%), black (11%) and grey (44%); small dewlap and hump; small to moderate ears in length and horizontal in orientation; small and black (72%) or grey (28%) horns with



A herd of Mizoram cattle

outward, upward and then curved towards face orientation; small (5–12 cm) and funnel (78%) shaped teats; brown (54%), black (39%) and grey (7%) tail switch. The cow and bullock weigh about 169 kg and 200 kg, respectively. The daily milk yield ranges from 1.0 to 3.5 kg with the average of 1.54 kg. A pair of bullock can plough about 0.5 acre of land in 5-6 h. The age at first calving, lactation length, dry period, service period and calving interval ranges from 28 to 42 months, 150 to 210 days, 4 to 6 months, 3 to 4 months and 12 to 24 months, respectively.

Adilabad (Jhari cattle): Jhari cattle are mainly reared for draught and agricultural operations. Average body length, height at withers, chest girth, paunch girth, ear length, tail length and body weight of Jhari cows are 96.24±2.09, 102.52 ± 1.66, 133.83±3.5, 136.60 ± 3.89, 19.40 ± 0.34, 78.03 ± 2.46 cm and 181.12 ±



13.01 kg, respectively. Animals have either white coat colour (60%) or brown (40%), and are medium in size with well-developed dewlap. Horns are small to medium in size, cylindrical, sickle shaped and curved

forward. The milk yield ranges from 1.5 to 2.0 kg/day.

Malnad Gidda – Dwarf cattle (Karnataka): The Malnad Gidda, a unique dwarf cattle of Karnataka state, is registered with Accession Number INDIA_CATTLE-0800MALNADGIDDA-03037. The coat colour is mostly black with light shades of fawn on thigh and shoulder region. Cows have bowl shaped small size udder; funnel shaped teats with pointed tips. They thrive on grazing and play a unique role in farming systems of heavy rain fall in Malnad and



Elite Malnad Gidda cow with calf; Malnad Gidda Bull at NDR1 Farm (inset)

coastal regions of Karnataka. Age at first calving is around 3 years and the cow gives milk for 8-9 months. Average lactation milk yield, daily milk yield, peak yield and inter-calving period are 522.33 litre, 2.17 litre, 3.42 litre and 14.91 months, respectively. Malnad Gidda cow milk and ghee are in huge demand due to preference for usage in ayurvedic medicine. The average fat and SNF in milk are 4.18 and 8.66% respectively. The animals have a short inter-calving period of 396 days even when thriving under low input regime. The cows yield 3–4 liters of quality milk per day and are well adapted to heavy rainfall conditions.

Malkangiri goat: Malkangiri goats are medium in size and are reared for meat only. The goats are mostly light brown or black brown, however, white and black are also seen. The face has strips of white or light brown colour extending from base of ear to nose in brown goats. The top line is black. In males black ring is present around the neck. Muzzle and hooves are generally black. These goats are reared on



semi-extensive management system. The average body length, height at withers, chest girth, paunch girth, face length, horn length, ear length and tail length in adult male and female are 62.67 ± 0.99 , 65.53 ± 1.02 , 67.53 ± 0.86 , 69.47 ± 1.21 , 15.80 ± 0.22 , 11.00 ± 0.76 , 15.13 ± 0.52 , 15.27 ± 0.44 cm and 61.79 ± 0.37 , 63.20 ± 0.39 , 67.37 ± 0.51 , 70.69 ± 0.61 , 15.62 ± 0.10 , 9.64 ± 0.33 , 13.94 ± 0.24 , and 13.80 ± 0.18 cm, respectively. Female animals sexually mature at about 12-18 months of age.

Raigari goat: Raigari goats, reared mainly for meat, are medium in size. Coat colour is light brown to dark brown; mixed colour animals are also seen in flocks. White or light brown colour strips extending from base of the



ear to muzzle are present on either side of the nose line. Muzzle colour is black or brown and hooves are black or grey. The averages of body length, height at withers, chest girth, paunch girth, face length, horn length, ear length, and tail length are 60.87 ± 0.53 , 61.35 ± 0.44 , 65.85 ± 0.62 , 70.06 ± 0.85 , 15.34 ± 0.17 , 9.38 ± 0.39 , 13.62 ± 0.18 , 12.66 ± 0.18 cm respectively, in females and 61.71 ± 1.43 , 63.43 ± 1.49 , 65.14 ± 2.10 , 67.14 ± 2.43 , 15.43 ± 0.78 , 10.57 ± 1.29 , 14.71 ± 0.42 , and 13.57 ± 0.69 cm, respectively in males. The average age at sexual maturity and first kidding are 10–12 months and 15–18 months, respectively. Marginal and small farmers and landless tribes of Raigarh district, Odisha rear them.

Narayanpatna goat: Narayanpatna goats of Narayanpatna taluk, Koraput, Odisha, are medium in size and reared by tribals (Kondhs) for meat purpose. Animals are mostly brown-black, however, brown, off white



and even mixed colour animals are also seen. The average body length, height at withers, chest girth, paunch girth, face length, horn length, ear length and tail length in adult male are 74.40 ± 2.77 , 69.60 ± 3.71 , 70.60 ± 4.39 , 71.40 ± 4.07 , 16.00 ± 1.05 , 9.60 ± 2.38 , 15.20 ± 0.86 , 16.20 ± 0.37 cm, respectively, and in female 68.47 ± 0.56 , 65.63 ± 0.57 , 70.86 ± 0.60 , 73.14 ± 0.73 , 16.34 ± 0.12 , 11.49 ± 0.46 , 13.96 ± 0.24 , and 13.96 ± 0.22 cm, respectively. The average body weights of adult female and male animals were 27.33 ± 0.61 and 32.80 ± 6.82 kg, respectively. Female animals attain sexual maturity at about 12-15 months of age.

Sindhi donkey: Sindhi donkeys are reared in Barmer and Jaisalmer districts of Rajasthan. Sindhi donkeys are able to carry about 100 kg of load in sandy tracts. The animals are of small size with lean built. Predominant coat colour is light brown, however, small



percentage of animals have brown and grey. The belly, inner surfaces of legs, ventral side of neck and inner sides of ears are generally white and mane is comparatively dark. The body length varies from 82 to 105 cm. The height at withers of male and female animals is 98.8 ± 3.9 and 97.93 ± 4.9 cm, respectively. The chest girth is 104.3 ± 5.35 in males and 106.52 ± 5.97 cm in females. The estimated weights of adult (above 3 years) male and female animals are 84.95 ± 10.12 and 89.54 ± 14.57 kg, respectively.



Geographically distinct donkeys: Systematic and scientific evaluation of donkeys was carried out for better utilization and improvement in health and reproduction efficiency. Fifteen biometric indices of donkeys from Leh area (Ladakh, Jammu and Kashmir) and Baramati area, Pune, Maharashtra were recorded. Coat colour of most of the donkeys at Baramati was grey, both light and dark with and without dark strip on back. Large white donkeys are mostly brought from Gujarat, but in Leh animals are bay black. Both Indian populations were found smaller than Poitu donkeys. Donkeys of Baramati area were significantly taller and bigger in size than donkeys of Leh area.



Donkeys from Baramati, Maharashtra (above); Leh (left) and Spiti (right)

Frieswal cattle: Coat colour is >75% black and <25% white in 43.75% of animals; 50-75% black and rest white in 28.52% of animals, and completely black with 1-2 small white spots in 15.63% of animals. Presence of white star (65%) on forehead and white patch on at least one fetlock (66.8%) are also among important features of Frieswal. Hoof colour is either black, creamy or black stripe over creamy base. The average heart girth, rear girth, height at withers, scrotal circumference, paired testicular volume and area of

pelvic triangle are 168.82 cm, 164.28 cm, 124.69 cm, 30.12 cm, 444.97 cm^3 and 324.88 cm^2 respectively.

In-situ conservation: A total of 451 Kilakarsal progenies of sheep were produced during 2012-13 at Tirunelvalli Station of TANUVAS. The tugging and lambing percentage at farm was 81.48 and 80.24, respectively. Inseminations (10,228) were performed for conservation of Krishna Valley cattle under the project operational in 25 cattle development centers of Department of Animal Husbandry, Karnataka. So far, 725 males and 627 females were born from 2,777 pregnancies.

Ex-situ conservation: Frozen semen doses from 19 bulls of 10 cattle breeds (Red Sindhi, Tharparkar, Sahiwal, Amritmahal, Dangi, Hallikar, Red Kandhari, Gangatiri, Frieswal, Khilar) and three bulls of Banni buffalo breed were added (14,150) to the gene bank repository of National Bureau of Animal Genetic Resources during the year 2012-13.

Molecular genetic characterization

The real time qPCR analysis revealed the up-regulation of CatSper1 gene in poorly motile sperm as compared to those with good motility of crossbred bulls. A whole-genome (Black Bengal breed, male, 2.8 GB, 30X) was sequenced and assembled. Knockdown of myostatin gene using siRNA and shRNA in caprine fetal myoblast was demonstrated in goats.

Spiti donkey: Evaluation of Spiti donkeys distributed in Spiti and Yangthang regions of Himachal Pradesh was done for within breed genetic diversity and genetic bottlenecks. The allele number and heterozygosity values observed across the studied loci indicated presence of reasonably high levels of genetic variability in Spiti donkeys. The polymorphic information contents (PIC) ranged from 0.51 to 0.79 with mean value of 0.68 ± 0.09 . The mean genetic diversity estimate (F_{IS}) was 0.048 indicating moderate levels of inbreeding. The normal 'L' shaped distribution of allelic frequency strongly indicated absence of any recent genetic bottlenecks in the Spiti donkeys.

Genetic relationship of Indian native cattle: Individuals (23), adapted to different agro-climatic regions, representing seven native cattle breeds viz. Amritmahal, Gir, Ongole, Red Kandhari, Sahiwal, Tharparkar, Leh cattle, and two exotic breeds, viz. Holstein and Jersey cattle were genotyped. The native cattle from Leh region were genetically distinct from the rest of the Indian cattle. This is the first study to assess population structure of Indian native cattle breeds using the high density SNP chip, and supports the genetic distinctness of zebu from taurine cattle.

Differential heat shock response: The quantification of different members of heat shock protein family, viz. *HSP27*, *HSP60*, and *HSP70* was achieved to understand the magnitude of transcriptional response of heat stressed peripheral blood mononuclear cells (PBMC) in Holstein, Sahiwal cows and Murrah buffaloes. Comparatively at 2h time point, *HSP70* peak was highest in buffaloes (~73.0 fold) followed by



Holstein (~65.0 fold) and Sahiwal (~54.0 fold). Similarly, *HSP60* and *HSP27* transcripts were maximally induced in buffalo at this time point. The higher abundance of *HSP* mRNA after heat stress showed evidence of transcriptional differences in PBMCs of different cattle types and buffaloes suggesting their differential cellular tolerance to heat stress.

Polymorphism and evolution of toll like receptors: Sequence characterization and genotyping of eight Toll like receptor (TLR 1,2,4,5,6,8,9 and 10) genes was undertaken in Indian native cattle breeds (*Bos indicus*) to identify novel single nucleotide polymorphisms (SNPs). Kankrej, Hariana and Gir cattle were found to have the highest number of SNPs and the Kangayam was the least polymorphic among the analysed indigenous cattle breeds. Comparison of protein domain architecture for different TLR gene clusters of Indian native cattle with other mammalian species revealed conserved regions in the TLR. The study brought out diversity within Indian cattle as well as the divergence from the taurine counterpart.

Nucleotide diversity in candidate genes for mutton quality traits: Indian sheep breeds namely, Bandur, Chokla, Deccani, Ganjam, Garole, Madgyal, Magra, Malpura, Muzzafarnagri and Nali were analyzed for genetic polymorphism at the growth differentiation factor 8 (*GDF8*), β 3 adrenergic receptor (*ADRB3*) and calpain (*CAPN*) gene. The analysis of the edited sequences of *GDF8* gene loci revealed an absence of SNPs in the exon 3 region. Three SNPs were identified in non-coding regions of *GDF8* gene in Indian sheep, out of which -16C>T was not reported earlier. Two SNPs identified in the Indian sheep are known to be associated with mutton quality and carcass traits in exotic sheep. The initial results showed genetic variability and presence of favourable alleles/SNPs in the *GDF8* gene. The sequence analysis of *ADRB3* gene revealed two synonymous SNPs in the exonic region (g.333C>T and g.497G>C). One SNP was detected in the 3'UTR (g.2621T>C), however, no SNP was detected in 5'UTR. The identified SNPs were present in the heterozygous state. A single C>T transversion in heterozygous state was detected in the intron 5 of ovine *CAPN* gene. The frequency of C and T alleles was 0.564 and 0.436 respectively.

BL41 microsatellite markers in Frieswal cattle: BL41, an autosomal microsatellite marker, located at the region of bovine chromosome 3 (BTA3), is well known for its lactogenic trait QTL property. Genotyping of the BL41 revealed that Frieswal cow genome has seven allelic pattern of BL41 microsatellite markers of which 245 bp allele is the most frequently distributed. A higher level of fat (4.45±0.05) and protein (3.09±0.09) percentages were observed among Frieswal cows, which had 238 and 234 allele of BL41 microsatellite marker respectively.

Novel SNPs in exon 2 and exon 3 of Leptin gene: Leptin affects tissue and endocrine system of the animal and influences production, reproduction and nutritional

traits. Unique SNPs in the leptin and its receptor gene were identified and its association with milk yield and milk constituents were also worked out. The synergistic effect of SNPs in exon 2, intron 2 and exon 3 (w1/m2/m3+ mA/mB) combination showed significant association with milk protein percentage.

Expression of interferon-gamma gene: Interferon-gamma gene of dromedary was cloned at EcoRI and NotI sites of bacterial expression vector-pET 32 (a) and the recombinant plasmid obtained was named as pETCAMELGAM. It was expressed as a fusion protein of 38kDa size.

Camelpox virus: The complete nucleotide sequences of epidermal growth factor (EGF) encoding gene of camelpox virus (CMLV) from India has the size of 418 bp, and in this there is an addition of one cytosine residue at position 132. The resultant protein is a truncated polypeptide due to this mutation. The complete amino acid sequences of golgi anti apoptotic protein (GAAP) encoding gene and its relation to GAAP gene of other orthopox viruses indicated that it was 714 bp in length, encoding 237 amino acids.

Heat shock protein 70 encoding gene: The gene sequences of heat shock protein 70 encoding gene (HSP A1B) of dromedary camel were amplified from the total cellular RNA isolated from blood. The open reading frame of *HSP 70* gene of Indian dromedary camel is 1926 bp and encodes a polypeptide of 641 amino acids.

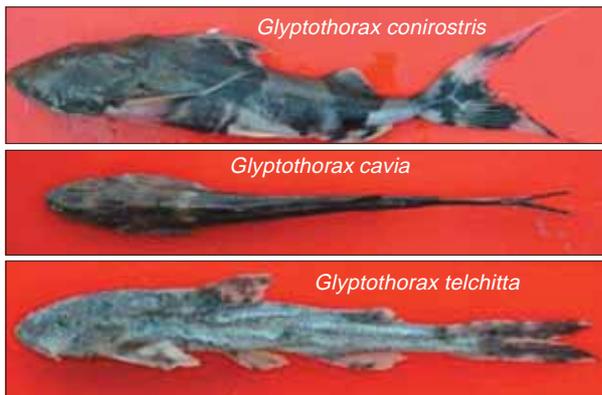
Gut metagenomes of camel: Based on Ribosomal Database Project, in the adults and camel calves, abundant hits were for the firmicutes followed by bacteroidetes, verrucomicrobia and proteobacteria. The genera mainly found in adult camels were *Bacteroides*, *Clostridium*, *Bacillus*, *Eubacterium*, *Ruminococcus* while camel calves had *Clostridium*, *Ruminococcus*, *Eubacterium*, *Treponema* and *Bacteroides*. The functional hierarchies in adult camels clustering based subsystems followed by carbohydrates, virulence, disease and defence showed more than 10% abundance whereas in camel calves DNA metabolism, RNA metabolism, metabolism of aromatic amino-acids, clustering based systems showed more than 10 % abundance.

Microsatellite characterization of mithun - first report: Thirty bovine microsatellite markers from FAO list of measurement of domestic animal biodiversity (MoDAD) were tested in mithuns and gaurs individually. Nineteen markers (63%) successfully amplified mithun and wild gaur genomic DNA. However, 14 out of 19 markers (74%) were highly polymorphic with high polymorphic information content (PIC) value (> 0.50) in mithun and gaur with allele numbers ranging from 10 to 26 in mithun and 2 to 7 in gaur, respectively. Inbreeding coefficient was 30 and 6.53% in mithun and gaur population, respectively. The present study will help in developing a suitable breeding policy for mithun.

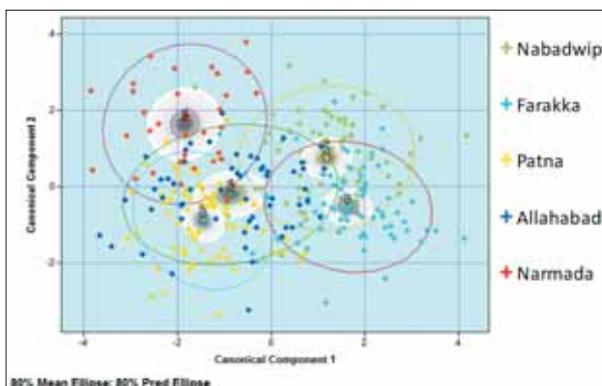


Fisheries

New biogeographically distribution of sisorid catfish: Genus *Glyptothorax*, sisorid catfishes, having 37 species, are widely distributed in India along fast flowing mountain streams and are benthic in habitat. The NBFGR collected, *Glyptothorax conirostris*, *G. telchitta* and *G. cavia* in the Ganga river basin which is a new distribution record. *G. conirostris* was collected from the Ganga canal at Roorki, and *G. cavia* and *G. telchitta* from upstream of river Gomti. Present report may be considered as the first evidence of a broader distributional range of *Glyptothorax* genus, indicating that the species may be more widely distributed than previously acknowledged.



Stock characterization of Indian major carps : Morphological differentiation in Indian major carps from different Indian rivers using truss morphometry showed that population of *Catla catla* in Ganga at lower stretch (Nabadwip and Farakka) was different from that of upper stretch (Patna-Allahabad) and Narmada, while *Labeo rohita* and *Cirrhinus mrigala* showed no such difference. Analysis of molecular variance (AMOVA) of PCR amplified partial cytochrome b (307bp) gene sequence from *L. rohita* (n=133) collected from Allahabad, Patna, Farakka, Nabadwip, Guwahati, Bharuch revealed that 92.16% of the total variation in the species was attributed to variation within population and 7.84% to differentiation among populations and population structuring. In *C. catla* (n=87) 69.93% variation was attributed to variation



Bi-plot of scores corresponding to two canonical variates expressing morphological difference in *C. catla* in lower Ganga and Narmada

within populations and 30.07% to variation among populations and population structuring. AMOVA within four populations (Guwahati, Allahabad, Farakka and Bharuch) of *C. mrigala* (n=89) revealed that 96.45% of total variation was attributed to variation within populations and 3.55% to variation among populations and population structuring.

Genetic characterization

Whole mitochondrial genomes of Indian fish species: The whole mitochondrial genomes of *Channa marulius*, the great snakehead (NCBI accession no. KF420268), *Clarias batrachus*, walking catfish (accession no. KC572134) and *Pangasius pangasius*, yellow fin catfish (accession no. KC572135) were sequenced. Two ornamental barbs, viz. *Puntius denisonii* and *P. chalakkudiensis* endemic to the Western Ghats were found to have mtDNA size 16899 bp and 16989bp, showing a difference of 90bp mainly in control region. The fish mitogenome is small, circular and haploid DNA molecule, which is maternally inherited. The size of mitochondrial genome in animals ranges from 15–20 kilobases and approximately 15–17 kb in fish. Structural composition comprises 37 genes, 13 protein coding, 22 tRNA and 2 ribosomal RNAs (*12S rRNA* and *16S rRNA*). The concatenated protein coding genes have comparatively high potential to resolve phylogenetic pattern.

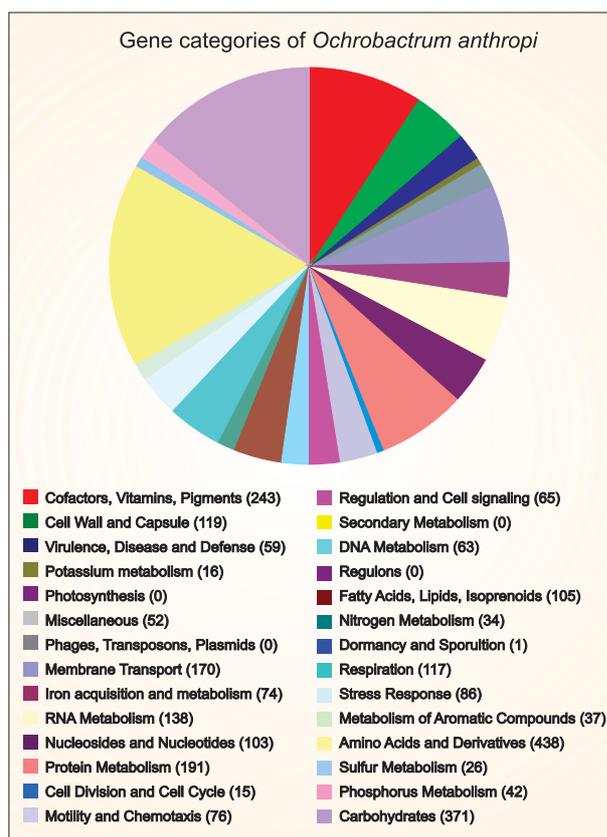
Mitochondrial genome organization of coldwater fish: The complete mitochondrial genomes of *Schizothorax richardsonii* and *Tor putitora* were sequenced for the first time. The mitochondrial genome of *S. richardsonii* and *Tor putitora* was found to be 16,592 bp (Accession number KC790369) and 16,576 bp (Accession number KC914620) respectively in length and both consist of 13 protein coding genes, 22 tRNAs, 2rRNA genes and one putative control region. Gene organization and its order are similar to other vertebrates. The present study will provide the rationale for the management and conservation of snow trout and mahseer species.

Microarray chip to identify genes against WSSV infection

To identify differentially expressed genes against WSSV infection, a challenge experiment (using $2.62 \times 10^6/\mu\text{l}$ viral copies) was carried out. Agilent microarray slide was custom designed for tiger shrimp gene expression studies, using the NCBI EST and nucleotide database. In addition, the microarray chip contained *P. monodon* gene sequences. A total of 42,013 sequences were used in the microarray chip to identify differentially expressed genes against WSSV infection.

Whole genome sequence of phenol degrading bacterium

The bacterium *Ochrobactrum anthropi* was isolated from polluted river and examined for its phenol and chlorophenol degradation. To examine all potential beneficial and harmful properties of the bacterium intended for bioremediation application in polluted environments, the whole genome of the bacterium was



sequenced. Genome analysis identified presence of genes involved in detoxification of formaldehyde, salicylate ester, toluene, quinate, benzoate, p-Hydroxybenzoate, chloroaromatic compounds and N-heterocyclic aromatic compounds, catechol branch of beta-ketoadipate pathway, salicylate and gentisate catabolism, protocatechuate branch of beta-ketoadipate pathway, aromatic amine catabolism, thioredoxin-disulfide reductase, alkanesulfonates utilization, and alkylphosphonate utilization, without presence of any important pathogenicity or virulence gene making it a potential candidate in pollutant degradation in field condition.

Testicular gene expression in Indian white shrimp:

Genes influencing testicular development in *Fenneropenaeus indicus* were studied and specific primers for genes functionally related to testicular development, were examined by semi-quantitative RT-PCR using *EF1- α* as the internal control. *MIPP2*, *Dmc1*, *TST1* and *IAG* exhibited male specific expression while *HSP90* exhibited higher expression levels in females compared to males. Semi-quantitative RT-PCR analysis revealed weak expressions of male specific reproductive genes (*TST1*, *MIPP2* and *Dmc1*) in ablated group compared to control.

