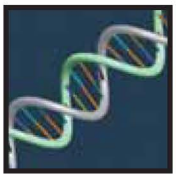


5.

Genetic Resources

Wide array of plant genetic resources with useful traits are deployed in different taxa to develop crop varieties that meet emerging environmental and biotic challenges.

Crops

Germplasm augmentation, conservation and use: Thirty explorations were undertaken, and 1,591 accessions, including 620 of wild species, were collected. About 334 herbarium specimens have been added to the National Herbarium of Cultivated Plants. Germplasm accessions added to the National Gene bank for long-term storage comprised 8,857 of orthodox seed species; 15 of non-orthodox species for cryopreservation and 18 for *in-vitro* storage.

A total of 40,879 accessions were imported from 38 countries, including international trial material. Promising introductions are – wheat genetic stocks, resistant to different rusts and powdery mildews (EC 799617-754), from Mexico; rice tolerant to lodging (EC 791959-70), shattering (EC 791930-44), heat (EC 792176-284) and blast (EC 803403-40) from the Philippines; maize showing resistance to maize streak virus, *Turcicum* leaf blight, common rust and grey leaf spot with excellent combining ability (EC 803523-40) from Mexico; bottlegourd resistant to powdery mildew, *Fusarium* wilt and anthracnose (EC 800995-8) from the USA; tomato resistant to tomato yellow leaf curl virus, bacterial wilt and *Fusarium* wilt (EC 798219-20) from Taiwan; muskmelon resistant to powdery mildew, *Fusarium* wilt, anthracnose (EC 802405-15) from the USA; watermelon resistant to bud necrosis virus (EC 800999-1022) from the USA; and wild papaya with resistance gene to *papaya ring spot virus* (EC 815412, 816070-71) from Australia. About 24,824 accessions were characterized and evaluated, including wheat for terminal heat tolerance, and rice tolerant to submergence and drought.

In rice, out of 1,250 genotypes, 53 were moderately resistant to sheath blight; of 1,670 lines, two were found resistant to brown spot and of 1,685 lines, 118 were resistant to bacterial leaf blight. Brown planthopper (BPH) resistance was confirmed in nine farmers' varieties, one CRRI (CR 3006-8-2), 14 IRRI lines and two wild accessions of *Oryza rufipogan* (AC 100174, AC 100444). Among 14 BPH resistant genotypes, nine genotypes, SSTL No. 142, 227, 317, 395, 405, 490, 609, 680 and 691, scored 1. Against yellow stem borer, among the 60 CRRI accessions, AC 42494, AC 42499, AC 42513 and AC 42532 had damage score of 2 at the vegetative stage, while wild rice genotypes, ZA/BCP 17, ZA/BCP 18, ZA/BCP 27, PM 117, PM 125, recorded stem borer damage score of 1 at the reproductive stage. Out of 150 rice breeding lines, C 226-9-2-1-1, C 226-10-3-2-1, C 226-11-4-1-1 and C 226-13-12-1-2, had no white ear-head (WEH) formation with a damage score of 0, while C 226-11-3-1-2 registered highest WEH incidence (54.3%), followed by C 226-12-4-1-1 (50%).

Indian mustard (*Brassica juncea*) genotypes, NPJ 182, TM 101, RH 1089, Pusa mustard 25 and BPR 540-6, based on the low seedling mortality (< 20%), have been rated as thermo-tolerant, while, BPR 349-9 and DRMR 541-44 have been identified for low light stress tolerance. Genotypes DRMR 1153-12, RGN 348, MCP 802, NPJ 182, DRMR 10-40 and NPJ 183 are found suitable for drought tolerance. RH 1230 and RH 1235 of Indian mustard and PPBN 2 and PPBN 3 of *Brassica napus* have been found resistant to white rust.

Vigna konkanensis, a new species described from Konkan Region, Maharashtra (*left*); Extra-long staple cotton (*Gossypium barbadense*), collected from backyard cultivation in Manipur (*middle*); Variability in fingermillet (*Eleusine coracana*), collected from Kandhamal, Odisha (*right*)

Groundnut advanced breeding lines, PBS 16038, PBS 11077, PBS 16023 and PBS 30055, showed moderate tolerance to drought, and PBS 12032 has been identified as resistant to leaf spot. Groundnut lines identified in Valencia mini core germplasm for high shelling (>70%) are NRCG 14379, NRCG 14335 and NRCG 14497; and for low oil content (47%) is NRCG 14444, and for high protein content (32.4%) is NRCG 14445. In Spanish germplasm lines, highest shelling outturn line is NRCG 14324 (74.6%), and of shortest duration is NRCG 14425 (109 days).The accession NRCG 12447, having low oil content (44.6%) coupled with high protein (34.8%), and another accession NRCG 10580 with high oil content (52.15%) coupled with low protein (26.9%), have been identified as donors for breeding confectionery groundnut types.

Out of 118 castor germplasm accessions collected from Rajasthan, RG 386 (IC 432910), RG 1624 (IC 373981) and RG 2787 (IC 374338/IC 346591) were confirmed for wilt resistance (0–10% wilt incidence) through root-dip inoculation technique. In linseed, trait-specific germplasm lines identified include three lines (CI 1924, ES 13239, GS 105) for higher root length (25–30 cm) and root volume, fifteen suitable for high temperature (45°C) at the seedling stage, one (EC 704) for rainfed and *utera* situation, and two (Kangra local, Mayurbhanj local) as the source of multiple disease resistance in natural fields.

A total of 10,295 accessions of pulse crops including chickpea (4,000), lentil (3,000), mungbean (570), urdbean (340), pigeonpea (1,000), lathyrus (450), rajmash (65) and fieldpea (870) are being maintained. For breeding programmes, 120 wild accessions of six *Cicer* species, 97 of 23 *Vigna* species, 364 of six *Lens* species and 50 of 12 wild relatives of pigeonpea as well as 118 Mediterranean landraces of lentil have been characterized. In sugarcane, two recently introduced CP clones (CPCL 4111 and CP 03-1912) and two Co canes (Co 12015, Co 13010) have been added to the collection. Seventeen accessions of *Saccharum edule* have been characterized for agro-morphological traits, including yield of inflorescence.

Germplasm registration

For germplasm registration, following proposals of cereals and millets (9), grain-legumes (4), vegetables (5), fruits (9), oilseeds (5), fibres (3), spices (2), medicinal and aromatic plants (1) and commercial crops (11) have been approved. Seventeen notified varieties of groundnut which are in the seed-chain have been registered as the 'extant notified' under the PPV & FRA.

Important registered germplasm of crop-plants

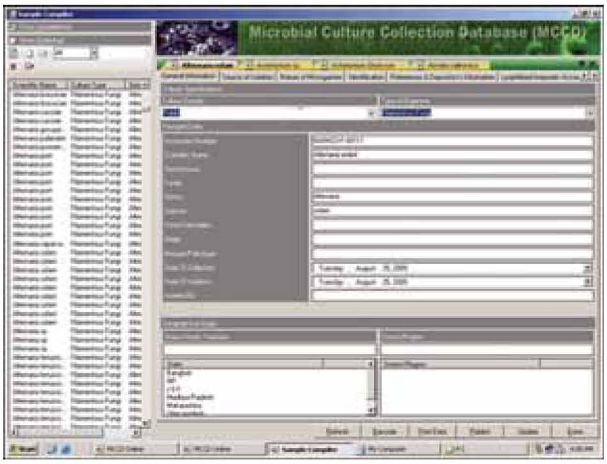
Crop	National identity	INGR No.	Unique features
Blackgram	IC 0144901	14056	Resistant to *mungbean yellow Mosaic virus* (MYMV), causing yellow mosaic disease
Castor	IC 0598621	14003	Pistillate line with unique morphotype of flowers and stem colour, and with the zero bloom hermaphrodite flower at the tip
Castor	IC 0346622	14004	Resistant to wilt (*Fusarium oxysporum* f.sp.*ricini*)
Castor	IC 0346626	14028	Resistant to root-rot (*Macrophomina phaseolina* Tassi (Goid))
Chickpea	IC 0598237	14001	Wilt resistant
Chilli	IC 0436231	14040	Purple phenotype as a morphological marker
Chilli	IC 0570408	14041	Immune to anthracnose, caused by *Colletotrichum capsici*
China-aster	IC 0610420	14048	Early flowering. More number of flowers/plant
China-aster	IC 0610421	14049	Early flowering. Higher number of flowers/plant
China-aster	IC 0610422	14050	Flower colour: Violet (83.A). Flower type: Pompon
China-aster	IC 0610423	14051	Flower colour: Creamy-white. Flower type: Powderpuff. Resistant to root-knot nematode (*Meloidogyne incognita* race 1)
Cotton	IC 0597395	14005	Inter-racial pigmented *arboreum*
Cotton	IC 0597397	14058	Cluster boll-bearing habit, deeply palmate leaf-lobe
Cotton	IC 0597398	14059	Cluster boll-bearing habit, zero monopodia and compact habit
Fingermillet	IC 0598201	14015	Partial sterile, useful in hybridization, and easy for maintenance
Garlic	IC 0596521	14009	Early, suitable for cultivation in *kharif*, ready for harvest within 72–77 days; in *rabi*, matures in only 85–95 days
Gladiolus	IC 611879	14052	Early blooming, flowers 76–80 days after planting and florets are red (41 C, RHS colour chart) with dark-red stripes on the inner two tepals (42A, RHS colour chart), and also red spots on the outer throat. Spike length is 93 cm and is with more than 16 florets. At a time 5–6 florets remain open on the spike. Each mother corm produces more than two corms

Crop	National identity	INGR No.	Unique features
Gladiolus	IC 611878	14053	Very early in flowering (74 days after planting) and florets are red (50C, RHS colour charts). Two red spots are noticed on the two central tepals. Number of florets is 18.44, and spike length is more than 100 cm. Each mother corm produces more than two corms
Guava	IC 0395191	14022	Medium-sized fruits, white coloured pulp, high TSS, good keeping quality and is soft
Guava	IC 0395190	14023	Medium-sized fruits, white coloured pulp, high TSS, good keeping quality and is with high pectin
Guava	IC 0395219	14024	Medium-sized fruits, pink coloured pulp, high TSS, and has good keeping quality
Isabgol	IC 0598208	14010	Golden-yellow coloured leaf mutant
Maize	IC 0594368	14012	Early maturing quality protein maize (QPM)
Maize	IC 0594269	14013	Medium maturity QPM
Maize	IC 0594373	14014	Resistant to pink-borer
Makhana	IC 0610820	14054	White flower mutant
Mango	IC 0391661	14017	Medium-sized fruits, yellow coloured fibreless pulp, good sugar: acid blend, good keeping quality for processing, and fruits have excellent red blush on the skin
Mango	IC 0391736	14018	Dwarf tree, produces medium-sized fruits with deep-yellow coloured pulp, high TSS, and with good keeping quality
Mango	IC 0391715	14019	Dwarf tree, produces medium-sized fruits with yellow coloured pulp of high TSS, has good keeping quality, and fruits have attractive red blush all-over
Mango	IC 0391622	14020	Dwarf tree, medium-sized round shaped fruits, yellow coloured fibreless pulp, and fruits are sweet to taste
Mango	IC 0391747	14021	Dwarf tree, produces medium-sized round shaped fruits with yellow pulp
Muskmelon	IC 0599709	14043	Monoecious sex form
Nutmeg	IC 0537218	14039	Bold nut and has high sabinene and myrecene content
Onion	IC 0598327	14057	Very early in maturity (harvested within 90 days after transplanting during *rabi*) Unique genotype for earliness and 100% uniform neck-fall
Papaya	IC 0599272	14016	*Papaya ring spot virus* (PRSV) tolerant
Pea	IC 0208366	14007	Resistant to four isolates of powdery mildew(*Erysiphe pisi*)—*rangway, trilkinath, stingri, kangra*
Pea	IC 0208378	14008	Resistant to four isolates of powdery mildew (*Erysiphe pisi*)—*rangway, trilkinath, stingri, kangra*
Physic nut	IC 0598611	14006	High yield, early flowering (125 days) with high oil content (38.01%)
Rice	IC 0575277	14025	Elongation ability of shoot
Rice	IC 0575273	14026	Submergence tolerant (20 days)
Rice	IC 0599689	14055	Tolerant (SES score 3) to salinity stress (EC=12 dS/m) at the seedling stage
Safflower	IC 013884	14002	Resistant to *Fusarium* wilt (*Fusarium* f. sp. *carthami*)
Sugarcane	IC 0598475	14011	An early maturing, red- rot resistant sugarcane clone with high sugar content of 18.36% as compared to 16.81% of Co C 671 at the eighth month stage
Tea	IC 0610184	14029	Very high Darjeeling flavour (147:100)
Tea	IC 0610185	14030	High Darjeeling flavour (141:100)
Tea	IC 0610186	14031	Unique Darjeeling flavour (138:100)
Tea	IC 0610187	14032	High flavour index (134:100) with high pubescence and spreading and dense frame
Tea	IC 0610188	14033	High Darjeeling flavour (131:100)

Crop	National identity	INGR No.	Unique features
Tea	IC 0610189	14034	High Darjeeling flavour (129:100) and early flusher
Tea	IC 0610190	14035	Good flavour Darjeeling clone (128:100) with high geranial content (20.74)
Tea	IC 0610191	14036	High Darjeeling flavour (121:100). Suitable for mid and low elevations
Tea	IC 0610192	14037	Good Darjeeling flavour (117:100)
Tea	IC 0610193	14038	Darjeeling flavour above average (110:100)
Tea	IC 0610194	14044	With thick cuticle
Tea	IC 0610195	14045	Thickest epidermal cell layer
Tea	IC 0610203	14046	Highest number of stomata per square mm
Tea	IC 0610207	14047	Rose- like-sweet aroma producing cultivar. Synthesizes highest hexanol and 1–2 hexanol
Wheat	IC 0599612	14027	Resistant to foot-rot
Wheat	IC 0611303	14042	Resistant to leaf rust

Agriculturally important microoganisms

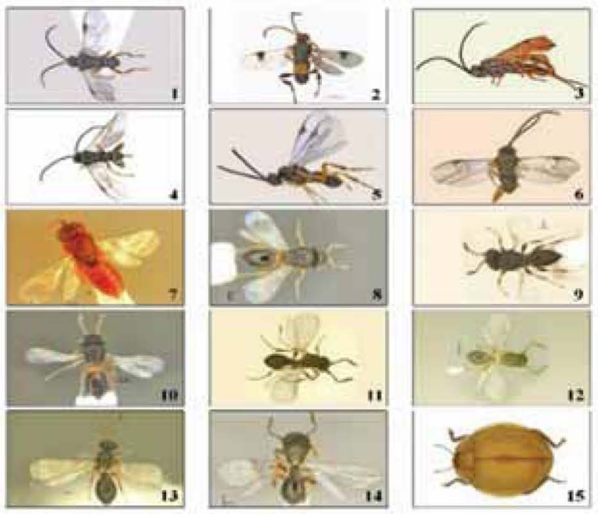
National Microbial Culture Collection: A software, 'Microbial Culture Collection Database (MCCD)', has been developed to enlist characteristics of microbes in terms of origin, ecology, morphology, physiology and biochemical parameters, pathogenic or non-pathogenic ones; molecular tools have been used for characterization of agriculturally important microorganisms.



Agriculturally important insects

Insect exploration and biosystematics: Surveys were conducted for collection of insects of agricultural importance. New species of parasitic hymenoptera (Platygastridae, Braconidae, Encyrtidae) and a predaceous coccinellid (Coleoptera: Coccinellidae) were described.

A new web portal 'Indian fauna of Pteromalidae' and a new web-based identification guide to the Indian genera of Mymaridae with illustrated factsheets were hosted on the National Bureau of Agricultural Insect Resources (NBAIR) website. Factsheets for 323 species of insect-pests (with 1,060 images) and 105 species of bioagents were uploaded on the NBAIR's website.



New species of insects described from India
Hymenoptera
A. Braconidae 1. *Glyptapanteles clonisae*, 2. *Buluka horni*, 3. *Microplitis murkyi*, 4. *Dolichogenidea c*, 5. *Glyptopanteles trilochae*, 6. *Parapanteles echeriae;* **B. Platygastridae** 7. *Mantibaribarta kerouaci*, 8. *Allotropa gundlupetensis*, 9. *Allotropa nigra*, 10. *Allotropa vanajae*, 11. *Amblyaspis fabrei*, 12. *Amblyaspis panhalensis*, 13. *Amblyaspis charvakae*, 14. *Ambhyaspis ashineadi*
Coleoptera
C. Coccinellidae 15. *Calvia albida*,

Barcodes using primers specific to cytochrome oxidase (CO1) were developed for over 500 insects and arachnids belonging to nine Orders (Hemiptera, Diptera, Lepidoptera, Coleoptera, Hymenoptera, Mantodea, Isoptera, Araneae and Ixodida). Fifteen new agriculturally important species of insects have been reported and described.

Bt-cry gene diversity in hot and humid regions

The dipteran toxic genes—*cry2A*, *cry17A*, *cry4A* and *cry44Ba*—were identified through PCR analysis. The gene sequence 2.37 kbVip3A (lepidopteran specific gene) and 3.686 kb*cry1Ac* (lepidopteran specific gene) was generated and sub-cloned into *Escherichia coli* expression system. Bioassay of coleopteran specific *Bt* against *Sitophilus oryzae* showed that the isolate *Bt*AN4 was on a par with the standard.

Barcoding of sugarcane insect-pests: DNA barcodes have been generated for following pest species of sugarcane — *Chilo infuscatellus, Scirpophaga excerptalis, Melanaphis sacchari, Aleurolobus barodensis, Neomaskellia bergii, Kiritshenkella sacchari, Sesamia inferens* and *Tertaneura javensis* and submitted in the GenBank with accession numbers KF986269-KF986271, KJ013410-KJ013412 and KM453721-KM453723

Horticulture

Fruit crops

Two indigenous mango cultivars, PRVRRN 3 (P. Reddyvaripalli V. Ramamoorthy Reddy Naati 3) and TMRM (Thumbavaripalle Munirathnam Reddy Manoranjitham), having high total carotenoids (>26 mg/100 g), were collected from Chittoor, Andhra Pradesh and are being propagated through grafting. *Mangifera camptosperma,* a related species from Andamans, was grafted on *M. indica* and first fruits were observed.


Wild accessions of *Mangifera griffithi* and *M. andamanica* are very promising

Collection of *M. griffithi* and *M. andamanica*, two salt tolerant *M. indica* accessions, from tsunami affected sites along with 42 other mango accessions from Andaman and Nicobar islands, 4 species of papaya, 36 accessions of jamun, 138 accessions of pomegranate and 14 accessions of guava were significant. Farlang, a new guava variety, was introduced from Thailand. The *Flacourtia montana* (Mountain sweet thorn), a potential fruit crop, was collected and planted in the field gene bank at Bengaluru. A large fruited (18.9 kg) jackfruit clone with coppery red flakes, high TSS (24°Brix) and flake: fruit ratio of 0.48 was added to the gene pool. Similarly, promising rambutan collections, CHESR-I-2, CHESX-9, CHES-XI-11, CHESR-XIV and CHES-XIV-11, were evaluated for fruit weight and yield.

To address the narrow genetic diversity in pomegranate, 132 trait-specific accessions from United States Department of Agriculture (USDA) were introduced. After quarantine, they were planted in the field and observations were recorded for traits such as plant height, growth and nodal blight resistance.

To protect, conserve, characterize and utilize precious mango germplasm of east India, a field gene bank was established at the State Horticulture Farm, Denkanal, Odisha. This is first of its kind in which a state and central organization have shown commitment for *ex situ* conservation of endangered mango accessions.

More than 200 pomegranate accessions representing both indigenous and exotic origin were established at Solapur, Maharashtra and promising accessions evaluated for processing. The accessions differed significantly for rind (26.67–41.30%), pomace (19.11-17.43%), juice (37.20–50.18%), TSS (14.44–17.63°Brix) and acidity (0.32–5.14%). Tabesta, Jyoti, China Orange, Saharanpur, Kabuli Yellow, P 13, P 16, G 137, KRS, Kandhari, IC 318762, IC 318734 and Ganesh recorded 44–50% juice. Significantly, highest TSS (17.63°Brix) and acidity (5.15%) were recorded in IC 318705 and IC 318706, respectively.

Thirteen unique trait-specific grape accessions were added to the existing germplasm at Pune. Evaluation of genotypes for loose bunch, bold berries, resistance to powdery mildew, cracking, suitability for raisin and juice was carried out. Seven accessions with a berry diameter of 18–20 mm were identified. Eight juice varieties were ranked based on organoleptic score and 2 varieties, Arka Shyam and Medika, were the most acceptable. Two Thompson Seedless mutant vines from the farmers' field were selected for bold berries.

Date palm accessions (7), ber (*Ziziphus mauritiana*) (3), wood apple (*Limonia acidissima*), khirni (*Mimusops hexandra*) and jamun (*Syzygium cumini*) (1 each), mulberry (*Moris nigra*) (5) and bael (*Aegle marmelos*) (31) were collected and conserved at Godhra, Gujarat. A number of underutilized genotypes of jamun (26), tamarind (*Tamarindus indica*) (24), mahua (*Madhuca longifolia*) (30), karonda (*Carissa carandas*) (40) and khirini (32) were evaluated for yield and other quality parameters. An early, short, precocious and high-yielding promising chironji (*Buchanania lanzan*) (CHES C-7) was identified.

Molecular characterization and documentation of arid zone fruit crops: Molecular characterization of 22 elite varieties/germplasm lines of arid zone fruits, *Ziziphus mauritiana* (ber), *Punica granatum* (pomegranate), *Emblica officinalis* (aonla), *Carissa carandas* (*karonda*) and *Cordia myxa* (*gonda*) maintained at CAZRI research farm were completed. RAPD banding patterns revealed genetic polymorphism amounting to 85.15% in *Ziziphus mauritiana*, 92.44% in *Punica granatum,* 56.18% in *Emblica officinalis* (*Phyllanthus emblica*), 25% in *Carissa carandas* and 59.04% in *Cordia myxa.*

Vegetable crops

At Bengaluru, tomato accessions (14), chilli and bell pepper (56), okra (13), cucumber (19), dolichos bean (35), ridge gourd (22) and bitter gourd (65) were collected and conserved. A total of 613 accessions including wild relatives (70) in 51 major and minor vegetable crops were augmented through import and inland explorations at Varanasi. These include tomato (37), brinjal (31), bitter gourd (10), bottle gourd (10), sponge gourd (14), chilli (27), okra (226), cauliflower (6), cucumber (36), muskmelon (20), pointed gourd (3), snake gourd (4), ridge gourd (7), satputia (*Luffa hermaphodita*) (7), ivy gourd (2), longmelon (4), watermelon (5), roundmelon (6), kakrol (*Momordica dioica*) (6), kartoli or spine gourd (*Momordica dioica*) (4), french bean (26), cowpea (3), radish (9), carrot (8), vegetable soyabean (38), faba bean (*Vicia faba*) (14), water spinach (3) and Amaranth sp (8). Similarly one accession each in *Aerva lanata*, *Amaranthus viridis*, *Anisochilus carnosus*, *Antidesma acidum*, *Basella alba* var. rubra, *Brassica napus*, *Cassia occidentalis*, *Cassia tora*, *Chenopodium album*, *Corchorus aestuarus*, *Eclipta prostrate*, *Ipomoea aquatic*, *Malva sylvestris* var. mauritiana, *Murraya koenigii*, *Oxalis corniculata*, *Portulaca oleracea*, *Trianthema portucastrum*, *Trigonella corniculata*, *Urena sinuate* and *Vicia sativa*; two each in *Basella alba*, *Basella alba* var. alba, *Celosia argentea*, *Cleome viscosa*, *Coriandrum sativum*, and *Melochia corchorifolia*; three each in *Lathyrus sativus*, *Spinacia oleracea*, and *Trigonella foenumgraecum*, *Hibiscus* (5), Chorcorus (7), *Amaranthus blitum* (10), *Amaranthus caudatus* (14), *Amaranthus dubius* (16), *Amaranthus hybridus* (19) and *Amaranthus oleraceous* (23) were collected.

Forty-nine onion accessions (including wild and cultivated) were collected from Arunachal Pradesh and Assam. Further, 40 accessions were introduced from the USA. A unique, white, multiplier onion accession (WM 514) having 4–6 bulblets in a cluster was identified at Karimnagar in Telengana. This unique accession that matures 110–125 days after transplanting recorded a mean yield of 20 tonnes/ha. It has the advantage of seed setting in the plains.

A number of red and white onion accessions were evaluated for their suitability in late *kharif* and *rabi* and superior accessions advanced for further evaluations. Similarly, 2 accessions (654 and 674) and 7 elite lines (AC-74-7, ACC-471, Col-AC-316.15, RG-37, Col-AC-36-0.5, CDT-14.6 and T-8-1) were found to be superior out of 104 garlic accessions evaluated. Based on phenotypic characters, a core set of 39 accessions was identified.

A unique native cucumber, mat kachari (*Cucumis pubescens*), tinda (*Praecitrullus fistulosus*) and 3 dual purpose clusterbean races were collected based on specific traits and conserved at Bikaner. A monoecious muskmelon (AHM/BR-8) was identified that could be exploited for hybrid seed production. AHLM-2, a promising line of long melon, was identified for its earliness, fruit length, weight and number of fruits/ plant. An advanced muskmelon genotype (CIAH-1), identified as potential crop under hot and arid agroclimate, was evaluated for growth and fruit characters.

Plantation crops

Of the total cashew germplasm (528), 478 accessions were evaluated and characterized as per the IPGRI descriptors for growth, yield and nut characters. Among hybrids, H-125 and H-126, a cross-combination of NRCC Selection 2 × Bhedasi recorded an average nut yield of 2.79 kg and 2.91 kg/tree at the third and the fourth harvesting, respectively and was on par with the ruling variety, Bhaskara. These hybrids fall under jumbo nut category (11–12 g).

H-126 is a promising jumbo nut cashew hybrid

Coconut accessions (14) collected from Tripura, Andamans, Lakshadweep, Karnataka and Kerala having distinct vegetative and yield traits were added to existing gene bank at CPCRI, Kasaragod.

Dura oil palms (4) belonging to Guinea Bissau and Zambia sources with high degree of drought tolerance were identified and utilized for development of Dura×Dura and Dura×Pisifera hybrids. These hybrids are recommended for cultivation in regions with limited water supply.

Drought tolerant Dura palm (ZS-1)

Tuber crops

A collection of 26 accessions was added to existing potato gene bank. In addition, 282 accessions of TPS (true potato seeds) representing 43 species were imported from the USA. Further, indigenous collection from plains of Assam, Lahul-Spiti, Manipur, West Bengal, Leh and Ladhakh regions were carried out.

A total of 5,832 germplasm of tropical tuber crops comprising cassava (1,383), sweet potato (1,483), yams (1,151), aroids (1,348) and minor tuber crops (390) were conserved in field gene bank at Thiruvananthapuram, Kerala. Further, 77 new accessions of tuber crops comprising cassava (20), sweet potato (10), *Ipomoea* sp. (1), greater yam (5), lesser yam (1), wild yams (2), taro (17), tannia (4), elephant-foot yam (8), Chinese potato (1), arrowroot (3), *Curcuma* sp. (3), *Canna* sp. (1) and giant taro (1) were also conserved.

Cassava clones having novel traits, viz. cassava mosaic disease (CMD) resistance (9S127,CR 20 A2, CR21-10, 11S20, 11S28, 11S33, IH5/15) with high starch content on fresh-weight basis (31.9, 31.6 and 30.8%, respectively), suitability for processing (CR 21-10, CR 20A-2, CMR 100), high dry matter (>45%) and keeping quality (CR 20 A2, CI-800, BR-105) were identified.

Taro accessions (21) having good cooking quality with no acridity and 3 accessions with leaf blight (*Phytophthora colocasiae*) resistance (U-64, TCR 125 and IC 204065) were identified. Da 293, a high-yielding quality, greater yam variety with compact tuber is widely adopted in Odisha. Promising genotypes, viz. Dr 246, Dr 169 (early bulking), Dr 29 (compact tuber) and Dr 128, Dr 130, Dr 140, Dr 147, Dr 21, Dr 281, Dr 29, Dr 324, Dr 7 (good cooking quality) with high yield were identified in white yam for further evaluation.

Flower crops

Tuberose germplasm (2), rose (7), carnation (18) and chrysanthemum (8) were collected. Digital rose repository was completed for 145 varieties at Bengaluru.

Medicinal and aromatic plants

The genetic resources of *Mandukaparni* (*Centella asiatica*) (12) and kalmegh (*Andrographis paniculata*) (14) were collected at Anand, Gujarat. Accessions of rare, endangered and threatened (RET) medicinal plants from Nandi Hills, Bengaluru and adjoining areas (5), *Decalepisha miltonii* from Savandurga and Devarayanadurga, Karnataka, 50 accessions from Dakshina Kanada and 7 RET species from Wayanad, Kerala and *Embelia ribes* from Ootacamund, Tamil Nadu and adjoining areas were collected. These represent the RET species of the Western Ghats and Plateau.

Distinctiveness, uniformity and stability (DUS) descriptors were identified for 10 morphological characters in kalmegh. Major characteristics identified were: plant habit, leaf type (narrow, broad), leaf colour, leaf lamina, branching pattern, canopy shape, flowering pattern, plant height, internode length and inflorescence type. Accordingly 45 distinct reference lines were identified.

Gudmad accessions (*Gymnema sylvestre*) and salaparni (*Desmodium gangeticum*) with distinct morphological characters were identified. DGS 31, a gudmad accession collected from Shimoga, Karnataka had distinct orange flower, whereas other accessions normally have yellow flowers. Three distinct accessions of *D. gangeticum*, viz. DDG 6 (prostrate type plant), DDG 15 (tall and erect plant) and DDG 29 (narrow and long leaves) were identified.

Five species of *Zingiber,* viz. *Z. squarrosum, Z. spectabilis, Z. odoriferum, Hedychium coronarium* and *Alpinia galangal* and 4 accessions of *Gloriosa,* viz. Accession 1 (Andhra local), Accession 2 (Tamil Nadu local), Accession 3 (Chidiyatapu) and Accession 4 (Rangat) were added through exploratory surveys from South and Middle Andaman. Six RET species of medicinal plants, viz. *Moringa oleifera,* Indian Trumpet (*Oroxylum indicum*), brown gold (*Holostemma adakodein*), Jyotismati (*Celastrus paniculatus*), Malabar Embilia (*Embelia tsejiam-cottam*) and swallowroot (*Decalphisha miltonii*) were collected and conserved at Bengaluru.

First ever variety of makhana

Swarna Vaidehi, first ever variety of makhana, was developed and released. The seeds of Swarna Vaidehi are bold with average productivity of 2.8–3.0 tonnes/ ha. This variety produced 60% higher seed yield compared to local check.

Spices

Promising black pepper genotypes (3), clove (1), nutmeg (6) and ginger (7) were collected from Kerala, Tamil Nadu, Karnataka and Nagaland, respectively. Fenugreek accessions, UM 301 and UM 112, from Jobner collections were evaluated for low moisture tolerance. CS 38 and LCC-232 coriander were identified as superior genotypes (as leaf), while 5 wild relatives and 21 accessions of black pepper were collected from Sirsi, Yellapur, Honnavar (Uttar Kannada) and Sagar (Shimoga) of Karnataka. Further, 2 local types with very long spikes were identified from Wayanad (Kerala). A seedless nutmeg from Kottayam (Kerala) and 14 monoecious nutmegs from Karnataka were collected and conserved.

The seed spices gene bank has been strengthened with an addition of 87 new germplasm of coriander (28), cumin (30), fennel (15), dill (6), ajwain (5), nigella (2) and fenugreek (1) at Ajmer.

One extra dwarf (35 cm) fennel plant was identified (average height 150 cm) and maintained through selfing. Seeds were preserved for hybridization programme.

Mushroom

More than 210 unique mushroom germplasm were collected from the forest of Himachal Pradesh, Mizoram, Arunachal Pradesh and Gujarat. Of them, 195 were identified up to genus level and 109 were cultured and deposited in national gene bank at Solan. In addition, two each high-yielding varieties of button, shiitake and paddy straw mushroom and one each of milky mushroom and Macrocybe were deposited. The retro element-based markers linked with fertility in *Agaricus*, strain-specific markers in different strains of *Agaricus* and also genus and species-specific markers in different mushrooms were identified. Presence of WRKY type transcription factor was confirmed in *Agaricus* mushroom.

Orchids

The taxonomic identity of scented species, viz. *Dendrobium ovatum* (NOAC-324) and *D. macrostachyum* (NOAC-329) were confirmed from BSI, (Botanical Survey of India), Gangtok. The assessment of compatibility and pod setting success were studied between species, hybrids *vs* species and hybrids *vs* hybrids among *Dendrobium*, *Vanda*, *Phalaenopsis*, *Renanthera*, *Phaphiopedilum* and *Coelogyne* genus from more than 400 pollinations. Species of wild orchids (45) were collected and maintained.

Livestock

In India about 20–25% of total livestock is descript and well recognised. Still there is a need to manage the genetic resources properly for improving the productivity of existing stock, while maintaining the unique and beneficial genetic characteristics of the Indian breeds.

Presently, India has 144 registered breeds of livestock and poultry including 37 breeds of cattle, 13 of buffalo, 39 of sheep, 23 of goat, 6 of horse and pony, 8 of camel, 2 of pig, 1 of donkey and 15 of poultry besides populations/breeds of other species like mules, yaks, mithun, ducks, etc., which are yet to be classified. About 20–25% of total livestock population in our country comprises descript and well recognized breeds. The remaining population of livestock is non-descript which is yet to be characterized systematically. Characterization of various populations of livestock species was undertaken during the year.

Phenotypic characterization and conservation of animal genetic resources

Sanchori cattle: Sanchori cattle is mainly distributed in Sanchore, Bhinmal and Raniwada tehsils of Jalore district of Rajasthan. The cows are generally white and bulls are grey, whereas muzzle and tail switch are mostly black. The size and circumference of horns are smaller as compared to that of Kankrej or Nari cattle found in the same area. Horns are predominantly black and orientated outward, upward and inward ending with pointing tips. The orientation of ear is horizontal but sometimes slightly drooping. Udder is mostly pendulous with cylindrical teats ending with rounded tip. The average body length, height at withers, chest girth, paunch girth, face length, ear length, horn length, horn circumference, tail length and tail length without switch of cows are 129.3±0.65, 122.95±0.34, 167.03±0.75, 183.5±0.97, 44.07±0.20, 31.66±0.17, 32.01±0.60, 22.87±0.28, 117.94±0.70, 87.95±0.58 cm, respectively. In bulls/bullock the corresponding values are 137.86±0.68, 138.57±0.35, 188.7±1.02, 199±1.43, 46.85±0.18, 32.5±0.1, 42.21±0.73, 21.38±0.20, 129±0.68, 94.6±0.68 cm, respectively. The overall daily milk yield is 9.08±0.16 kg/day, and peak milk yield 6–18 kg/day in a lactation period ranging from 8 to 15 months. The animals are kept in open houses (*Dhanis*), adjacent to the farmers' house made in the agricultural fields. Natural breeding is adopted.

Sanchori cattle

Belahi cattle: A migratory cattle population, also referred to as Desi, Morni and Gujari, is mainly reared by Gujjars of Haryana and Punjab. The animals are medium statured. Coat is reddish with a white face and a black muzzle. Average body weights in males and females are 17.6±0.51 kg and 15.2±0.58 kg at birth, 31.6±1.22 and 33.75±1.42 kg at 3 months and 304.8±1.35 and 266.74±2.15 kg for adults, respectively. The average test day milk for Belahi cow is 4.0 kg in third lactation and 3.0 kg in sixth lactation. Average values of milk constituents like fat, lactose and SNF are 5.25, 3.45, 5.20 and 9.39%, respectively. Males are used for transport and agricultural operations.

Belahi cattle

Manipuri cattle: The local cattle population in Manipur is small, well built, stout, with cylindrical body. Majority of the animals are dark brown. The birth weight ranges from 8 to 15 kg. Daily milk production ranges from 2.0 to 4.50 kg and average per day milk yield is 2.65±0.18 kg. A pair of bullock may plough about 1.0 acre of land in 6–8 hr. The age at first calving, lactation length, dry period, service period, calving interval, herd life and number of calving during life time range from 30 to 45 months, 120–270 days, 6–9 months, 3–9 months, 12–18 months, 12–15 years, 6–8 calvings, respectively. The average body length, height at wither, heart girth, paunch girth, horn length, ear length, face length and tail length without switch in cows are 100.32±0.59, 106.22±0.51,

Manipuri bull

Manipuri cattle

137.69±1.01, 142.12±0.98, 11.85±0.38, 19.59±0.17, 38.06±0.2 and 74.30±0.50 cm, respectively. Herd size ranged from 2 to 20. Cattle are generally reared for bullock power and manure (100%), however, 18% of farmers reared them for milk purpose also.

Gojri buffalo: Geographic distribution and migration pattern of Gojri, a migratory buffalo population in Himachal Pradesh and Punjab region were identified. Gojri buffaloes are black with thick brown hair. They have black face and muzzle though white patches may be present on the face. Horns are of medium to large size with curved orientation which move backwards and then towards front to complete the loop, locally called '*Pattih wale seengh*'. Udder is small, round shaped but well-placed with cylindrical teats and prominent milk vein. Gojri buffaloes graze for about 6–7 hr/day on the hilly terrains in Himachal Pradesh but herders from Punjab region do not migrate and stall feed their animals. Gojri buffaloes are reared for milk, draught and manure/dung. Compared to Murrah and Nilli Ravi, the Gojri buffalo is lighter, smaller and shorter. The average height at withers, body length, chest girth, paunch girth, face length, horn length, horn circumference, ear length, tail length and tail length without switch of she buffaloes are 128.66±0.32, 133.33±0.35, 195.91±0.67, 213.91±1.34, 48.58±0.11, 44.61±0.61, 19.82±0.12, 28.76±0.09, 90.57±1.15, 104.15±0.67 cm, respectively. In buffalo bulls/bullock the corresponding values are 136.63±1.22, 138.91±1.59, 203.47±1.99, 230.88±2.48, 48.97±0.44, 35.75±1.32, 21.41±0.48, 29.00±0.16, 95.81±1.44, 109.16±1.31 cm, respectively.


Gojri buffalo

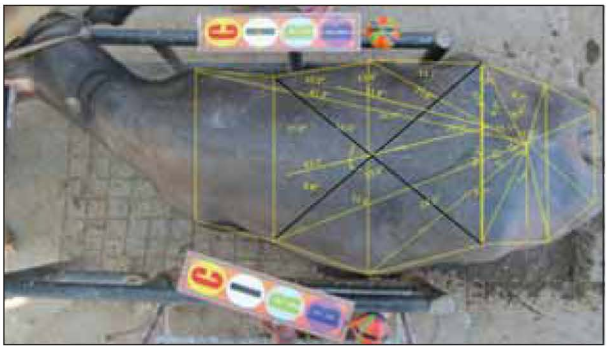
Harringhata Black chicken: Survey of Nadia and North 24 Pargana districts of West Bengal revealed that estimated population of Harringhata Black in the breeding tract is 63,600. The birds are used for both meat and eggs. Colour of plumage is black; comb is red and mostly single; earlobe is red or white; beak is blackish in appearance; wattles are small and red; and shank is blackish grey or yellow. Some cocks have brown feathers on neck and wings. Body weight at 10 months of age is 1.1 kg in hens and 1.3 kg in cocks. Average age at first egg is 5.63 months. Average number of eggs per cycle is 12.32 and annual egg production is 45 with brooding and 98 without brooding. Average number of chicks per hatch was 9.45 with 77.4% hatching on total egg basis.


Harringhata Black chicken

Ex-situ conservation

Frozen semen doses of breeding males of Tharparkar cattle (13,000), Osmanabadi sheep (491), Mehsana buffalo (1,000), Assam Hill goat (500), Zanskari horse (330), Marwari horse (160), French donkey (240) and Arunachali yak (100) were added to the repository in National Gene Bank of NBAGR.

Digital imaging for buffalo conformation/body condition score: A new instrument "Kalrumpscale" was designed for linear measurements of body parts (length, height, pin-shoulder length etc.) in Murrah and Nili-Ravi buffaloes. The instrument measures 3D angular and linear orientation of external rump/pelvic surface for digital quantification of dairy characters in buffaloes.


Digital imaging angles of buffalo

Types of horn curves in Murrah and Nili-Ravi buffaloes

Screening of curve pattern of horn of buffaloes will be useful for identification of purity and sustainability of Murrah and Nili-Ravi buffaloes.

Molecular genetic characterization

Production traits for milk and meat production—Leptin gene: Individual effect of mutation (A125G) in Exon 2 showed significant association with the protein percentage at 24 weeks during whole lactation in Murrah buffaloes. Leptin gene showed synergistic effect [w1m2/m1/w1w2] of SNPs in Exon 2, Intron 2 and Exon 3.

Conception rate in Murrah buffaloes: Seminal acidic fluid protein gene governs sperm stability and fertilization efficiency in many species. Four haplotypes were identified in exon 4 and 5 of the gene from 35 Murrah bulls with variable conception rates. These SNPs, indirectly, can be used for screening of bulls with respect to conception rate.

Genetic characterization and functional genomics

Microsatellite markers in cattle: Genetic characterization of Belahi cattle was accomplished using microsatellite markers. Genomic DNA was isolated from 50 random blood samples collected from animals and data for 16 microsatellites markers (INRA35, ILSTS005, INRA05, INRA63, BM1824, ILSTS11, CSSM60, CSSM66, TGLA122, MM12, CSSM33, MM8, ILSTS06, CSSM8, TGLA227, HEL1) were generated. The mean observed and effective number of alleles were 9.3125 and 4.3894, respectively. The average observed and expected heterozygosity values were 0.6890± 0.1688 and 0.7196±0.1543, respectively.

Genetic variability in the bovine cytokines: Twenty SNPs were found spread across 3.4 Kb region of IFN-γ gene in 40 cattle of Tharparkar, Rathi, Sahiwal, Hariana and Kankrej breeds. Microsatellite repeat $(GTTT)_n$ in the intron-1 region of the gene exhibited high degree of polymorphism. Polymorphism present across the complete TNF β gene (3.5Kb) in these animals revealed 31 SNPs across 3.5 Kb long region. The SNP 1412 (A>G) in exon 2 resulted in amino acid change Gly>Asp. The observed heterozygosity for all the loci for SNPs was almost the same as the expected heterozygosity. The overall negative Fis value indicated little level of inbreeding. The Fst value was 0.1354.

Sequencing of cytokine gene(s) in camel: The PCR amplification, cloning and sequencing of poly-U binding splicing factor of the Dromedary camel and sequence analysis of poly-U binding-splicing factor gene revealed that Indian Dromedary camel shared 96.1 and 96.8% identity at the nucleotide level with wild Bactrian and Alpaca camels, respectively.

Genomic profiles of chicken lines: Candidate gene analysis revealed presence of 12 haplotypes in IGF-1 gene and 8 haplotypes in GHR gene in control broiler and layer chicken lines. The haplogroups showed significant effect on body weight at day-old and 6 weeks of age, and daily gain between 4 and 6 weeks of age in control broiler population. *In vivo* studies of MSTN expression and effect indicated specificity of the protein and reiterated the negative effect on growth in chicken. The whole genome of Aseel bird was sequenced indicating presence of approximately 23,000 genes. Six mitochondrial genes, viz. *CO-II, CO-III, ATPase6, ATPase8, ND-3* and *ND-6* were characterized in different breeds of chicken. To explore impact and mitigation of climate change in chicken, an experiment on chicken embryos exposed to heat was conducted for studying the exact role of heat shock protein genes. All Hsp genes (*Hsp-70, Hsp-27, Hsp-90a* and *Hsp-60*) were found significantly up-regulated in naked neck birds. The body weight at 6 weeks of age was significantly lower in heat exposed birds (37.5°C up to 42 days of age) as compared to the normal birds.

Characterization of male specific genes of yak—first report

Decline in yak population has become a cause of concern and male fertility plays the central role in maintaining the genetic health of a small population. Systematic discovery and functional characterization of genes on Y chromosome of yaks, which play a role in male fertility, are required. MicroRNA (miRNA) helps many cell functions by which it can regulate expression of number of genes. During the present investigation 12 male specific genes of yak were identified, and related six miRNAs were found expressed significantly in yak sperms. Presence of these miRNAs in normal yak sperms is the basis for investigation of their likely association with yak bull fertility.

Genetic characterization of Indian horse and pony breeds

Genetic diversity analysis of Indian horse and pony breeds along with thoroughbred horses revealed high values of allele number, observed and expected heterozygosity, polymorphism information content for all Indian breeds except Spiti ponies in comparison to thoroughbred horses, indicating high genetic diversity in them. Genetic differentiation between Spiti and thoroughbred was maximum followed by Spiti and Kathiawari; while Zanskari and Manipuri were the least differentiated. Individual assignment indicated admixture in all the breeds except thoroughbred horses. Three distinctive clusters of Indian horse and pony breeds were observed—first of Kathiawari, the most prominent cluster as horse breed; second of Zanskari, Spiti and Manipuri ponies; and third of Bhutia and a sub population of Marwari horses. Clustering of one sub-population of Marwari with Bhutia indicated their common ancestries, which need further investigations as both these are distinct at phenotypic level and geographically isolated. Kathiawari represents the oldest stock and has contributed to other Indian breeds. Similarity of Kathiawari and Marwari horses is attributed to contiguity of their breeding tracts.

Development of livestock traceability database system: Livestock traceability database system (www.livestocktraceindia.com) was established to store information of animals, farm and abattoir on web based module. Farm was enrolled in the database, RFID tags were ear tagged on to buffaloes, and corresponding information was updated on traceability database.

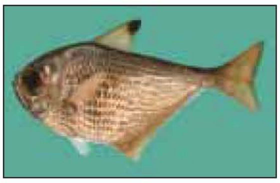
Cytogenetic screening: NBAGR provided consultancy service of cytogenetic screening of breeding males to check the spread of chromosomal defects as per the policy of Government of India. During the year 372 breeding bulls were screened for their cytogenetic parameters and all except two, showed normal karyotype, representative of the respective species.

Genetic polymorphism in receptor gene associated with FMDV: Cloning, characterization and sequence analysis of integrin alpha beta 6 (*ITGB6*) receptor of zebu cattle were carried out. The complete CDS of zebu ITGB6 was 2367 base pair in length with 788 amino acid residues, and they share common structural and functional elements with taurine and other species. Three amino acid substitutions (S_{665} to F_{665}, Q_{781} to F_{781} and L_{785} to F_{785},) were identified in *Itgb6* gene among zebu and taurine.

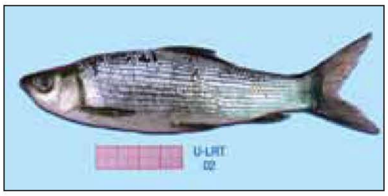
Fish

New fish species characterized: Two fish species, *Plectranthias alcockii* and *Pempheris sarayu*, discovered from the Arabian Sea were portrayed based on morphomeristic and molecular parameters. The specimens of *Plectranthias alcockii* were caught over the continental shelf of the Arabian Sea, off Kollam (Quilon) at depths of 180–320 m and landed at Sakthikulangara fisheries harbour, Kerala. It is a small benthic species generally found in tropical and subtropical sea on coral or rocky reefs at depths of 20 to over 300 m. The species *Pempheris sarayu,* popularly known as sweepers was collected from Kovalam, Kerala. Freshwater fish species, *Labeo icarae* was identified from western Rajasthan.

Plectranthias alcockii



Pempheris sarayu

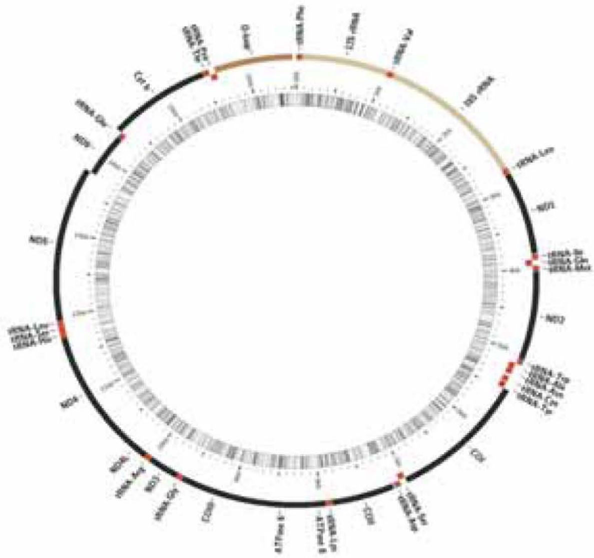


Labeo icarae

Genetic diversity of silver pomfret: Genetic stock identification of silver pomfret, *Pampus argenteus,* populations along the coasts of West Bengal, Andhra Pradesh, Tamil Nadu, Gujarat and Kerala represents existence of three distinct genetically structured management units namely, one stock along western coast (Gujarat to Kerala) and two stocks along eastern coast (West Bengal to Andhra Pradesh and Tamil Nadu).

Novel DNA chip for genotyping economic traits: Tiger shrimp, *Penaeus monodon*, a species of commercial importance is susceptibile to white spot syndrome virus (WSSV) disease, which impacts its production to a great extent. Further, its females grow more rapidly than males, so mono-sex culture is advantageous. To determine loci associated with resistance to WSSV and sex, a chip containing 6000 SNPs was developed. The markers for disease resistance and sexual differentiation would be useful for marker assisted selection to improve resistance to WSSV and for identifying homogametic female individuals for mono-sex (all female) production.

Mitogenome of *Clarias batrachus*: From the whole genome of *Clarias batrachus,* mitochondrial whole genome was retrieved as the longest contig of 16,510 base pairs. Gene annotation of mitochondrial contig yielded 13 coding, 22 tRNA and 2 rRNA genes along with D-loop information. Identified 51 single nucleotide variants (SNVs), of which 49 SNVs were in the genic region and two in the inter-genic regions.



Mitogenome of *Clarias batrachus*

Draft genome sequence of *Mangrovibacter* spp. *MFB070*: The genome of *Mangrovibacter* spp. *MFB070,* a facultative anaerobic, nitrogen-fixing bacterium, associated with the rhizosphere of mangrove-associated plants was sequenced and annotated. The bacteria encodes for mdtABCD, the multidrug resistance cluster that increase resistance to novobiocin and deoxycholate. It also encodes genes for heavy metal resistance to cobalt, cadmium, zinc, arsenic and copper. Several phage proteins and genes involved in iron acquisition and nitrogen were also found in the genome.

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