

## 6. Crop Improvement

### Rice

Five hybrids and four varieties of rice were notified by the Central Sub-committee of Crop Standards, Notification and Release of Varieties.

The promising lines of rice under coastal saline soil conditions are IET 21235 (CR 2218-41-2-1), Nona Bokra, SR 26B, IR 72049-B-R-22-3-1-1, CSR 2 and Canning 7 for shallow water, Purnendu and Nalini for semi-deep water, and CSRC(D) 12-8-12 and CSRC(D) 2-17-5 for deep water.

### Wheat

Eight wheat varieties were released for different

production systems.

**Salt-tolerant wheat:** Two salt-tolerant varieties (KRL 210 and KRL 213) of wheat were identified. KRL 210 wheat has shown good yielding ability and salt tolerance with superiority in grain yield. This variety has shown 26.8% gain over Kharchia 65. It is found resistant to yellow and brown rusts, loose smut, Karnal bunt and flag smut. The variety has also shown tolerance to shoot fly. It is a semi-dwarf variety and matures in about 143 days. Its grains are amber coloured, bold in size and contain about 11% protein. The hectolitre weight of the grain is 77 kg with sedimentation value

#### Rice hybrids/varieties released

Variety	Reaction to pests/diseases	Recommended State/Region
CO(R) 50	MR – BLB, RTV, BS	Irrigated areas of Andhra Pradesh, Karnataka, Tamil Nadu
<b>DRH 775</b>		Irrigated areas of Chhattisgarh, Jharkhand, West Bengal
<b>HRI 157</b>	MR – RTV, BS	Irrigated areas of Chhattisgarh, Uttar Pradesh, Madhya Pradesh, Karnataka, Puducherry, Gujarat
<b>PAC 835</b>	MR – BLB, RTV	Irrigated areas of Odisha, Gujarat
<b>PAC 837</b>	MR – RTV, BS, GLH	Irrigated areas of Gujarat, Chhattisgarh, Jammu and Kashmir, Andhra Pradesh, Karnataka
Narendra Usar Dhan 2008	–	Irrigated saline/alkaline areas of Odisha, Andhra Pradesh, West Bengal
DRR Dhan 38	MR – BLB, WBPH	Irrigated areas of Gujarat, Andhra Pradesh
DRR Dhan 39	MR – BLB, RTV	Irrigated coastal saline areas of Odisha, Kerala, Gujarat
<b>DRRH 3</b>	MR – LBI, NBI, BS, ShBI, ShR	Irrigated areas of Madhya Pradesh, Odisha, Uttar Pradesh, Gujarat, Andhra Pradesh

R: Resistant; MR: Moderately resistant; BL: Blast; BLB: Bacterial leaf blight; BS: Brown spot; BPH: Brown planthopper; GLH: Green leaf hopper; GM: Gall midge; LF: Leaf folder; LBI: Leaf blight; NBI: Neck blight; RTV: Rice tungro virus; ShBI: Sheath blight; SB: Stem borer; ShR: Sheath rot; WBPH: White backed planthopper; Hybrids are in **bold**.

#### Wheat released varieties

Variety	Production condition	Adaptation area
VL 907	Timely sown irrigated and rainfed areas	Hills of Jammu and Kashmir (excepting Jammu and Kathua districts), Himachal Pradesh (excepting Paonta Valley and Una district), Uttarakhand (excluding <i>tarai</i> region), Sikkim and hills of West Bengal and north-eastern states
PDW 314 (d)	Timely sown irrigated area	Punjab, Haryana, Delhi, Rajasthan (excepting Kota and Udaipur divisions), western Uttar Pradesh (excepting Jhansi division), Jammu and Kathua districts of Jammu and Kashmir, Paonta Valley and Una district of Himachal Pradesh, and <i>tarai</i> region of Uttarakhand
DBW 39	Timely sown irrigated area	Eastern Uttar Pradesh, Bihar, Jharkhand, West Bengal (excluding hills), Odisha, Assam and plains of north-eastern states
MPO 1215 (d)	Timely sown irrigated area	Madhya Pradesh, Chhattisgarh, Gujarat, Kota and Udaipur divisions of Rajasthan and Jhansi division of Uttar Pradesh
MACS 6222	Timely sown irrigated area	Maharashtra, Karnataka, Andhra Pradesh, Goa and plains of Tamil Nadu
AKAW 4627	Late sown irrigated area	Maharashtra, Karnataka, Andhra Pradesh, Goa and plains of Tamil Nadu
KRL 210	Timely sown irrigated area	Saline/alkaline soils across the country
KRL 213	Timely sown irrigated area	Saline/alkaline soils across the country

### Faster wheat-breeding technologies

Key parental materials were profiled with markers and the populations segregated for markers were identified and screened using marker-assisted selection for key genes. Marker-assisted identification of genes in selections from each of the F<sub>2</sub> bulks was done to take advantage of markers in terms of precision breeding. In the initial phase, markers linked to the genes *Sr2*, *Lr24*, *Lr34*, *Lr37*, *Lr10* and *Lr26* were applied.

Amplification reactions were adjusted to obtain fragments of the expected size for the markers associated with the genes for vernalization (*Vrn1A*, *Vrn1B*, *Vrn1D*), reduced plant height (*Rht1*) and photoperiod responsiveness (*Ppd1*).

of 39. Its yield potential is 5.2 tonnes/ha in normal soils, and in salt-affected soils (*pH* up to 9.3 and *EC<sub>e</sub>* up to 6 dS/m), it is 3.5 tonnes/ha.

KRL 213 showed salt tolerance and good yielding ability with superiority in grain yield. The variety showed 24.1% gain over Kharchia 65, and it is resistant to yellow as well as brown rust, leaf blight, Karnal bunt and hill bunt. It has an excellent plant type with semi-dwarfness, and flowers in 97 days, and matures in 145 days in the north-western plains zone. However, in the north-eastern plains zone, the variety attains flowering and maturity at 91 and 128 days, respectively. It has been specifically bred for salt tolerance to saline (*EC<sub>e</sub>* 6.0 dS/m) as well as alkaline soil (up to *pH* 9.2) conditions. It also performed well in areas where groundwater was either brackish and/or saline (*EC<sub>iw</sub>* 15 dS/m; *RSC* 12–14 meq/litre). This variety has amber colour grain with 11% protein, 77 kg hectolitre weight of grain and sedimentation value of 29. It has a good yield potential (average yield is 3.3 tonnes/ha) under the salt stress condition. The variety can produce up to 5.1 tonnes/ha in normal soils.

### Rust-resistant wheat sources

Eleven of the released wheat varieties under cultivation, showed resistance to Nilgiri flora of black and brown rusts. Molecular characterization of Indian wheat varieties for stem rust resistance was done and breeding materials have been generated by making specific crosses. Segregation analysis is in progress.

Stripe rust exhibited variations in the resistance level in the phenotypic distribution of double haploid (*Ducula* 4/2\*Brookton and *Camm/HD2329*) populations. Analysis for Karnal bunt score indicated that some of these lines possessed good level of Karnal bunt resistance.

## Maize

Eight hybrids/composites were released for different agro-climates.

Vivek QPM 9 is an early-maturing hybrid. Based on its performance, it has recently been released for commercial cultivation in the Himalayan states as well as in the peninsular India. This new hybrid possesses all good qualities of Vivek Hybrid 9 with added

## Maize released hybrids and composites

Hybrid/Composites	States
<b>Hybrids</b>	
HM 11	All states for <i>rabi</i> season
Pinnacle	Punjab, Haryana, Delhi, western Uttar Pradesh
JKMH 502	Delhi, Punjab, Haryana and western Uttar Pradesh
PAC 740	Delhi, Punjab, Haryana and western Uttar Pradesh
SMH 3904	Punjab, Haryana, Delhi, Uttar Pradesh, Bihar, Jharkhand, Odisha, Karnataka, Andhra Pradesh, Tamil Nadu, Maharashtra, Rajasthan, Gujarat, Chhattisgarh, Madhya Pradesh
DKC 7074R	Punjab, Haryana, Delhi, western Uttar Pradesh
<b>Composites</b>	
VivekSankul 35	Jammu and Kashmir, Himachal Pradesh, Uttar Pradesh, north-eastern hills
VivekSankul 37	Karnataka, Andhra Pradesh, Tamil Nadu, Maharashtra

advantage of 30% higher lysine and 44% higher tryptophan.

## Pearl millet

Five pearl millet hybrids were released for various agro-ecologies.



### Pearl millet released varieties

Hybrids	States
MH 1468 (HHB 223)	Rajasthan, Gujarat, Haryana, Punjab, New Delhi, Uttar Pradesh and Madhya Pradesh
MH 1421 (HHB 216)	Western Rajasthan and drier part of Gujarat and Haryana
MSH 199 (Nandi 64)	Summer growing areas of Gujarat, Maharashtra, Rajasthan and Tamil Nadu
MH 1548 (Nandi 61)	Rajasthan, Gujarat, Haryana, Uttar Pradesh, New Delhi, Madhya Pradesh and Punjab
MH 1549 (Nandi 65)	Rajasthan, Gujarat, Haryana, Uttar Pradesh, New Delhi, Madhya Pradesh and Punjab

### Minor millets released varieties

Varieties	Adaptation area	Traits
Fingermillet GPU 67	Karnataka, Chhattisgarh, Jharkhand, Maharashtra, Tamil Nadu and Uttarakhand	Semi-dwarf, erect flag leaf, profuse tillering, moderately resistant to blast; fodder yield equivalent to tall varieties
Barnyard millet CO 2	Tamil Nadu	Short-duration, high-yielding, maturing in 95 days, suitable for contingency planting
Kodo millet RK 286	Madhya Pradesh, Tamil Nadu, Chhattisgarh and Karnataka	Short-duration, high-yielding
Foxtail millet SiA 3085	Andhra Pradesh	Moderately tillering, non-lodging type, suitable for rainfed and irrigated areas, with desirable qualities for cooking and for fodder
Proso millet TNAU 194	Tamil Nadu	Early-maturing, non-lodging type, tolerant to shoot-fly and grain-smut disease, optimum number of productive (5–6) tillers, with bold and golden-yellow grains, suitable for contingency planting

#### Minor millets

Five varieties of minor millets were released.

#### Forage crops and underutilized crops

Bundel Guinea 2 (JHGG 04-01), an excellent perennial **forage** variety, was released for the rainfed areas of Punjab, Himachal Pradesh, Central Uttar Pradesh, Maharashtra and Tamil Nadu. It is a robust growing variety and remains green throughout the year under irrigation. It has shown adaptability to rainfed areas and resistance to drought under semi-arid conditions. It produced 45–75 tonnes of green fodder, 15–20 tonnes of dry matter and 1.3–1.5 tonnes of crude protein in rainfed areas.

RMA 7 **amaranth** variety has been recommended for cultivation in Rajasthan and Gujarat.

#### Oilseed crops

**Groundnut** Girnar 3, a Spanish bunch variety, was released for commercial cultivation in West Bengal, Manipur and Odisha for *kharif*. Nine lines—PBS 21095, PBS 21087, PBS 16038, PBS 26019, PBS 26015, PBS 24022, PBS 11084, PBS 11058 and JUN 27, and Girnar 3 have been found drought tolerant. They gave appreciable yield even under prolonged (~ 40 days) end-of-the-season drought.

**Sunflower** hybrid PSH 569 with high seed yield and 40% oil content was released for Punjab, and **Castor** hybrid YRCH 1 with seed yield of 1,800 kg/ha and oil content of 49% was released for Tamil Nadu.

**Linseed** varieties PKV NL 260 and SLS 67 were recommended for general cultivation in the linseed-growing areas of Maharashtra, Bundelkhand region of Uttar Pradesh, Madhya Pradesh and Rajasthan.

**Sesame** RT 351 was recommended for Rajasthan, Uttar Pradesh, Maharashtra, Gujarat, Karnataka, Himachal Pradesh, Punjab, Haryana and Jammu and Kashmir.

#### Pulse crops

**Kabuli chickpea** IPCK 2002-29 (Shubhra) for Madhya Pradesh and Maharashtra, **mungbean** IPM 02- 3 in *kharif* for Punjab, Haryana and western Uttar Pradesh, **urdbean** IPU 2-43 in *kharif* for Andhra

Pradesh, Karnataka and Tamil Nadu and **fieldpea** IPF 5-19 for Punjab, Haryana and western Uttar Pradesh were released and notified for cultivation. Fieldpea IPFD 5-8 and IPFD 4-6 gave higher seed yield in all sowing dates, and showed minimum effect of temperature on yield.

#### Commercial crops

Early-maturing **sugarcane** Co 0314 and mid-late maturing Co 0218 were found superior in the Advanced Varietal Trials. Co 0314 (Co 7201 × Co 86011), a high-yielding, good quality clone was found moderately resistant to red-rot and resistant to smut. Across the locations, its mean sugar yield, cane yield and sucrose % juice for two plants and one ratoon crop were found 13.97 tonnes/ha, 103.8 tonnes/ha and 18.99%. Co 0218 (Co 8353 × Co 86011) gave mean sucrose % juice of 19.64, cane yield of 119.6 tonnes/ha, and sugar yield of 16.85 tonnes/ha. This clone also showed moderate resistance to red-rot and smut along with good ratooning and tolerance to drought and salinity. Co 0124 (Karan 5), a mid-late maturing variety, and Co 0239 (Karan 6), an early-maturing variety, were also identified for release for commercial cultivation in the north-western zone—Punjab, Haryana, Rajasthan and western Uttar Pradesh.

**Cotton** *Gossypium hirsutum* variety Suraj was released and notified for commercial cultivation in Maharashtra, Gujarat, Madhya Pradesh Tamil Nadu, Karnataka and Andhra Pradesh. It is spinnable at 60s counts, and is found tolerant to jassids in these states. Cotton CNHO12 was identified for release for the irrigated areas of Maharashtra, Gujarat and Madhya Pradesh. The variety is characterized by dwarf stature, early maturity, high seed-oil content with synchronous boll bursting. Owing to shortage of short staple and medium staple cottons in the country, this new variety, spinnable at 20s counts, is found suitable for manufacturing denim.

CISA 614 *desi* cotton variety was notified for commercial cultivation in Punjab, Haryana and Rajasthan.

**Jute** CO 58 (Sourav) was developed from TJ 40 × Tanganyika 1, following pedigree method, and showed

yield potential of 3.4 tonnes/ha. It is found suitable for rainfed and for tossa-jute growing regions and areas where jute is cultivated following transplanted *aman* paddy. Its pods are non-shattering type, and it has also shown resistance to premature flowering.

JBC 5 (Arpita) white jute variety has shown yield potential up to 2.8–3.0 tonnes/ha, and has been recommended for cultivation in West Bengal, Asom, Bihar and Odisha. JBO 1 (Sudhanshu), tossa jute, recommended for West Bengal and Asom under rainfed agro-system has shown yield potential up to 3.0–3.5 tonnes/ha. For the traditional **mesta**-growing belt of the country, JRM 3 (Sneha), a kenaf variety with yield potential up to 2.5–3.8 tonnes/ha was recommended. *Kenaf* variety JRM 5 (Shrestha) was recommended for growing in rainfed areas of Andhra Pradesh, Odisha, Asom, Maharashtra, Bihar and West Bengal.

**Tobacco** FCV hybrids—TBSh 1, NLSH 1, SH 12 and KLSH 10 with yield potential of ~3,000 kg/ha and chewing tobacco hybrid VDH 3 with yield potential of ~4,000 kg/ha were developed. High seed-yielding lines with high oil content from crosses A 119 × Abirami (2,213 kg/ha) and HDBRG × A 145 (1,666 kg/ha) were identified at Rajahmundry and Veda sandur.

### Fruit crops

Out of 1,711 hybrid population evaluated, hybrid-949 in **mango** was found to have attractive peel colour, and regularity in cropping. A total of 440 new hybrids from 21 cross combinations were planted for evaluation and 150 accessions were genotyped using SSR markers.

Among the SSR primers, that could be validated, primer LMLY 1 amplified four alleles against expected 10. Cultivar Shahi was characterized by allelic configuration of 87/92, while China by 88/93. Primer LMLY 3 could discriminate CHL 3 and Bombay No.1 by generating unique profiles. Primer LMLY 8 was the most descriptive locus for the Indian cultivars, generating six alleles. It generated unique profile for Late Bedana, Longia, CHL 7, Dehradun and Dehrrase. *In vitro* regeneration protocol for rootstocks of *Citrus* mainly *C. macrophylla*, Troyer citrange, Rangpur lime were developed. Hybrid rootstocks were evaluated against *P. nicotianae*. Out of these, Rough lemon × Trifoliolate hybrid was found moderately resistant. The selection for seedlessness in Nagpur santra was evaluated and superior lines were multiplied for testing.

The RAPD marker for red pulp in **guava** was developed. A new cultivar, Arka Kiran was identified for release which has high yield, quality and colourful pulp.

Sixty accessions in **banana** were screened in the field for BBTv, BBrMV, BBMySv and CMV viruses. All of them were negative for CMV and BBTv and 20 accessions were positive for BBrMV.

In **papaya**, Arka Prabhat was identified for release, since this variety is deep red in colour and has potential to replace imported variety, Red Lady. Transgenic papaya cultivar solo ( $T_2$ ) was developed expressing non-translatable coat protein of PRSV, and event

selection was approved by RCGM. A cost-effective PCR-based sex identification of dioecious papaya was developed using crude leaf extract. Two events of papaya developed from gene construct (CP + rep) were advanced to  $T_1$  stage under containment condition.

Berry weight in **grape** was found to be the most variable character in genetic diversity analysis. Phenotypic co-efficient of variation was higher than genotypic coefficient of variation for fruit characters. Berry weight and diameter, seed weight and number and TSS were observed to be heritable traits. The analysis of expression of  $Na^+/H^+$  antiporter gene in rootstocks 110R and 1613C under salinity and moisture stress showed differential response by different rootstocks. The expression of  $Na^+/H^+$  antiporter gene was affected by different levels of salt and moisture stress. DDRT-PCR of 110R RNA identified differentially expressed transcript specific to salinity, moisture and combined stress.

Under field conditions in **pomegranate**, accessions, nana, IC 1182, IC 1198, IC 1199 and IC 1205 showed partial resistance. The genotypes, M 300A, M 424, M 500 and M 528, showed higher photosynthetic rate ( $> 10 \mu\text{mol CO}_2/\text{m}^2/\text{second}$ ) during March–April. Fruit setting was 50–60% when *Punica granatum* var. nana was used as the donor parent. Regeneration protocol from non-auxiliary plants were standardized for transformation. A variety in deciduous type, Goma Khatta was identified for release. In addition, a promising clones of pomegranate was identified through exploration and multiplied for further testing.

In **chironji**, 3 germplasm lines (CHES C 1, CHES C 2 and CHES C 7) were found to be promising. Out of 16 types of Bhagawa, Selection 4 was selected for yield and quality. Maximum powdery mildew incidence was recorded in Hybrid 12, Hybrid 13 and minimum in Hybrid 9 and Hybrid 10, while Hybrid 3 and Hybrid 4 were free from powdery mildew incidence. Four varieties, namely Goma Yashi (bael), Goma Priyanka (jamun), Goma Prateek (tamarind) were identified for release.

In **temperate fruits**, 100 new germplasm lines superior in yield, quality and economic traits were evaluated. Coe-Red Fuji, Granny Smith, Royal Gala and Spartan (pollinizer) cultivars in apple; Crest Heavan,



Spartan—a promising apple variety

Gloe-Heaven, Red Globe and Fantasia (Nectarine) in peach; and Tilton, Chinese Apricot and Rival in apricot were found very promising.

Five genotypes of walnut superior in yield and kernel quality and three of apricot having high yield potential and better table quality were identified for release. Among 12 early-maturing apple cultivars evaluated for fruit yield and quality, Mollies Delicious and Vista Bella recorded highest yield of 21.1 and 17.30 tonnes/ha, respectively, with TSS above 14° Brix and were found very suitable for mid to high-hills. Out of 11 spur type cultivars evaluated, Oregon Spur, Star Krimson, Red Fuji, Red Chief and Silver Spur recorded higher fruit yield (25–30 tonnes/ha).

### Plantation crops

Microsatellite analysis of DNA isolated from 308 samples of 58 coconut accessions exhibited gene diversity of 0.215 and heterozygosity of 0.617. Clustering with Neis' genetic distance indicated two distinct clusters of coconut accessions. First web-based utility for phytoplasm information containing 776,165 RNA sequences, 1,514 genes and 2,102 proteins entries was developed. Coconut varieties, Kalpasree and Kalpa Sankara, were recommended for release in root (wilt) prevalent tracts of Kerala. Kalpasree was recommended for release as a variety suitable for cultivation in homesteads in root (wilt)-diseased tract owing to its superior quality of oil and sweet tender nut water (240 ml/nut) containing total sugars 4.80 g/ml, potassium 2150 ppm, sodium 22.40 ppm with a TSS of 4.8° Brix. Kalpa Samrudhi hybrid of coconut was recommended for release in Kerala and Asom based on high copra yield under rainfed condition and good tender nut quality. The hybrid is high-yielding (117 nuts/palm) and has high copra yield (25 kg/palm/year) and oil yield of 3.04 tonnes/ha under rainfed condition. Kalpatharu coconut was recommended for release in Kerala and Karnataka. High recovery of ball copra without much spoilage of kernel (3.92%) is another beneficial trait of Kalpatharu variety.

A high-yielding arecanut variety, Kahikuchi (VTL-64), has been recommended for release in Asom and north-eastern region. The maximum yield of 607 nuts/palm (4.50 kg of chali/palm) was observed in Nalbari accession. Based on high yield record, Shriwardhan and Nalbari varieties were recommended for release to farmers. In cocoa, 274 accessions were maintained and evaluated and during the year under report, 44 new accessions were also added.

In **oilpalm**, 3 promising dwarf interspecific hybrids, namely 47 (361Eg × 11Eo), 48 (16Eo × 18Eg) and 6 (12Eo × 82Eg) were identified, which can be used for backcrossing programme. Screening of Duras collected from four African countries (Cameroon, Guinea Bissau, Tanzania and Zambia) for drought tolerance and/or high water-use efficiency is being done at different locations in India. Among African germplasm, Zambian accessions, in general, performed better under both irrigated and stressed conditions. Bunch index was

highest in Zambian material. Fatty acids composition of 18 palms from 5 African accessions (GB22/311, GB5 10, ZS 01, ZS 02, TS 04) and 1 indigenous accessions (204D × 281D) was also carried out.

In **cashew**, 29 accessions were evaluated while 67 accessions were genotyped using ISSR and SSR markers. The Jaccard's similarity coefficient values (0.38–0.89) indicated low-diversity existing among the accessions. High shelling (30%) was observed in accessions, JGM 147 and JGM 151. Accessions, RFRS 173 and RFRS 177, had higher number of panicles/m<sup>2</sup>. The genotype, T.No 10/19, produced highest cumulative nut yield (78.69 kg/tree), followed by T No 30/1 (66.49 kg/tree) in 14 harvesting. Under hybridization trials, at Jhargram centre, the highest annual yield of 14.7kg/tree was obtained in H 41, followed by H 57 (13.60 kg/tree) and H-23 (13.2 kg/tree).

### Vegetable crops

Arka Samrat and Rakshak in **tomato**; Arka Muthu, Arka Akash and Arka Aishwarya in **watermelon**; Arka Sharath in **French bean**; Arka Neelachal Sabuja and Arka Neelachal Kunkhi in **ivy gourd**; Arka Neelachal Kirti in **pointed gourd**; Arka Neelachal Shree in **spine gourd**; Arka Neelachal Gaurav in **teasel gourd** and Arka Dhanvantri and Arka Aswini in **velvet bean** were identified for release. **Chilli** high-yielding F<sub>1</sub> hybrid Arka Harita, tolerant to powdery mildew and chilli veinal mottle potyvirus, and high-yielding **carrot** variety, Arka Suraj, were recommended for release in Southern Karnataka. Kashi Harittima, a variety of **pole bean**, was recommended for release. In **Dolicos**, Arka Soumya, Arka Sambhran and Arka Amogh; in **Amaranth**, Arka Samraksha and Arka Varuna were recommended for release. Multiple disease resistant (LCV, bacterial wilt, early blight, root-knot nematode) line of tomato was found promising. In chilli and Capsicum, powdery mildew resistant line and in brinjal bacterial wilt resistant line were found promising.

In **onion**, nine new red and white type improved varieties, Bhima Kiran, Bhima Shakti, Bhima Shweta, Bhima Shubra, Arka Ujjwal, Arka Swadista, Arka Vishwas, Arka Sona and Syn 6 for different seasons with better quality and high yield potential were identified for release. Onion variety, RO 597, was identified for release in Zones III and VI, while Line 355 was identified for release in Zones III, IV and VI. In **muskmelon**, 60 lines, **bottle gourd** (20 lines) and **chilli** (45 lines) were evaluated for morphological and yield parameters. Efforts are being made to incorporate heat tolerance and virus resistant genes from *Citrullus colocynthis* into *C. lanatus*. Four varieties, Thar Mahi (sword bean), Thar Kartiki and Thar Maghi (Indian bean) and Thar Bhadavai (cluster bean) were released for arid region.

The varieties LS 2 and Iceberg of **lettuce**, SH-K-28, SH-K 30, CITH-K 6 and SH-K 29 of **kale**, CITH-P-4 of **parsley**, Ford Hook of **celery**, CITH-CC 3 of **Chinese cabbage**; Green Head and Palam Samridhi of **broccoli**; CITH Green of **artichoke** and CITH-A 1 of **Asparagus**



Lettuce is a potential high-value vegetable for NWH region

were found promising for high yield and net returns.

In **tomato**, 16 transgenic events for resistance to tospovirus (PBNV) were generated in four genetic backgrounds, 8 events for resistance to TLCV. Twenty events in four genetic backgrounds for resistance to TLCV and tospovirus were approved for trial by RCGM. In **watermelon**, four events for resistance to bud necrosis were also approved for field trials. Two transgenic events with chitinase gene in tomato, two transgenic events with cry gene in tomato and brinjal and two transgenic events with Dreb 2A were advanced to T<sub>3</sub>.

Suitable tomato varieties/hybrids having resistance to bacterial wilt, were developed for protected condition by making eight F<sub>1</sub> crosses using Swarna Lalima having resistance to bacterial wilt as female parent and eight exotic lines as male parent. One promising F<sub>1</sub> hybrid Swarna Lalima EC 596741 (yield 187.79 tonnes/ha; resistant to bacterial wilt, fruit weight 65 g, TSS 5.2 °B, titratable acidity 0.3%) was identified. Harvesting period ranged from 180 to 200 days.

### Potato and tuber crops

In potato, *Solanum verrucosum* was identified to have high yield and resistance to late blight. The hybrid, JX 576, was released as Kufri Gaurav for north-western plains. The variety possess higher N, P and K efficiency, thereby enabling lesser use of N, P, K fertilizer and restoration of soil health. Similarly, processing hybrid, MP/01 916, (released as Kufri Chipsona 4) was found promising for Karnataka, West Bengal and Madhya Pradesh. Hybrid, MS/4-2261 has 15.41% dry matter with good keeping quality and field resistance to late blight. LBY 15 and LBY 17 having combined resistances to late blight and PVY were selected for multilocal trials. Hybrid, OS/01-516, resistant to cyst nematode and late blight outyielded Kufri Giriraj at Ootacamund. Sequencing of chromosome 2 covered 2.4 Mbp sequence with 877 large contigs. Transgenic lines of potato with durable late blight resistance using RB gene were selected for further evaluation. A cold chipping line developed using RNAi gene was further evaluated and found highly promising. Putative somatic

hybrids developed earlier were confirmed using molecular and phenotypic markers.

Sixteen cassava landraces with very good chip making quality were identified, of which, Ci-24 had low cyanogens and was free from symptoms of cassava mosaic disease. Eighty-seven accessions were evaluated for drought tolerance, of which 34 were found tolerant.

In **sweet potato**, 10 orange-fleshed clones showed total carotenoids of 11–14 mg/100g fresh weight and  $\beta$ -carotene of 9–13 mg/100g fresh weight and the dry-matter content was 21–25%. Clones, CIP-440127 and Samrat, were promising for salt tolerance at Erasama in Orissa and Canning in West Bengal, respectively. The Single Marker Analysis (SMA) of DNA isolated from 250 hybrid sweet potato seedlings using 5 ISSR primers resulted in identification of one marker ISSR Y818 3/1 associated with  $\beta$ -carotene. Six accessions of *D. alata*, viz. Da 10, Da 11, Da 60, Da 62, Da 64 and Da 157, were found to be tolerant to anthracnose disease from screening of field gene bank of greater yam. The *Amorphophallus* hybrid, Am H 102, gave significantly higher yield of 43.8 tonnes/ha with resistance to collar rot and in taro, hybrid Co H 4-3 with high yield (22.2 tonnes/ha) have been identified for on-farm trials.

A cassava transformation protocol was optimized. Cassava transformation was done with three hairpin constructs of Sri Lankan cassava mosaic virus (SLCMV)/Indian cassava mosaic virus (ICMV) in cassava cultivar H 226. Transformation efficiency was 0.6–1%. Full genome of SPLCV (2.8 kb) was amplified through rolling circle amplification and amplified product (2.8kb) has been cloned in pUC18 vector.

### Spices

Microsatellites developed for *Piper* species were successfully used to detect polymorphism in its cultivars. The *Piper ornatum*, a wild species related to black pepper, find resistance to *Phytophthora capsici*, *Radopholus similis* and *Meloidogyne incognita*, pathogen involved in quick and slow wilt of black pepper. Cardamom hybrid, GG × NKE 19, was promising with more than 70% of 8 mm capsules and showed field tolerance to rhizome rot and leaf blight. Of the 68 second generation seedling progenies of 5 seedling progenies, most of them showed very high multiplication rate.

Among 13 genotypes analyzed for biochemical parameters, oil content varied from 1.2 to 2.8%, maximum being in Acc.162, followed by Acc.95, while oleoresin content was 2–4.6% and fibre 1.87–5.13%. Chromosome number of ginger collection Acc.195, which has high pollen fertility, was found to be 2n=44 in majority of cells, indicating that it is a tetraploid. In **Garcinia**, using the model of GIS, the existence in north-east Himalayan region was assessed. Four species of *Garcinia*, namely *G. kydia* (Kuji Thekera), *G. lancifolia* (Rupohi Thekera), *G. pedunculata* (Bor Thekera) and *G. xanthochymus* (Tepor Tenga) were located in Meghalaya and Asom.

## Floriculture

Arka Naveen, Arka Gold and Arka Amar varieties of gladiolus; Arka Tejas of Dianthus; Arka Nirantara of tuberose; Arka Kanaka and Arka Ambara of crossandra and Arka Pinkstar of chrysanthemum were identified for release. Rose varieties, Impertice Farah, Gold Medallion, Taj Mahal, Papa Meiland and Paradise in hybrid tea group; Summer Snow, Valentine, Saratoga, Candian Centenary in Floribunda group and Wild Plum and Bhargava in miniatures group were found promising in western region. Rose, Valentine, Summer Snow Saratoga and Canadian Centenary (floribundas) and Small Virtue and Rise-n-Shine (miniatures) flowered during summer months. For cut flowers, chrysanthemum varieties, Reagan White, Reagan Emperor, Majoor Bosshardt Wit, Kelvin Mandarin, Kelvin Tattoo, Nanako, White Bouquet, Ajay, White Staphour, Obsession, Statesman and Kermits were found suitable, while Baggi, Birbal Sahni, Ratlam Selection and Basanti for loose flowers and Mother Teresa, Gum Drop, Tomiko, Dolly Pink, Kotai No Kori, Yellow Charm and Little Dipper for pot plants. Tuberose variety, Prajwal was found to be most promising for Punjab.

In **orchids**, 350 species are maintained under protected conditions, including 20 species under terrestrial conditions and 30 species under natural conditions on tree logs. A large number of hybrids of *Cymbidium*, *Dendrobium*, *Vanda*, *Phalaenopsis*, *Aranda*, *Mokara*, *Cattleya* and *Oncidium* were also maintained and evaluated. A total of 13 hybrids of *Dendrobium*, 'Bangkok Blue', 'Larvia', 'Madam Pampodur', 'Big White'; 8 of *Vanda*, 'Robert Delight Blue' and 7 of *Phalaenopsis*, 'Brother and Sister' were found promising. Genotyping using RAPD was done for *Dendrobium* and descriptors have been developed for DUS testing.

## Mushroom

Twenty single spore isolates of *Pleurotus sajor-caju* and 57 hybrids evolved by compatible mating were compared for qualitative estimation of laccase using ABTS and fruit body formation. Three parent strains of *Volvariella volvacea* and 4 single spore isolates were pre-screened for various characteristics. Strain, OE-272, produced highest number of fruiting bodies. A large-sized *Scleroderma* sp. has been identified using morphological and molecular taxonomy ITS-1 and ITS-4, a new world record. Intensive explorations were undertaken and 14 endangered species were collected, characterized and planted in field gene bank. The S 130 strain of *Agaricus bisporus*, *P. florida* hybrid, PF 03 and *P. sajor-caju* hybrid PSc 5 and PSc 4, and Vv 11, Vv 09 and Vv 12 of *V. volvacea* were superior to other strains within the groups.

## Medicinal and aromatic plants

A molecular technique to detect common adulterant of Ashoka raw drug was developed. Species-specific RAPD bands of both species were cloned and sequenced. Primers were designed to amplify sequence characterized amplified region (SCAR) markers from

individual species. The SCAR primer designed from *S. asoca* produced an amplified product of 193 bp from this species only. Similarly, species-specific amplification of a 395 bp product was achieved from *P. longifolia* using another set of primers.

Progeny rows of single plant selections of ashwagandha resulted in wide variability. The lines obtained included an extra dwarf plant (15–20 cm), plant with open type calyx, clustered flowering type, compact plant type with less fibrous roots and procumbent plant type. Plant types with four different berry colours, viz. red, yellow, orange and creamy white were also identified. A male sterile plant was identified, first time in this species.

Forty-three giloe accessions were characterized based on starch granule size (perimeter) and their frequency distribution. Based on the frequency distribution of starch granules of different classes, germplasm was also classified into five classes. Majority of them have small starch granules (46–75  $\mu\text{m}$ , L1 10–25  $\mu\text{m}$  and L2 of 10–20  $\mu\text{m}$ ). Fresh stem yield varied from 0.09 to 5.44 kg/plant and dry stem yield 0.03 to 1.43 kg/plant. Highest dry stem yield was recorded in IC 283650 (1.43 kg/plant), followed by Kalyani (0.71 kg/plant), IC 310602 (0.64 kg/plant) and GUJ 4 (0.60 kg/plant). Stem starch content varied from 12 to 52% on dry-weight basis among the accessions.

In M3 generation progeny, rows of isabgol were grown from chemical mutagen (DES, EMS and Colchicine) treatments. Among these, an early-flowering (30–35 days after sowing) and-maturing (80–85 DAS) mutant, DPO 14, was identified. It had an average plant height of 37.6 cm, 60 leaves/plant, 37 spikes/plant, 9.84 g biomass/plant and seed yield of 2.25 g/plant. From the colchicines treated plant progenies of GI 2 variety, a tetraploid plant, was isolated. Tetraploid plants were more vigorous than the diploids. Fifteen germplasm lines of asalio (*Lepidium sativum*) were evaluated. The highest seed yield was recorded in genotype HLS 5 (2,048.21 kg/ha), followed by HLS 7 (1,938.36 kg/ha). Out of 13 germplasm lines evaluated, highest mean seed yield was recorded in MLS-7 (1,941 kg/ha).

## BIOTECHNOLOGY

**Bioprospecting of genes and allele mining in microbes:** A total of 548 microbes (381 bacteria, 35 fungi, 104 cyanobacteria and 28 phytoplanktons) tolerant to a wide range of abiotic stresses, moisture, cold, heat, salinity and anoxia, were isolated. Transcriptome sequencing of salt-tolerant halobacillae and cold-tolerant *Arthrobacter sulfurous* revealed a set of known and unknown genes for the target traits.

Phenotyping was initiated in the core collections of targeted crops like rice (7,227), sorghum (242), *Lathyrus* (295), *Cucumis* (175) and mothbean (223); 300 inbred lines in maize and 40 accessions of *Ziziphus* were identified as the core set for association mapping, gene discovery and allele mining. Genome



re-sequencing of six genotypes of rice was completed for Single Nucleotide Polymorphisms (SNPs). Functional validation of two stress-responsive rice genes, using model plant system *Arabidopsis*, revealed that one of the genes was promising in imparting tolerance. One drought-responsive promoter from sorghum was characterized in *Nicotiana tabacum*.

**Development of transgenics:** Quality trait loci (QTLs) markers in **wheat** were identified for root biomass. In **rice**, QTLs were mapped for aroma, grain length and salt tolerance, and functional markers were developed for *BADH2* gene for aroma in aromatic rice.

Putative rice transgenics were developed in cultivars PusaSungandh 2, IR 64 and BPT 5204 with *DREB1a* gene for drought tolerance, and in cultivars IR 64, BPT 5204 and Swarna with *cryIac* and *cryIab* for resistance to stem borer.

#### QTL for grain-filling in rice

Nine quality trait loci for grain-filling on chromosomes 1, 2, 3, 4, 5, 7 and 10 were identified in F<sub>2</sub> mapping population derived from Rasi, a rice variety, with >90% grain-filling; and IC 114927, a landrace, with <45% grain-filling, using selective genotyping approach.

In **mustard**, crosses were made for development of mapping populations for *Alternaria* blight resistance and drought tolerance.

Transgenic mustard expressing *osmotin* that confers tolerance to salinity, transgenic **potato** expressing *RB* gene from *Solanum bulbocastaneum* that confers

#### CLCuV-resistant cotton plants

*Gossypium hirsutum* genotypes H 777 and HS 6 were transformed into CLCuV (cotton curl leaf virus)-resistant plants with antisense *rep* (replicase protein), sense coat protein and antisense coat protein gene constructs mediated through *Agrobacterium*. Transgenics were characterized for transgene presence by the PCR and Southern hybridization and were evaluated for tolerance to CLCuV.

#### Sugarcane streak mosaic virus coat-protein gene recombinant expression

Efforts were made to produce antisera for major sugarcane viruses. Preparation of antiserum against recombinant coat protein has strategic advantage, hence cDNA fragment coding for the partial ORF of the sugarcane streak mosaic virus (**SCSMV**) coat protein gene (~850bp) was cloned by the RT-PCR using gene specific primers. The cloned cDNA fragment in the protein expression vectors pMAL-C4X and SCSMV-CP expressed as an MBPSCSMV-CP fusion-protein after induction with the IPTG. Proteolytic enzyme cleaved fusion-protein into two fragments of ~42 and ~30kDa corresponding to MBP and SCSMV-CP, respectively. The MBP-SCSMV recombinant protein was affinity purified, and polyclonal antisera were raised in rabbit.

#### *Mesorhizobium ciceri* Ca 181 genome sequenced

*Mesorhizobium ciceri* Ca181 is an agriculturally important nitrogen-fixing symbiont strain widely adapted to superior nitrogen-fixer strain of chickpea. Its genome sequencing was done by Next Generation 454 pyro-sequencing technology. About 849 million base pairs sequence data were generated in the form of 2.68 millions sequence reads. This huge sequence data were assembled through De novo Genome Assembler (Newbler Assembler) software. The complete assembled genome is about 8.0 Mb, estimated genome size and 70x coverage depth. A total of 64 contigs were formed having average length of 0.11 Mb base pairs and the largest contig was 0.57 Mb base pairs. A total of 6,461 genes were predicted out of 64 contigs used and operon prediction through *FGENESH-B*. Two thousand short plasmid (0.5–2.0 kb inserts) clones were also generated by shearing sym plasmid. Sequencing of 0.5 to 2.0 kb inserts was done by shotgun method (Sanger method). And 1,344 reads were generated from sequencing 672 clones with end-to-end sequencing.

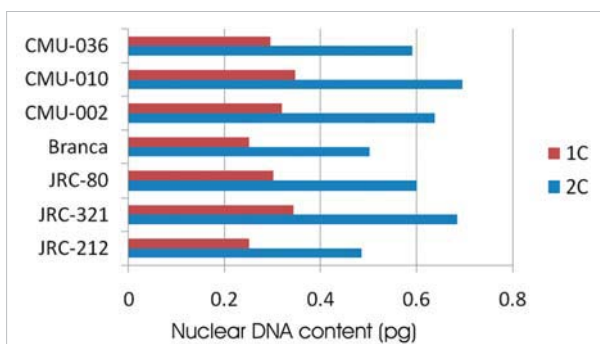
resistance to late blight disease and transgenic **sorghum** expressing *cryIB* gene that confers resistance to stem borer are ready for field testing.

Biosafety tests on **cotton** transgenics (Anjali and LRK 5266 with *cryIac* and *cryIF* genes) showing resistance for American bollworm were carried out.

**Sugarcane-specific promoters— identification and cloning:** Out of the three 5' upstream sequences of three different ubiquitin genes isolated, two were cloned in pCAMBIA vector in place of CaMV35s promoter to get a gene regulatory region—*gus* fusion. Suitable constructs were used for transforming sugarcane, rice, tobacco and *Arabidopsis* through *Agrobacterium*/biolistics with appropriate controls for validation studies. This regulatory region could drive *gus* gene expression in rice and sugarcane tissues but not in tobacco and *Arabidopsis*, indicating monocot-specific nature of the regulatory sequence. To understand the role of different domains of 5' upstream region in gene expression, six deletions of the region were cloned in pCAMBIA vector for transformation studies.

**Jute nuclear DNA content and haploid genome estimation:** Cultivated jute species *Corchorus capsularis* L. (seven genotypes) and *C. olitorius* L. (five genotypes) nuclear DNA content (2C values) and haploid genome (1C) sizes were estimated by the laser flow cytometry. There were significant ( $P \leq 0.05$ ) differences in 2C values not only between two cultivated species, but also between genotypes within the species. In *C. capsularis*, 2C values ranged from 0.502 to 0.695 pg, with the lowest value recorded in JRC 212 or Branca and the highest in the X-irradiated soft-stem mutant CMU 010. *C. capsularis* JRC 212 or Branca has the smallest genome of ~246 Mb, and the mutant CMU 010 has the largest (~341 Mb). *C. olitorius* cv. Sudan Green, with a genome size of ~315 Mb is the smallest genome among the *tossa*-jute cultivars and JRO 524 or S 19 has the largest genome, with an average of ~330 Mb.





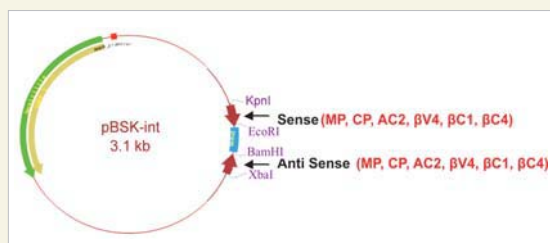
Nuclear DNA (2C content in different genotypes and mutants of *C. capsularis*) as determined by laser flow-cytometric measurement of the relative fluorescence of propidium iodide-stained nuclei in comparison with chicken red blood cell (CRBC) used as an internal standard

### Shootfly QTL for marker-assisted breeding:

Quality trait loci (QTL) for component traits (glossiness, trichome density and seedling vigour) for shootfly resistance in sorghum, using a recombinant inbred population of cross 296B (susceptible) × IS 18551 (resistant), were identified. LG SBI 10 has two quality trait loci regions between SSR markers, Xgap1-Xnhsbm1011 and Xnhsbm1044-Xnhsbm1013. Similarly, SBI 05 carries a major gene for glossiness between SSR markers Xtxp65-Xtxp30.

### RNAi construct for resistance against CLCuV in cotton

To engineer RNA interference-mediated resistance against CLCuV, five inverted repeat constructs of target sequences — pBSK-int-AC2-SA (3.3 kb), pBSK-int-CP-SA (3.4 kb), pBSK-int-MP-SA (3.2 kb), pBSK-int-βC1-SA (3.4 kb) and pBSK-int-βV4-SA (3.4 kb) in *Agrobacterium tumefaciens* were generated. Plasmids pBin-CP-S-int-A and pBin-βC4-S-int-A were transformed in *Gossypium hirsutum* HS6 by *Agrobacterium*-inoculation. Putative transformants were characterized for integration of transgenes.



Inverted repeat plasmid pBSK-int (3.1 kb) with sense and antisense strands of 6 viral target sequences

### DNA fingerprinting

Cotton germplasm (156) were characterized, and could be discriminated using simple sequence repeat (SSR) primers. DNA fingerprinting was done in oats (110), pearl millet (20) and finger millet (67) using SSR markers; in *Jatropha curcas* (257) using random amplified polymorphic DNA primers, inter simple sequence repeat (ISSR) primers and amplified fragment length polymorphism (AFLP) primers; in flax (20) using RAPD, ISSR and sequence related amplified polymorphism (SRAP) markers. In *Cucumis*, sequence variation was

### Cytoplasmic male sterile system (CMS) in cauliflower

To develop CMS-based hybrids in cauliflower, attempts were made to transfer male sterility genes of wild brassica plants, viz., *Moricandia arvensis* and *Erucastrum canariense* to *Brassica juncea* and *B. napus* of cauliflower by sexual hybridization and backcrossing. Interspecific hybrids were recovered successfully by embryo-rescue technique. BC<sub>2</sub> generation plants were successfully obtained from the crosses. Some of them showed characteristic *oleracea* phenotype.

identified in *rbcL* locus to distinguish *C. sativus* from *C. melo*. Novel expressed sequence tag-simple sequence repeat (EST-SSR) markers were developed in finger millet (75) and watermelon (122). Hexaplex polymerase chain reaction (PCR) assay for simultaneous amplification of commonly used marker genes—*nptII*, *aadA*, *bar*, *pat*, *hpt* and *uidA*—was developed for initial screening of genetically modified crop materials. Qualitative detection using real time PCR was carried out in GM crops—tomato (*AVPI*), cotton (*EPSPS*) and potato (*cryIAb*). Molecular testing was done in 216 imported transgenic planting materials.

Genomes of cucumber mosaic virus (RNA1) (Delhi isolate, GU111227, 3358 nt), papaya ringspot virus (Pathotype W, EU475877, 10335 nt) and citrus tristeza virus (Kpg3, 19253 nt) were sequenced.

### Seed

Nucleus seed production technology was optimized for different premier and popular rice varieties—PusaSugandh 4, PusaSugandh 5, Sarju 52, Naveen, Pratikshya, MTU 7029 and BPT 5204 for breeder seed production.

During the current year, 629 tonnes of nucleus seed, 9,554 tonnes of breeder seed, 7,745 tonnes of foundation seed, 3,471 tonnes of certified seed, and 10,443 tonnes of truthfully labelled seed were produced.

Under participatory seed production using the ICAR Seed Project Revolving Fund, appreciable amount of quality seeds were produced of wheat varieties compatible to eastern Uttar Pradesh—PBW 343 (4.8 tonnes), HD 2733 (1.36 tonnes), WR 544 (2.96 tonnes) HD 2851 (1.92 tonnes) and Kundan (0.76 tonne). Total quality seed production of field crops and horticultural crops was 63,761.8 tonnes against the target of 43,454.6 tonnes. Besides, 604.16 lakh planting materials and 2.01 lakh tissue-culture plantlets of field crops were produced against the target of 194.51 and 1.58 lakh, respectively.

It was demonstrated that CO<sub>2</sub>-rich atmosphere (40%) provided zero-insect infestation without impairing germination of paddy and maize seeds in 12 months' of storage; hitherto not possible excepting with chemical fumigants. CO<sub>2</sub> storage technique can be upscaled and can be used for storing other crop-seeds also.

Following grading sieves are recommended for different crop seeds—safflower: 2.2 mm; soybean: 3.6 mm; chickpea: 5.0 mm; paddy: 1.4 mm for fine-grained



varieties, 1.6 mm for coarse-grained varieties; and *ragi*: 1.30 mm.

### Honeybees and pollinators

At Solan, pollen inserts from apple pollinizer flowers fixed in *Apis mellifera* colonies resulted in 73.68% fruit set as compared to 48.43% when colonies were placed in the apple orchard without pollen inserts. In Bhubaneswar, pollination by *A. mellifera* in mustard (*Brassica juncea*) increased seed yield by 12.16 to 21.26%. Highest berseem yield in Ludhiana was recorded in open pollination (97.98%), followed by plots caged with *A. mellifera* colony (90.90%) as compared to plots excluded from pollinators. Five hives of *A. cerana* were found optimum to obtain significant increase in fruit set and yield of cucumber in Jorhat. Open pollination in cucumber in Bengaluru gave highest fruit set (98.23%), followed by *A. cerana* (95.56%), *A. florea* (93.13%) and *Trigona* species (90.45%)

#### Stingless bees and their management

Four stingless bee species, *Trigona canifrons*, *T. iridipennis*, *T. atripes* and *T. laeviceps* were identified from the north-east. Peak foraging activity of stingless bees was recorded in September and June in Odisha. Wooden boxes (15 cm × 10 cm × 10 cm) were found most suitable for domesticating stingless bee colonies in Odisha as compared to earthen pots and bamboo pieces in Kerala and Uttar Pradesh.

pollinated crop. Greater number and weight of onion seeds per umbel were recorded in Hisar in open-pollinated plants as compared to selfed plants. Carpenter bee *Xylocopa fenestrata* was found effective pollinator of ridgegourd in Jorhat; resulting in 250% increased yield over no pollination. Pollination by stingless bee resulted in 83.16% fruit set in winged-bean *Psophocarpus tetragonolobus* as compared to just 2.2% plants when excluded from pollinators.

In Bhubaneswar, pollen substitute consisting of brewer's yeast (42%), dehusked parched gram-flour (4%), skimmed milk powder (4%) and sugar solution (50%) was found best for dearth period management and colony development of *A. mellifera*. ELISA test kit was developed for detection of European Foul Brood disease. Thaisac brood virus (TSBV) and sac brood virus were identified at Solan and their molecular characterization was done. Aqueous extracts of *Mimosa pudica* and *Philanthus niruri* at 2 ml/100 ml sugar syrup fed to *A. cerana* reduced incidence of TSBV in Kerala.

Population dynamics of *Varroa destructor* at Ludhiana indicated increased mite population with increase of worker brood honeybee colonies. Non-chemical methods such as dusting of finely ground sugar with sticky paper at bottom board and garlic powder (13.35%) mixed with icing sugar were effective in management of *Varroa* mite in Ludhiana, Pantnagar and Solan.

