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Crop Improvement

Global demand of crops for food, feed and fodder is increasing rapidly to meet requirement of ever-increasing population of human and also of livestock. Researches on genetic improvement of crops strive at improving productivity of crops in view of the shrinking arable land. Crop genetic improvement also aims at realizing nutritional security besides development of climate-resilient crops (biotic and abiotic stresses) and also crops suitable for diverse cropping systems.

Crop improvement programmes have been reoriented with a greater emphasis on the development of genomic resources for targeted traits and crops. Pre-breeding for accessing desirable genes from the related and the wild species has also been employed to broaden narrow genetic base and introgress desirable alleles. Characterization of economically important genes/alleles, their functional validation, marker-assisted selection of phenotypes encoded by such genes/functional alleles and ultimately cloning of genes for transgenic/cisgenic deployment holds a great promise for genetically improving crops.

Cereals

Twenty-one high-yielding varieties of rice, eleven of wheat, six hybrids of maize, three of pearl millet and four of sorghum were released for cultivation in different production ecologies of the country.

Commercialization of wheat variety 'HD 3086'

With a mission of "Translating Research into Prosperity", ZTM & BPD Unit at the IARI launched a marketing campaign of the variety, and commercialized it successfully in the Indo-Gangetic Plains (Punjab, Haryana, western Uttar Pradesh and Rajasthan).

Swarna Shreya rice for drought-prone areas: A medium duration (120-125 days) aerobic rice variety, Swarna Shreya (IET 24003), has been developed by the

ICAR Research Complex for Eastern Region, Patna, Bihar, and released by the Bihar State Seed Sub-Committee on 14 May 2015. It has capacity to withstand drought and is also tolerant to major diseases and insects. Average



Swarna Shreya—A new rice variety for drought-prone areas

Biofortified CR Dhan 310 for high protein



Panicle, grains and kernel of CR Dhan 310 (IET 24780)

This protein-rich rice variety evolved from a cross between ARC10075 and Naveen is suitable for cultivation in medium-rainfed lands during *kharif* and irrigated areas during *boro/rabi* season. It has semi-dwarf plant type (100-110 cm), maturing in 120 days in *kharif* under transplanted conditions. In *rabi*, it matures in 125 days under trans-plantation. The variety has medium slender grains with 69.7% head rice recovery. It yields 4.5-5.0 tonnes grains/ha during *kharif* and 5-6 tonnes/ha in *rabi*.

Released varieties/hybrids of cereals

Variety	Area of adoption	Salient features
Rice		
Arize 6444 Gold	Andhra Pradesh, Maharashtra, Uttarakhand, Uttar Pradesh, Tripura, Odisha, Karnataka	IRM; R-BLB, GM
INH 97288	Punjab, Chhattisgarh, Uttar Pradesh	IRM, high-yielding with long bold seed
RC Maniphaou 12	Manipur	IRE; MR- SB
Indira Aerobic 1	Gujarat, Chhattisgarh, Tamil Nadu	Aerob; R-NBI, ShR, MR-LBI, ShBI, BS, RTD





Variety	Area of adoption	Salient features
Basmati 564	Jammu and Kashmir	SCR; MR-BI, R-NBI, BPH
6129	Punjab, Tamil Nadu	IRE; MR- LBI, ShBI, BS
BNKR1	West Bengal	Late (RSL); MR- NBI, ShR
Pushpa	Karnataka	IRE; R-BPH
Vallabh Basmati 24	Uttar Pradesh, Haryana, Jharkhand	SCR; MR-BS, ShR
IR 64 Drt 1	Andhra Pradesh, Madhya Pradesh, Telangana, Tamil Nadu, Jharkhand, Chhattisgarh	IRME; MR-LBI
DRR Dhan 41	Bihar, Karnataka	Aerob; T-Nematode, GLH,LF
CO 51	Tamil Nadu	IRME; MR-LBI, BPH
Birsa Vikas Dhan 111	Jharkhand	RUP; MR-LBI, BS, SB
Sambha Sub 1	Uttar Pradesh	NIL-Sub; MR-RTV
Birsa Vikas Dhan 203	Jharkhand	RUP; MR-LBI, BLB, BS, SB
Vallabh Basmati 23	Uttar Pradesh	SCR; R-RTV, GM
Sabour Shree	Bihar	IRM, Medium slender grain type with 108 days to 50% flowering
PR 124	Haryana, Punjab	IRE; MR-BS, LBI, ShR, GMB1
Shalimar Rice 2	Jammu and Kashmir	HRIR; MR-LBI
Shalimar Rice 3	Jammu and Kashmir	HRIR; MR- ShBI, LBI
SAVA 127	Uttar Pradesh	IRE, short statured; and moderately tolerant to lodging
Wheat		
Pusa Kiran	Hills of Jammu and Kashmir, Himachal Pradesh, Uttarakhand	Rainfed, early sown; R- yellow rust and good for <i>chapati</i> quality
RSP 561	Plain and mid- hills of Jammu Division of Jammu and Kashmir	Irrigated, timely sown; MR- to yellow/ stripe, leaf and stem rust
Shalimar Wheat 2	Kashmir Division of Jammu and Kashmir	Early maturing
WH 1142	Punjab, Haryana, northern Rajasthan, western Uttar Pradesh, foot hills and plains of Jammu and Kashmir, Himachal Pradesh and Uttarakhand	Restricted irrigation, timely sown; is lodging resistant
Pusa Vatsala	Uttar Pradesh, Bihar, Jharkhand, West Bengal	Irrigated, late sown, good for bread industry
DBW 107	Uttar Pradesh, Bihar, Jharkhand, West Bengal	Irrigated, late sown; R- leaf blight and MR - leaf rust
DBW 110	Uttar Pradesh, Maharashtra, Gujarat, Madhya Pradesh, Chhattisgarh	Restricted irrigation, timely sown, higher yield gains at one and two irrigations
DBW 93	Maharashtra, Karnataka	Restricted irrigation, timely sown;R- stem and leaf rusts; high protein content, high test weight, high flour recovery
Pusa Anmol (Durum)	Uttar Pradesh, Maharashtra, Gujarat, Madhya Pradesh, Chhattisgarh	Irrigated, timely sown;R- stem and leaf rusts; suitable for pasta preparation
UAS 446 (Durum)	Maharashtra, Karnataka	Rainfed, timely sown; lustrous grains with high protein content and yellow pigment
Nilgiri Khapli (Dicoccum)	Tamil Nadu, Karnataka	Irrigated, timely sown; high degree of seedling resistance to most stem, leaf and yellow rust pathotypes



Variety	Area of adoption	Salient features
Barley		
DWRB 101	Punjab, Haryana, northern Rajasthan, western Uttar Pradesh, foot- hills and plains of Jammu and Kashmir, Himachal Pradesh and Uttarakhand	Two-row malt barley, good grain quality; timely sown conditions; resistant to stripe and leaf rusts
BH 959	Uttar Pradesh Maharashtra, Gujarat, Madhya Pradesh, Chhattisgarh	Six-row feed barley; tolerant to yellow and brown rust
Maize hybrids		
CoH (M) 10	Andhra Pradesh, Tamil Nadu, Karnataka, Maharashtra, Rajasthan, Gujarat, Madhya Pradesh and Chhattisgarh	<i>Kharif</i> season: medium maturity, orange-yellow, semi-dent; R- MLB, RDM ,MR- C. rust and TLB
HM13	Jammu and Kashmir, Himachal Pradesh and Uttarakhand	<i>Kharif</i> season, early maturity, yellow with cap, flint ;R- MLB, TLB, BLSB, C.rust and PFSR
PMH 6	Bihar, West Bengal, Jharkhand, Odisha and Uttar Pradesh	<i>Kharif</i> season, medium maturity, yellow, flint
NMH 713	Uttar Pradesh, Bihar, Jharkhand, Odisha, Andhra Pradesh, Karnataka, Tamil Nadu and Maharashtra	<i>Rabi</i> season, late maturity, yellow, dent
NMH 731	Gujarat, Rajasthan Chhattisgarh, Madhya Pradesh, Andhra Pradesh, Karnataka, Tamil Nadu , Maharashtra	<i>Kharif</i> season, late maturity, orange-yellow, semi-dent
NMH 1242	Andhra Pradesh, Tamil Nadu, Maharashtra, Karnataka, Punjab, Haryana, Delhi, Uttar Pradesh, Rajasthan, Gujarat, Chhattisgarh, Madhya Pradesh	<i>Kharif</i> season, medium maturity, yellow, dent; MT- MLB
Pearl millet		
NBH 5767	Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu	Medium maturing, purple anther colour, medium plant height, compact lanceolate ear-heads, deep grey-coloured grains
NBH 5061	Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu	Late maturing, purple anther colour, medium plant height, compact lanceolate ear- heads, grey-coloured grains
Dhanshakti	Rajasthan, Haryana, Madhya Pradesh, Gujarat, Uttar Pradesh, Punjab, Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu	Early-maturing variety with high iron (76-91 ppm) and zinc (39-48 ppm); bold, globular, shining slate- grey- coloured seeds, cylindrical -lanceolate ear-head; R- downy mildew
Sorghum		
SPH 1635	Maharashtra	<i>Kharif</i> hybrid, dual- purpose, mid- late group maturity; grain yield: 4.5 tonnes/ha ,dry fodder yield: 13 tonnes/ha; T- major insects and pests
Phule Suchitra	Maharashtra	<i>Rabi</i> variety, medium maturity, tall (235 cm) white midrib, compact cylindrical panicle, medium bold pearly -white seeds; T- shoot-fly, stem-borer and drought
CSH 33	Rajasthan, north Gujarat, south Andhra Pradesh, Tamil Nadu	<i>Kharif</i> hybrid, medium tall, early maturity; long bold panicles and bold grains, grain yield: 4.4 tonnes/ha, dry fodder yield: 11.8 tonnes/ha.; T- grain-mould and shoot-fly
CSV 32F	Maharashtra, Karnataka, Tamil Nadu	Forage sorghum variety, well- exerted panicle with clustering of grain in panicle branches, green fodder yield: 46.2 tonnes/ha, dry fodder yield: 17.8 tonnes/ha; R- anthracnose, sooty stripe and grain-mould.

BL : Blast; **BLB**: Bacterial Leaf Blight; **RTV**: Rice Tungro Virus; **ShBI** : Sheath Blight; **BS** : Brown Spot; **GLH** : Green Leaf Hopper; **SB** : Stem Borer; **BPH**: Brown Plant Hopper; **MLB**: Maydis Leaf Blight, **TLB**: Turicum Leaf Blight, **BLSB**: banded Leaf and Sheath Blight; **C. rust**: Common rust, **PFSR**: Post Flowering Stalk Rot; **WBPH** : White Backed Plant Hopper; **GM** :Gall Midge; **LF**: Leaf Folder; **T**: Tolerant; **R**: Resistant; **MR**: Moderately Resistant





Improved rice variety DRR Dhan 41 (IET 22779)


BC₃ F₁ rice-plants in glasshouse

productivity of this variety is 4.5 to 5.0 tonnes/ha. Under severe drought, it can produce 2.0 to 2.5 tonnes/ha. Under dry direct-seeded aerobic condition, it saves up to 40% water as compared to transplanted rice. It produces long bold grains, and quality-wise, it possesses 77.0% hulling, 69.7% milling, 60.2% head rice recovery (HRR) with desirable intermediate alkali spreading value (ASV=4.0) and amylase content (22.26%).

Marker-assisted breeding of abiotic stress tolerant rice: This project was aimed to transfer major quantitative trait loci (QTL) for salinity tolerance into locally adapted, high-yielding varieties of rice through marker-assisted backcross breeding. Genotype FL 478 was used as donor parent, whereas Sarjoo 52, PR 114 and Pusa 44 were used as recipient parents to transfer salinity tolerance genes. After crossing recipient parents with donor parent, F₁ seeds were obtained for Sarjoo 52 × FL 478, PR 114 × FL 478 and Pusa 44 × FL 478. Ten to fifteen per cent of F₁ seeds were obtained from each cross. A total of 250, 100 and 150 F₁ seeds were obtained from Pusa 44 × FL 478, PR 114 × FL 478 and Sarjoo 52 × FL 48, respectively. The available F₁ seeds were divided into two sets for advancing generation to BC₁F₁. In the first set, the experiment was conducted in glasshouse, and for second set, a field experiment was conducted to produce BC₁F₁ population. F₁s were used as male parent and recipient parent of the last year was used as female parent in cross.

True BC₁F₁ plants were selected using *Saltol* markers, through foreground and recombinant marker selection, for their further use in crossing programme. RM 3412 was used as marker for foreground selection. For recombinant selection, RM 493, RM 10748 and RM 10893 were used as markers. The selected true BC₁F₁ plants were backcrossed with their respective parents (Pusa 44, PR 114 and Sarjoo 52), and BC₂F₁ seeds were harvested. The seeds of parents and BC₂F₁ were sown on floating grids under hydroponics in Yoshida culture solution. After thirty days, seedlings were transplanted in field for further maintenance. True BC₂F₁ plants were selected using *Saltol* markers RM 3412 (foreground selection) and RM 493 and G11A (recombinant selection) for their further use in crossing programme to produce BC₃F₁ population. The selected true BC₂F₁ plants were backcrossed with their respective parents (Pusa 44, PR 114 and Sarjoo 52) and BC₃F₁ seeds were harvested.

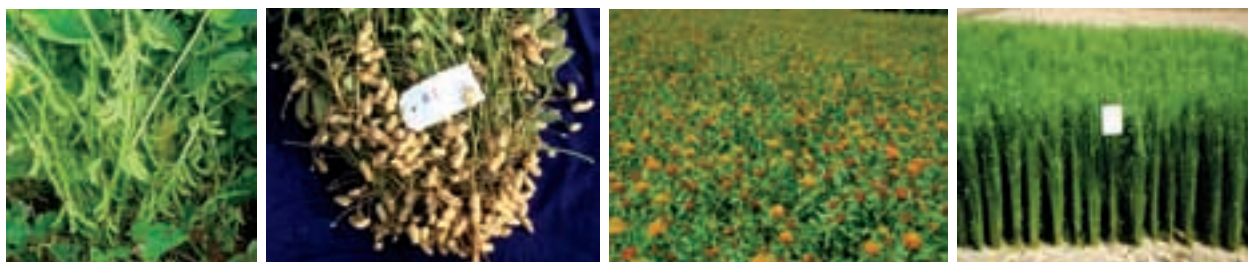
Oilseeds

Sixteen high-yielding varieties of oilseeds were released for different agro-ecologies.

High oleic safflower genotypes: Nine hundred and twenty-seven F₅ progenies possessing >70% oleic acid oil content ranging from 19.0 to 40.1% were developed. The best check, A-1, recorded 27% oil content and 12% oleic acid.

Released varieties/hybrids of oilseeds

Variety/hybrid	Recommended state/region	Salient features
Rapeseed-mustard		
Gujarat Dantiwada Mustard 4	Gujarat	Irrigated conditions; recorded 11.1 -24.7% higher yield over checks; tolerant to powdery mildew and aphids
Albeli1	Eastern Rajasthan, Madhya Pradesh, Uttar Pradesh, Uttarakhand	Irrigated conditions; average seed yield 1,973 kg/ha; tolerant to <i>Alternaria</i> blight, white rust and powdery mildew
RSPN 25	Jammu	Irrigated conditions, 145-155 days to maturity; average seed yield 1,500-1,800 kg/ha; 36-39% oil content
GSC 7	Punjab, Himachal Pradesh, Jammu	Timely- sown, irrigated conditions, 139-232 days to maturity low erucic and low glucosinolate content; average seed yield 1,793-2,190 kg/ha, 38.6-42.0% oil content



Phule Agrani (KDS 344) variety of soybean; Raj Mungfali 2 of groundnut; NARI 57 of safflower and Tiara of linseed (fibre flax type) (from left to right)

Variety/hybrid	Recommended state/region	Salient features
Soybean		
NRC 86	Maharashtra, Madhya Pradesh, Chhattisgarh, Rajasthan	95-97 days to maturity; average yield 2,128 kg/ha, 19.8% oil content, 40.60% protein content; highly resistant to charcoal-rot, moderately to highly resistant for girdle beetle and moderately resistant to bacterial pustule, pod-blight, collar-rot and stem-fly
KDS 344 (Phule Agrani)	Karnataka, Andhra Pradesh, Telangana	94 days to maturity; average yield 2,555 kg/ha, 16.8% oil content, 34.6% protein content; tolerant to rust, moderately resistant to stem-fly, pod-borer and leaf-roller
Pusa 12	Punjab, Haryana, Himachal Pradesh	124-131 days to maturity; average yield 2,286 kg/ha, 19.6% oil content, 37.8% protein content; resistant to yellow mosaic virus, <i>Rhizoctonia</i> aerial blight and bacterial pustules
DSB 21	Karnataka, Andhra Pradesh, Telangana	90-95 days to maturity; average yield 2,500-3,000 kg/ha, 18.2% oil content; 38.2% protein content; resistant to rust
Groundnut		
Gujarat Junagadh Groundnut 18	Odisha, West Bengal, Jharkhand, Manipur	<i>Kharif</i> season, maturity 120 days; 1,557 kg pod/ha and 1,215 kg kernel / ha, oil content 48%
Raj Mungfali 2 (RG578)	Odisha, West Bengal, Jharkhand, Manipur	<i>Kharif</i> season; semi-spreading (Virginia bunch type); 1,480 kg pod/ha and 1,071 kg kernel / ha, large seeds (53 g / 100 kernels); tolerant to thrips
Phule Bharati	Northern Maharashtra, Madhya Pradesh	<i>Rabi</i> -summer, erect type (Spanish bunch); yield: 2,110 kg pod and 1,461 kg kernel per ha, oil content 50%, high proportion of sound mature kernels (92%); tolerant to <i>Spodoptera litura</i>
Safflower		
NARI 57	Maharashtra, Madhya Pradesh, Karnataka, Uttar Pradesh, Rajasthan, West Bengal Jharkhand, Punjab	151 days to maturity; yield 1,500 kg/ha, 29% oil content; resistant to wilt
Sesame		
Smarak	Odisha	<i>Kharif</i> , pre- <i>rabi</i> and summer season, white seed, 78-82 days to maturity; average yield 800-900 kg/ha, 48-51% oil content; tolerant to <i>Macrophomina</i> , leaf curl and <i>Alternaria</i> , resistant to lodging
Subhra	Odisha	<i>Kharif</i> , pre- <i>rabi</i> and summer; 80-85 days to maturity; Golden yellow bold seed, average yield 800-900 kg/ha, 48-52% oil content, delayed shattering, synchronous maturity; tolerant to <i>Macrophomina</i> , powdery mildew and <i>Alternaria</i> , resistant to water-stress
Linseed		
Pratap Alsi 2	Rajasthan	Blue flowered, shining brown large seeds, yield potential 1,957 kg/ha with 41.8% oil content; moderately resistant to <i>Alternaria</i> blight, powdery mildew, wilt and bud-fly
Tiara	Himachal Pradesh, Jammu and Kashmir Uttarakhand, North Eastern States, Uttar Pradesh, West Bengal	Average fibre yield 1,294 kg/ha, fibre strength 25.55 g/tex; resistant to wilt and <i>Alternaria</i> blight



Released varieties of pulses

Variety	Recommended state/ region	Salient features
Chickpea Bidisha (BG 1084)	West Bengal	Moderately resistant to wilt
Vallabh Kabuli Chana 1	Punjab, Haryana, Rajasthan, Uttar Pradesh, Delhi, Jammu and Kashmir	Yield potential 2,300 kg/ha; moderately resistant to wilt
Raj Vijay Gram 202	Madhya Pradesh, Gujarat, Maharashtra, Uttar Pradesh, Rajasthan	Early maturing; yield potential 2,000 kg/ha; resistant to wilt and moderately resistant to dry root
Mungbean CO 8	Tamil Nadu	Early maturing (60-65 days); average yield 1,000-1,100 kg/ha; resistant to yellow mosaic virus
Shalimar Moong 2	Kashmir valley, up to an altitude of 1,850 mean sea level	Early maturing; average yield 1,000-1,100 kg/ha; resistant to <i>Cercospora</i> leaf spot, moderately resistant to aphid
Urdbean Vallabh Urd 1	Uttar Pradesh	Resistant to yellow mosaic virus
Lentil Shalimar Masoor 2	Kashmir valley, up to an altitude of 1,850 mean sea level	Average yield 1,300 kg/ha, large seeded; moderately resistant to rust
Fieldpea Shalimar Pea 1	Jammu and Kashmir	Matures in 210-215 days; yield potential is 1,300-1,400 kg/ha, is dwarf

Pulses

Eight varieties of pulses including three of chickpea, two of mungbean and one each of urdbean, lentil and fieldpea were released for cultivation.



Raj Vijay Gram 202 variety of chickpea

Goa Cowpea 3– A grain variety for Goa: It is an indeterminate type of local cowpea selection with bold pods and high yield. Under ideal conditions, it grows to a height of about a feet with profuse dense foliage (up to 40 trifoliate leaves/plant) with vine growth up to one metre having 4-5 primary branches. The selection takes 68-70 days for flowering with total crop duration of 100-

105 days. Each plant produces 14-20 smooth greenish white pods in clusters measuring 23-25 cm and each pod has 13 to 17 light brownish seeds with a test weight of 25 g for 100 seeds. The selection has a potential seed yield up to 2 tonnes/ha and haulm yield of 4.30 tonnes/ha. The variety is highly tolerant to pests and diseases. It is fairly tolerant to drought situation and is suitable for residual moisture condition in rice fallows. This local cowpea is preferred in many of the culinary preparations



Goa Cowpea 3



Desirable genes introgressed from exotic lentil lines

Introgression of alien genes from wild lentil species widened genetic variability in segregating populations of wild x cultivated cross. Early vigour was introgressed in the background of improved lentil variety IPL 315 from exotic line ILL 7663, Minerals-rich breeding line IPL 220 was validated for Fe and Zn content. Lentil lines, ILL 755, ILL 364, ILL 6100, ILL6882, ILL 2556, KL 67, K 96, EC 267441 and PBJ/SSC 2/28, showed tolerance to Imazethapyr herbicide and EC 78503, EC 225503, ILL 1915, VKS 13/15, ILL 916, ILL 4551, ILL5902 to Metribuzin.



Exotic line ILL 7663



Improved lentil IPL 315

Introgression of alien genes from exotic line ILL 7663 in improved breeding line of lentil (IPL 315) for early vigour

owing to its unique taste, bold size and better cooking quality. As such, it fetches a premium price in the market. The variety was released during Group Meet on mung-bean and urdbean for spring/summer and rice fallow cultivation.

Forage crops

Six varieties of forage crops, three of oat and one each

of Napier Bajra Hybrid, Marvel grass and lucerne were released for cultivation.

Commercial crops

Nirmal18 of cotton, JRJ 610 (Prankur) of sunnhemp, JROG 1 (Rithika) of tossa jute and CoP 2061 of sugarcane released for cultivation are high-yielding varieties for different agro-ecological regions.

Released varieties/hybrids of forage crops

Hybrid/ variety	Area of adoption	Salient features
Oat		
Jo 03-93	Uttar Pradesh, Maharashtra, Gujarat, Madhya Pradesh, Chhattisgarh	Superior green and dry forage yield
OS 377	Uttar Pradesh, Maharashtra, Gujarat, Madhya Pradesh, Chhattisgarh	Irrigated conditions in single-cut system in <i>rabi</i> ; superior green fodder and dry matter yield; tolerant to major diseases
Shalimar Fodder Oats 4	Jammu and Kashmir	A medium maturing variety that fits well in rice-fodder oat system in the valley; bold seeded and high seed yield potential; resistant to leaf -spot and loose smut, armyworm
Napier Bajra Hybrid		
BNH 10	Punjab, Haryana, Rajasthan, Asom, Odhisa, Maharashtra, Gujarat, Uttar Pradesh, Madhya Pradesh, Andhra Pradesh, West Bengal, Telangana, Tamil Nadu, Karnataka	Superior for green forage, dry matter yield and per day productivity
Marvel Grass		
Phule Marvel 06-40	Maharashtra	Recommended for pasture land in rainfed areas; high green forage yield, high tillering ability, high L/S ratio; resistant to leaf-spot and rust
Lucerne		
Co2	Tamil Nadu	High crude protein content (23.5 %) and dry matter yield (21.94 tonnes/ha/yr), profuse flowering, enhanced seed yield, superior ratooning ability and early flowering results in 14 harvests a year





Released jute and allied fibres varieties

Variety	Area of adoption	Salient features
Sunnhemp (<i>Crotalaria juncea</i>) JRJ 610 (Prankur)	Sunnhemp-growing belt of India	Suitable for irrigated as well as rainfed and mid as well as highland situations; average fibre yield is 1,016 kg/ha and its potential is more than 1,400 kg/ha; it is tolerant to vascular wilt. Fibre quality is better in terms of strength (13.19 g/tex) than the check varieties K 12 yellow (11.19 g/tex) and SH 4 (11.93 g/tex)
Tossa Jute (<i>Corchorus olitorius</i>) JRJO 1 (Rithika)	Tossa jute-growing belt of India	Average fibre yield is 2,780 kg/ha and yield potential is about 3,300-3,500 kg/ha; it is tolerant to semilooper and yellow mite

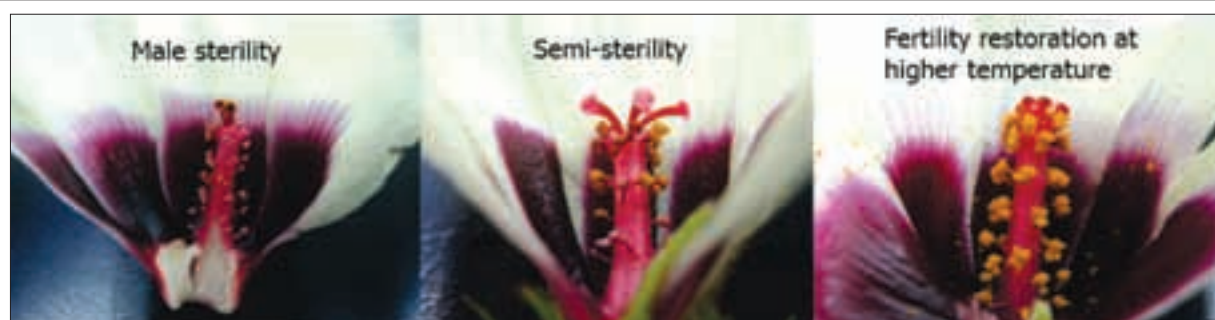


Tossa jute variety
Rithika

Male sterility in mesta: Three sets of mesta (kenaf) male-sterile lines were identified from interspecific hybridization and natural mutation. The sterility was functional in nature, manifested by formation of rudimentary anthers, inhibited anther dehiscence and a combination of two. Sterility is induced under low temperature, while under high temperature anther dehiscence. The male-sterile lines can be maintained by

either growing them at high temperature regions or by sib-mating with the fertile lines derived from the single plant. Tolerance to premature flowering in pre-breeding materials of *Corchorus olitorius* was studied in F₄ progenies. The population exhibited high tolerance to premature flowering when sown on 1 March 2014. Progenies were harvested from individual plants and a total of 42 F₅ progenies were evaluated for tolerance to premature flowering by sowing on 17 February 2015. Three F₅ progenies did not flower at 35 DAS, but exhibited 36% flowering at 65 DAS.

Transcriptome sequencing for resolving lignin biosynthesis pathway in jute: Employing comparative RNA-seq-based transcriptomics that used a deficient lignified phloem fibre (dlpf) mutant and its wild-type (WT) jute (*Corchorus capsularis*), genes and their isoforms involved in lignin biosynthesis via upstream shikimate-aromatic amino acid (AAA) and downstream monolignol pathways in jute fibres have been identified.



Phenological studies on male sterility in mesta

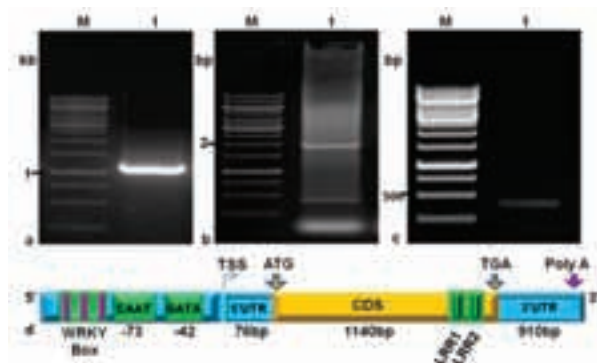


Altogether 60 WT and 57 mutant unigenes were mapped to shikimate-AAA pathway. While 91 WT and 85 mutant unigenes were mapped to monolignol pathway. Following cross-validation, a total of 38 isoforms of 16 genes involved in shikimate-AAA pathway were identified. The sequence and coding region length of these genes varied from 515 to 2,749 bp and 73 to 670aa.

Molecular approaches

Cereals

Cloning and characterization of a new orthologue for rice-blast resistance: Using allele mining an orthologue of *Pi54* was cloned from *Oryza officinalis* and designated as *Pi54of*. Gene conferred broad-spectrum resistance to rice blast, caused by *Magnaporthe oryzae*, which was also functionally validated. The full length gene has a small CC-NBS-LRR domain, a typical signature of disease resistant genes and a unique Zinc-finger domain. Its 1140 bp open-reading frame is the longest of the *Pi54* alleles cloned. It showed a basal expression that has been enhanced further by 23-fold, 72 h post-inoculation with *M. oryzae*.

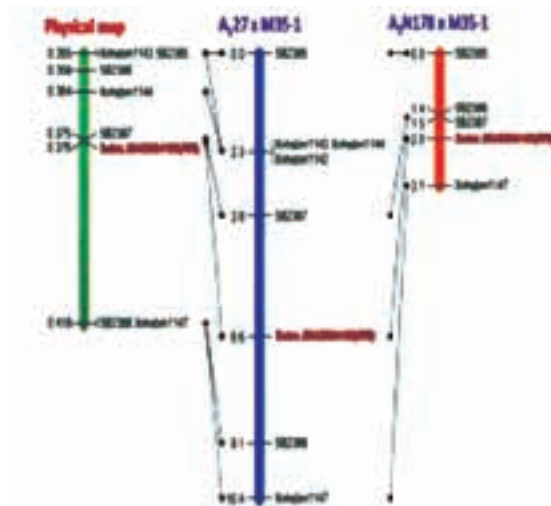


Cloning of full length *Pi54of* gene from *Oryza officinalis*. (a) PCR amplified ORF region; (b) inverse PCR for deducing 5' upstream and 3' downstream of the *Pi54of* allele in *O. officinalis*. (M: 100 bp DNA ladder and lane 1: 2 kb amplicon using IL1 and IR1); (c) RLM RACE product of *Pi54of* orthologue. M: 1 kb ladder, lane 1: amplicon (400 bp) generated by 5' RACE inner primer and AAP primer (provided with kit); (d) Schematic representation of *Pi54of* orthologue

Antioxidant genes cloned from Indian maize lines:

Antioxidant defense is a major mechanism employed by plants to mitigate environmental stresses. Five different antioxidant genes were cloned from two Indian maize inbred lines— HKI 335 (drought tolerant) and MGUD 22(drought susceptible). The cloned genes were registered with GenBank as a part of the International Nucleotide Sequence Database Collaboration (INSDC). Subtle sequence polymorphisms, including polymorphisms in the putative miRNA binding sites, were observed between sequences from drought-tolerant and drought-sensitive genotypes. This could be the key for unravelling tolerance mechanism in maize.

Molecular tagging of a fertility restoration (*Rf6*) gene in sorghum: Of the several cytoplasmic male-sterility (CMS) systems, *A₂* CMS was found a better



Map position of *Rf6* along with its linked markers (cM) in relation to physical map (Mb) in *A₁27xM35-1* and *A₂N178xM35-1* crosses

alternative to widely exploited *A₁* (*milo*) cytoplasm. A major gene for male-fertility restoration, *Rf6*, in sorghum was mapped on chromosome 4. Fertility restorer ability of the gene on both *A₁* and *A₂* CMS systems was ascertained using *F₂* populations of 27A x M35-1 and A2 x M35-1 crosses. The *Rf6* locus is tightly linked to SSR markers SB2387 and SB2388. Sequence comparison of the CDS and peptide sequences of parents showed deletions and insertions in non-restorers, leading to truncated peptide. The marker SB2387 was very tightly linked with *Rf6* locus (603bp away) on SBI 04, and it could successfully discriminate all restorer lines from maintainers (non-restorers) of *A₁* and *A₂* cytoplasm with higher accuracy of 94-97%. An additional gene (*Rf6*)-based marker, MS-SB04 266, was validated in a set of 37 genotypes and could be employed for selecting potential restorers on *A₁* and *A₂* cytoplasm.

Oilseeds

Abiotic stress-tolerant transgenic groundnut lines:

Characterization of groundnut lines having *AtDREB1A* gene showed improved tolerance to drought and salinity stresses over wild type genotypes. Transgenic plants were characterized by delayed and less severe leaf wilting and improved growth parameters correlating with physio-

Use of somatic embryogenesis

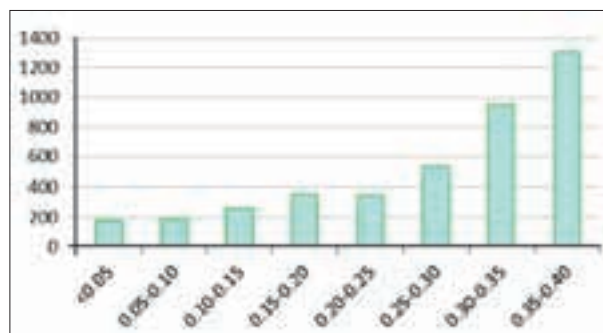
Complete plantlets of *C. reticulata* cv. Nagpur Mandarin and *C. sinensis* cv. Sweet Orange were successfully regenerated from hybrid endosperm tissue via somatic embryogenesis. The surviving plantlets were tested for ploidy and DNA content. The triploid plants were mini-grafted on Rough lemon rootstocks for greenhouse acclimatization. These results demonstrated the recovery of stable viable triploids from hybrid endosperm via somatic embryogenesis and can overcome the barriers to sexual hybridization resulting from apomixes, a step forward for breeding seedless scion cultivars of Nagpur mandarin.





biochemical parameters such as proline content, total chlorophyll content, osmotic potential, electrolytic leakage and relative water content.

Castor SNP genotyping array: A newly designed 6K SNP (Single Nucleotide Polymorphic) array was validated by genotyping 318 diverse castor accessions (comprising core set of germplasm, trait-specific germplasm, elite inbreds/parental lines of hybrids etc.), representing fairly wide genetic diversity available in castor. A total of 4,098 SNPs were called successfully with high quality. The call rate of these SNPs ranged from 80 to 100% with an average of 98%. The reproducibility of all the SNPs across biological and technical replicates was 100%. Of the 4,098 informative SNPs, 2,690 (65.64%) have MAF >0.2 and can be considered as markers with normal allele frequencies. About 18% have a MAF of 0.1 - 0.2 while 291 SNPs have MAF of <0.05. In addition, 489 SNPs (12%) have showed almost equal allele frequencies (with MAF close to 0.5) for two alternative alleles. The polymorphism information content (PIC) suggests usefulness of markers for diversity and linkage analyses, which ranged from 0 to 0.5 for a bi-allelic marker such as SNP. The gene diversity ranged from 0.003 to 0.500 with an average of 0.351; indicating a moderate level of genetic diversity in castor as validated by SSR, ISSR and AFLP. Thus, the array developed is of superior quality in terms of performance, polymorphism and reliability, which can be readily used for any genome-wide research applications in castor.

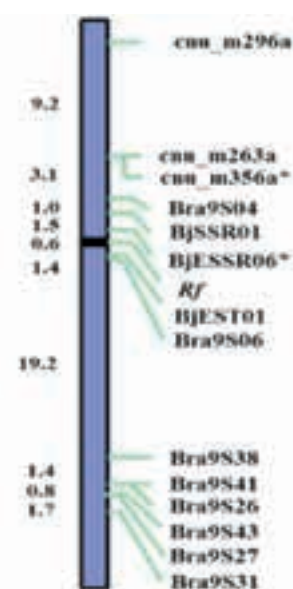


Frequency distribution of polymorphism information content (PIC) of SNP markers (X axis: PIC values of SNP; Y axis: Number of SNPs)

Marker-assisted selection for high oleic acid in safflower: A point mutation in the candidate gene, *fatty acid desaturase 2-1 (fad2-1)*, which is responsible for high oleic acid content was detected in a set of high oleic safflower genotypes. A gel-based marker assay was designed to predict high and low oleic genotypes using mutation specific primer-pair. Marker-assisted validation of F_2 population ($n=96$), produced from low oleic (~20%) and high oleic (~80%) cross, showed segregation 3 (presence):1 (absence) ratio. As heterozygotes carrying *Olo1* alleles could not be detected through this analysis, a 'sequencing based assay' was developed. Using this assay, perfect co-segregation of marker-genotype with high oleic acid trait was established by analyzing oleic acid content of F_3 seeds ($n=64$) through gas chromatography.

Fine mapping of fertility restorer gene of CMS (*Moricandia arvensis*) *Brassica juncea*:

Closely linked markers were identified for fertility restorer (*Rf*) locus on chromosome A9 using differentially expressed anther transcriptome sequences in *B. juncea*. From 842 differentially expressed unigenes, 45 SSR markers and 22 STS markers were designed and used to genotype BC_1F_1 population. Two markers, one each of SSR and STS, were found very closely linked to *Rf* gene.



Fertility restorer gene map of CMS (*Moricandia arvensis*) *B. juncea*

Pulses

Genetic transformation of chickpea and pigeonpea:

Explants of chickpea (41,217) and pigeonpea (22,309) were subjected to *Agrobacterium*-mediated genetic transformation with *Bt-cryIAC* gene. Kanamycin-tolerant putative transformants were established in transgenic containment facility. Molecular analysis (PCR, RT-PCR, ELISA, Southern and Western blot) of putative transformants indicated presence and expression of *Bt* gene in progenies of selected events of chickpea and pigeonpea (T3, T2 and T1). Insect bioassay (detached leaf assay) of selected lines of chickpea (T3 and T4) and pigeonpea (T5, T3 and T2) exhibited larval (*Helicoverpa armigera*) mortality in the range of 20-100%.

Pod-borer resistant transgenic pigeonpea:

Transgenic pigeonpea containing *cryIAa* and *cryIEC* genes individually were characterized for expression of transgenes and levels of insecticidal proteins. A total of 6,800 embryo explants were subjected to *Agrobacterium*-mediated transformation with a transformation frequency of 0.05%. The concentration of insecticidal protein in *cryIAa* events (804, DTS-43 and AK1304-PB-1) ranged from 0.16 to 0.978 ng/mg of fresh leaf tissue while that in *cryIEc* lines (AMT-1, NBRI-PB-1), ranged between 0.192 and 2.4 ng/mg.

Allele-mining in chickpea and pigeonpea: Allele-mining of drought-responsive factors (DRFs) *CcCDP* (Acc. No. GU 444041.1) and *CcHyPRP* (Acc. No. GU 444042.1) and *CAP2* gene (homolog of the *DREB2A* gene, Acc. No. DQ 321719.1) was accomplished in selected set of chickpea and pigeonpea genotypes. Chloroplast transit peptide (cTP) sequence from chickpea and pigeonpea genomes was isolated. In addition, eleven stress-induced miRNAs including those responsive to heat stress in pigeonpea were identified.

Molecular breeding in pulses: Marker-assisted backcross breeding generated five progenies with resistance to *Fusarium* wilt (*Fusarium oxysporum* race

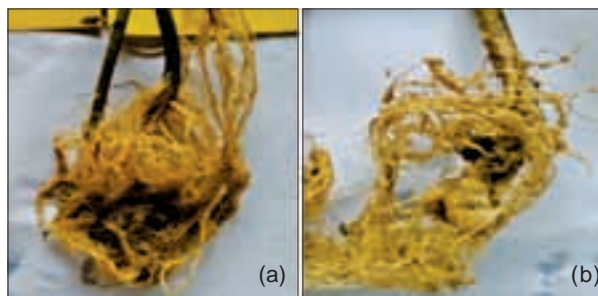


2) in the background of chickpea variety Pusa 256. Similarly, seven SSR markers identified polymorphic between parental lines were used in molecular mapping of wilt resistant genes in pigeonpea, and these identified true F_1S were from a cross Type 7 \times ICP 8863. In mungbean, 53 polymorphic SSR markers grouped 53 accessions of wild species into 5 distinct groups and one admixture group.

Commercial crops

Whole genome and transcriptome analysis of *Colletotrichum falcatum*: Using next generation sequencing (NGS) technology, whole genome (WGA) and whole transcriptome analysis (WTA) were done. Analysis of highly repetitive ~48.2 Mb genome and ~27Mb transcriptome assemblies of *C. falcatum* resulted in prediction of nearly 12,270 protein-coding genes. Global view of syntenic alignments between genome and transcriptome of *Colletotrichum falcatum* led to its delegation to linkage group of *C. graminicola* with about 93% similarity in base pairing and gene clustering. The WGA and WTA resulted in nearly all subunits of protein complexes like carbohydrate metabolism, putative proteins (characterized and uncharacterized), respiratory electron transport chains, the V-ATPase, and ubiquitin-proteasome systems. This is the first report on whole genome and transcriptome sequencing of *Colletotrichum falcatum*; red- rot pathogen of sugarcane.

Characterization of parasitism genes in root -knot nematode : More than thirty parasitism genes known in root-knot nematode *Meloidogyne incognita* were evaluated for their critical role in pathogenesis through RNAi-mediated silencing, using dsRNA specific to each gene. Two oesophageal genes – *MSP6* and *MSP13*– have been found to seriously affect parasitism and impair infectivity of root-knot nematode on cotton. As plant parasitic nematodes including juveniles of root-knot nematodes reduced oral uptake; four bio-molecules were evaluated for enhancing ability of second stage juveniles to acquired sRNA. Two molecules, Octopamine and



Uptake of *msp6 dsRNA* by root-knot nematode rendered it defective in infecting tomato (a) *dsRNA*-treated nematode; (b) healthy nematode

Resorcinol, have been found most effective as inducer of dsRNA uptake.

Pink bollworm resistance to cry toxins: Populations of pink bollworm were collected from 34 locations in Gujarat on Bollgard-II and non Bt cotton hybrids during 2014-2015. F_1 progenies of pink bollworm populations were subjected to diagnostic assays with Cry1 Ac and Cry2Ab toxin proteins at 10 ppm, 5 ppm, 1ppm and 0.1 ppm. Populations from Surat and Anand sourced from non-Bt were most tolerant as they recorded lowest corrected mortality of 62% and 69% at 10 ppm Cry 1Ac toxin compared to susceptible population. Pink bollworm collected on Bollgard-II hybrids in Junagadh and Vadodara were most tolerant as they recorded lowest corrected mortality (62% and 67%) as compared to susceptible population at 10 ppm Cry1Ac. Populations collected from Amerli Bt, Bhavnagar Bt and Surat NBt recorded lowest corrected mortality, 25.00%, 49.00% and 62.00%, respectively, on Cry2Ab at 10 ppm diagnostic dose. Resistance to Cry1Ac and Cry2Ab log dose probit assays with pink bollworm F_1 population from non-Bt cotton was monitored. Population from Jalna, Mansa, Bharuch, Amreli, Akola and Khandwa recorded 3, 4, 7, 9, 11 and 19 fold resistance to Cry1Ac over susceptible check. Population from Faridkot, Rahuri Sirsa, Mansa, Amreli, Junagadh and Khandwa recorded 26, 34, 35, 37, 125, 142 and 335 fold resistance over the susceptible



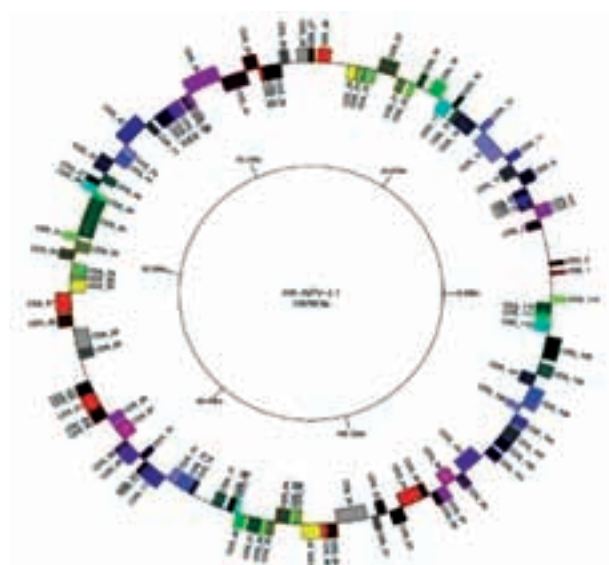
Pink bollworm infestation on Bollgard-II cotton hybrids in Gujarat



check to Cry2Ab.

Whole genome sequencing of economically important microbes: *Staphylococcus xylosus*: Genome sequence of psychro-tolerant bacteria *Staphylococcus xylosus* strain LSR_02N isolated from water (sediment) at the confluence of river Zaskar and Indus at Leh (Jammu and Kashmir) was deciphered. The 3.7 Mb genome sequence of the strain LSR_02N (JXAV00000000) contained 38 scaffolds and 2,971 total genes including 1,419 unique and 553 hypothetical genes. Presence of heat and cold shock protein encoding genes support its ability to survive under low temperature conditions.

***Helicoverpa armigera*:** Nuclear Polyhedrosis Virus



Circos plot for gene arrangement in *Helicoverpa armigera* NPV whole genome [Different colours represent protein-coding genes. Gene arrangements are depicted counterclockwise]

(NPV) is a member of family Baculoviridae having high specificity to insects belonging to Lepidoptera. These rod-shaped, double-stranded DNA viruses are one of the most potent biocontrol agents of *Helicoverpa armigera*, particularly on pulses and vegetables in India. The genome of *H. armigera* NPV (GenBank accession number KT013224) from Ludhiana was sequenced. The whole genome sequencing comprises 136,760bp circular DNA, with a total of 113 protein-coding genes with four repeat regions. Altogether, 73 named proteins were identified. The gene arrangement and orientation of the assembled NPV whole genome were identical to the reported single-capsid NPV genome from G4 strain of China, NNg1 of Kenya and LB1 of Spain. All these strains are known for their enormous infectivity against Lepidopteran insects.

***Virgibacillus*:** The whole genome sequence of *Virgibacillus* sp. bacterium known from Rann of Kutch, Gujarat, revealed presence of genes for 3,459 coding sequences and 910 hypothetical proteins. There are 26 genes for osmo-regulation and 37 for oxidative stress tolerance. Exploring genome has paved the way for understanding mechanism of osmotolerance. Genes

critical for osmoregulation are potential candidates for engineering plants and microbes for stress tolerance.

DNA fingerprinting

Genetic diversity analyses were done using SSR (Simple Sequence Repeat) and other markers in rice (6,984), wild *Oryza* (48), barnyard millet (94), kodo millet (96), proso millet (16), sponge- gourd (45), bread wheat (48), pearl millet (90) and giloe (24). New markers were developed for cultivar identification and genetic diversity analyses in sesame (~70, 000 SSR and SNPs-Single Nucleotide Polymorphisms markers), bottlegourd (44,823 genome-wide and 108 SSR markers through cross-transferrability) and rice (129 SSR markers using conserved microRNA genes). Trait-specific markers were developed for terminal heat tolerance gene *HKT2:1* and rust and spot blotch resistant genes *Adc* and *AdoMetDC* in wheat, yield -related genes in rice, long-chain fatty acid genes *FAE1/KCSI* in Indian mustard, transcription factor families in giloe, and abiotic stress tolerance in horsegram and pigeonpea. Visual and real-time LAMP (Loop mediated isothermal amplification) assays targeting *cry* genes and glyphosate tolerant genes were developed using fourteen GM events in corn, cotton, eggplant and soybean. Adventitious presence of transgenes was monitored in cotton (*in-situ* collection) and okra (*ex-situ* collection) using multiplex PCR targeting genes.

Seed technology

Alternative areas for hybrid seed production:

Considering uncertain weather owing to climate change and for ensuring steady supply of quality seeds, the alternative areas for economic hybrid-seed production of various crops have been identified.

Crop	Alternative areas for hybrid seed production
Paddy	Balaghat (Madhya Pradesh); Dhamtari, Mahasamund and Gariaband (Chhattisgarh); Chilkalpurpeta, Guntur (Andhra Pradesh)
Sunflower	Gudibande and Gowribidanur, Sira (Karnataka)
Maize	Nandiyal (Telangana); Sira, Hiriya and Siruguppa (Karnataka); Pathera (Haryana)
Pearl millet	Sriganganagar, Bharathpur (Rajasthan)
Castor	Surendranagar (Gujarat), Gadwal, Reddipalli, Nandyal and Banaganapally (Andhra Pradesh)
Jute	Tadikonda, Tulluru, Macherla, Sattanapalle, Chilakalpurpeta and Marturu (Andhra Pradesh)

Quality seed production: During 2014-15, 978, 17,562, 12,847, 14,000 and 3,418 tonnes of breeder, foundation, certified, truthfully labelled seed and planting material, respectively, were produced. Further, 2,026 lakh of planting material and tissue-cultured plants were produced. The production of different classes of seed and planting material was higher than the envisioned targets.



Target and production of seed and planting material during 2014-15

Pollinators

Sunflower: Significant variations were observed among the genotypes for luring honeybees. Among genotypes evaluated significantly high honey production potential (36.60 kg/ha) was recorded in DK 3849, followed by SH 3322 (34.52 kg/ha).

Mustard: Honeybees and other pollinators exhibited significant role in enhancing seed yield of mustard-crop. Different modes of pollinations in mustard-crop revealed that number of siliquae/plant were highest in open pollination–(OP) (188), followed by bee-pollinated plants (155) and was lowest in case of pollinator exclusion (PE) treatments (132). The highest seed yield per plant was recorded in OP (8.50 g), followed by BP (6.37), and PE (4.37) plants

Bt Cotton: In Bt cotton hybrid RCH BG 11 open-pollination treatment recorded maximum number of pollinators, followed by *Aphis cerana indica* confined treatment and pollinator excluded plots. The seed-cotton yield was 38% higher in open-pollinated plot and 17.5% higher in *A. cerana* pollinated plots compared to pollinator excluded plots.

Horticulture

Fruit crops

Arka Udaya, a semi-vigorous mango hybrid (Amrapali × Arka Anmol) with medium-sized fruits (250g), firm and deep yellow pulp, 23-24% TSS was released.



Arka Udaya mango

Arka Rashmi, a guava hybrid (Kamsari × Purple Local), bearing round and medium-sized fruits (200-210 g) with pink pulp and moderately hard (9kg/cm²) seed was released. Dhawal, a half-sib selection from Allahabad Safeda with round, smooth and medium to large fruits (200-250 g), white pulp, TSS 13%, acidity 0.42%, ascorbic acid (250mg/100 g pulp) was released.



Guava Dhawal

Lalima, a half-sib selection from Apple guava with attractive crimson fruits, good yield (50kg/tree) with higher shelf-life (5-6

days) at ambient was released.

The PDKV Bahar, an acid lime Clone 2, with 22% more fruit yield over the existing varieties was identified for high yield (143 kg/tree) and released for cultivation in Maharashtra.



Guava Lalima

Bael variety, Thar Divya, with compact canopy, semi-spreading growth, early-maturity (second fortnight of February), attractive dark yellow and high pulp (70.5%) content, TSS (pulp-37%, mucilage-49.5%) was released for cultivation in Rajasthan and Gujarat.

Thar Rituraj, a variety of khirni (*Manilkara hexandra*) with 12-14 kg fruit yield/tree, 5.2g fruits having 24-25% TSS and 0.3% acidity was released for cultivation.

Karonda, CHESK-2, with 5g fruit weight, 9-10% TSS, 0.64% acidity, 13.4 mg ascorbic acid/100g pulp and 13 kg/plant fruit yield was identified and released as Thar Kamal. The fruits of Thar Kamal are suitable for candy- and jelly-making.

Plantation crops

Kalpa Jyothi and Kalpa Surya, dwarf coconut lines, suitable for tender nut, were developed. Kalpa Haritha, a tall, dual-purpose variety suitable for copra and tender nut and; hybrid Kalpa Shreshtha (D × T); a high-yielding (167 nuts equivalent to 35.9 kg copra/palm/year), were accepted for release and notification by the Central Sub-Committee



Kalpa Shreshtha

on Crop Standards, Notification and Release of Varieties of Horticultural Crops. Kodinar, a high-yielding (3.82kg/palm/year), arecanut selection, with recovery of 62.5% A-grade nuts was recommended for release. The coconut varieties Kalpa Pratibha, Kalpa Dhenu, Kalpa Mitra, Kalpa Raksha, Kalpa Sree and Kalpa Sankara, were registered with the Protection of Plant Varieties and Farmers' Rights Authority, Government of India.

A hybrid cashew line (H126) with jumbo nut (11-12 g), kernel weight (3.3 g) and kernel grade of above W150 was found promising at Puttur.



Fruiting in H-126

Vegetable crops

Of the 10 determinate F₁ hybrids evaluated, Hybrid 369 with Arka Vikas fruit type possessed triple disease resistance (ToLCV+BW+EB), whereas Hybrid 371 possessed combined resistance to ToLCV and early



blight and Hybrid 373 recorded the highest yield (24 tonnes/ha). Similarly of the 25 indeterminate F_1 hybrids evaluated, maximum yield was recorded in IIHR 2042 \times IIHR 2834 (76 tonnes/ha), followed by IIHR 2042 \times IIHR 2856 (76 tonnes/ha) and PH 4225 (73 tonnes/ha). Fruit firmness was highest in IIHR 2867 \times IIHR 2834 (8.7 kg/cm²). These hybrids possessed triple disease resistance (ToLCV+BW+EB).

Six promising populations of chilli with combined resistance to thrips, CMV and ChiVMV were identified and advanced. Four advanced breeding lines of brinjal, viz. IIHR 37-36-4-4, (38 tonnes/ha), IIHR 37-36-4-20, (35 tonnes/ha), IIHR 37-36-13-7 (32 tonnes/ha) and IIHR 37-36-3-4 (30 tonnes/ha) were promising for high yield and resistance to bacterial wilt.

A total of 116 advanced lines of okra were evaluated. Of them, IIHR 11-1-50 and IIHR 299-1 were identified for high yield (23.54 and 27 kg/3.4 m² plot, respectively) along with combined resistance to YVMV + powdery mildew (no incidence) during summer.

Kashi Vardaan (VRO-25) is an early, medium tall (120-125 cm) hybrid, taking 42-44 days for first flowering. Its fruits are harvested 47-100 days after sowing. It has yield potential of 150-155 q/ha, resistant to yellow vein mosaic virus (YVMV) and okra enation leaf curl virus (OELCV). It is recommended for cultivation in Uttar Pradesh, Bihar, Jharkhand and Punjab.

Of the 30 pole type photo-insensitive advanced breeding lines (F_6) evaluated, seven high-yielding and photo-insensitive advanced breeding progenies, viz. IIHR15-5, IIHR 15-7DG, IIHR 15-7G, IIHR 15-8, IIHR15-15, IIHR 15-21, IIHR15-23 with 30-35 tonnes/ha pod yield were selected. A ridge gourd variety, Thar Karni, with 3.5m vine length, light green and cylindrical fruits (95g) and 140-150q/ha fruit yield was released for cultivation in Rajasthan.

Of the 20 selective crosses of onion (four male sterile, disease resistant lines and seven male fertile disease resistant lines), two F_1 progenies, viz. PBRMS 319 \times PBRC 339 (26.50 tonnes/ha and PDI 10.50%) and PBRMS 318 \times PBRC 338 (24.80 tonnes/ha and PDI 12.20%) were found tolerant to purple blotch disease during rainy season. Bhima Safed (NRCWO-3), a white onion line with 22-25 tonnes/ha bulb yield was recommended for cultivation during *kharif* in Chhattisgarh, Gujarat, Karnataka, Madhya Pradesh, Maharashtra, Odhisa, Rajasthan and Tamil Nadu. Onion, Bhima Super, Bhima Dark Red and Bhima Shweta, with 500-600 sets/m² production were recommended for set production in *kharif* season in areas prone to heavy rainfall. These varieties have bulb yield potential of 22-25 tonnes/ha in *kharif*.

Four advanced breeding lines of onion, viz. DOGR Hy-5, a F_1 hybrid with uniform, dark red and global bulbs and thin neck, 20.11% more bulb yield (387.25

q/ha) than the best check Bhima Dark Red (322.4 q/ha), matures 101 days after transplanting, free from double bulbs and bolters, suitable for *kharif* cultivation and; RGP-1, an open-pollinated line with red and flat-globe bulbs having thin neck and free of doubles and bolters, 17.5% more yield (328.6 q/ha) than the best check Bhima Shakti (279.65 q/ha), matures 118 days after transplanting and suitable for *rabi* cultivation; RGP-2, an open-pollinated line having uniform, global, dark red bulbs with thin neck and free of doubles and bolters, suitable for *rabi* season, with 32% more bulb yield (369.15 q/ha) than best check Bhima Shakti (279.65 q/ha) and matures 116 days after transplanting, were recommended for multilocal testing.

Potato

A potato variety, Kufri Lalit, with red peel and light yellow pulp was released for commercial cultivation in Bihar, West Bengal, Asom, Odhisa and Jharkhand. It is field resistant to late blight.



Patato Kufri Lalit

Ornamental crops

Arka Aayush, a gladiolus variety, with thick open-faced florets, slightly ruffled, double rowed, red (41.C) having red (41.A) margin, blotch red (46.B) with yellow (13.C) border and resistance to *Fusarium* wilt was recommended for release. Arka Manorama, another gladiolus variety with open-faced florets, medium, wavy, red-purple (65.B) having red purple (62.A) streaks, red-purple (67.B) splash was identified for release. Arka Agni, a petaloid male sterile (IIHRMGYP-1 \times 9-2) marigold hybrid with medium plant height (80-85 cm), high-yielding (7-7.5 tonnes/acre), compact but large (7.5-8 cm) and orange flowers (RHS colour N25C, orange group). Flowering starts at 40-45 days after planting and continues for 60 days was identified for release.

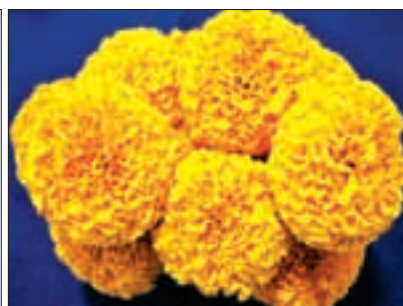
Arka Alankara, another petaloid male sterile marigold hybrid (IIHRMGYP-1 \times 9-2) with compact and large (7-7.5 cm), golden yellow (RHS colour 9A, yellow group) with high yield (6-6.5 tonnes/acre) was released. Flowering starts 40-45 days after planting and continues for 60 days. The *Zygopetalum intermedium*, a Brazilian orchid with scented flowers was observed to produce true-to-the-type apomictic progeny lines on hybridization with *Vanda coerulea*, *Vanda hybrids* and several species of



Onion Bhima Safed



Arka Aayush



Arka Alankara



Gene pyramiding

For pyramiding tomato leaf curl virus (ToLCV) resistance genes *Ty-2* and *Ty-3* into elite tomato lines, Marker Assisted Selection (MAS) was done. Among four backcross progenies, four plants homozygous to both *Ty-2* + *Ty-3* were identified and advanced. In addition, for introgression of *ToLCV* resistance genes from *Solanum habrochaites*, 30 BC₁F₄ families derived from an inter-specific cross, 15 SBSB × *S. habrochaites* (LA-1777), were screened using *Ty-2* and *Ty-3* markers and 28 individual plant selections were made for the presence of *Ty-2* and *Ty-3* genes.

genus *Coelogyne*. However, there was marked reduction in vigour in second selfing cycle due to inbreeding depression.

Spices

Appangala 2 (NHY-35); developed through heterosis breeding (moderately yielding 'Appangala 1' × mosaic resistant 'NKE 19') and resistant to Cardamom Mosaic Virus (katte) with 9.3 q/ha dry capsules yield was recommended for cultivation in hilly zones of Kodagu, Hassan and Chickmagalur in Karnataka and North Wyanad in Kerala. Ajmer Fenugreek 4 (AFg-4) variety with 12.53% higher seed yield (19.25 q/ha) than Hisar Sonali (National check), moderately resistant to powdery mildew and root rot was identified and released for cultivation in Rajasthan. Ajmer Ajwain 93 (AA-93), an early-maturing variety, was released for cultivation in Rajasthan. This variety is erect in growth, lodging resistant, matures 40-45 days early (123-125 days) and yields 9 q seeds/ha at 40 cm × 20 cm plant spacing.

Ajmer Nigella 20 (AN-20), with 42-43% more yield (10.25 q/ha) than Azad Kalonji and Ajmer Nigella 1 was released for cultivation in Rajasthan.

Medicinal and aromatic plants

A temperature sensitive, male sterile line (DWS-10) of Ashwagandha (*Withania somnifera*) producing sterile pollens during cool seasons (December-January), which gets converted into male fertile during warm season (March onwards), was identified. Eight promising advance breeding lines of Ashwagandha with higher dry root yield (569.5 – 1624.3 g/4m row) than check (Arka Ashwagandha, 432.3g/4m row) were selected in F7 generation.

Two promising selections of Mandukaparni (*Centella asiatica*, viz. IIHR-CA-13 with higher dry leaf yield (303.63 g/plant), asiaticoside (3.72%) and total tri terpenes (8.94%) and IIHR-CA-1 with higher leaf yield (349.26g), ascorbic acid (69.11mg/100g) and total carotenoids (26.58 mg/100g) contents were identified.

Promising advanced lines of *Mucuna* spp., viz. IIHR PS 10-2 and IIHR PS 10- 1 with higher seed yield (310 and 275g/plant) and L-dopa content (5.38 and 5.03%, respectively) over the check Arka Dhanvantari (304g, 4.82%), were identified.

Coconut selection for Goa: Tender coconuts of Benaulimpani coconut selection were harvested at 6, 7 and 8 months of maturity, where the volume of the water was 300, 280 and 250 ml/nut, respectively. TSS of the water was 6.86, 6.66 and 7.36 degree Brix in 6, 7 and 8 month old nuts. Sodium content was 22–23 ppm and potassium content ranged from 1,267 to 1,366 mg/l. Orgnaoleptic test revealed the taste of the water with very good score. Annual yield of selected palm ranged from 67 to 74 nuts/palm. Fruit component analysis of mature nuts revealed that it contains water of 160 ml/nut with 6.53 degree Brix. Copra wet and dry weight of the fruits was 266 and 194 g/nut respectively. The nuts had minimal damage due to eriophyiid mite. Benaulimpani has good scope for cultivation in Goa for tender coconuts.

