6.

Crop Improvement

Emphasis is laid on the development of trait-specific high-yielding crop varieties and hybrids in the crop improvement programmes to hasten the cherished goal of enhanced crop productivity and, in turn, food and

Released rice varieties/hybrids

Crop/Variety/Hybrid	Recommended state/region	Salient features
US 305 (IET 21827)	Andhra Pradesh, Tamil Nadu and Maharashtra	Medium slender grains, 50% flowering in 100 days, high yielding
CSR 43 (IET 18259)	Uttar Pradesh	Moderately resistant to brown spot
JKRH 01 (IET 18181)	Uttar Pradesh/2013 (area extension)	Moderately resistant to blast, rice tungro virus, sheath blight, brown spot and stem borer
SHIATS Dhan 1 (IET 20928)	Uttar Pradesh/2013	-
CR Dhan 300 (IET 19816)	Maharashtra, Odisha, Bihar and Gujarat	-
CR Dhan 303 (IET 21589)	Madhya Pradesh, Uttar Pradesh and Odisha	Moderately resistant to blast, neck blight, sheath rot and rice tungro virus
ARB 6	Karnataka	-
CR Dhan 201(IET 21924)	Chhattisgarh and Bihar under aerobic conditions	Moderately resistant to leaf blast, sheath rot, stem borer, leaf folder, whorl maggot and rice thrips
CR Dhan 202 (IET 21917)	Jharkhand and Odisha under aerobic conditions	Moderately resistant to stem borer, leaf folder, whorl maggot and rice thrips
CR Dhan 304 (IET 22117)	Odisha and West Bengal under irrigated conditions	Resistant to gall midge
CR Dhan 305	Jharkhand, Maharashtra and Andhra Pradesh under irrigated conditions	Moderately resistant to white-back planthopper, brown planthopper, leaf blight and blast
CR Dhan 407 (IET 21974)	Odisha and West Bengal under rainfed shallow lowlands	Moderately resistant to bacterial leaf blight and leaf blast
CR Dhan 505	Odisha and Asom under deep -water conditions	Moderately resistant to leaf blast, sheath rot, sheath blight, rice tungro virus, stem borer, leaf folder, whorl maggot and rice thrips
Gangavati Sona (GGV 05-01)	Karnataka	-
Gontra Bindhan 3 (IET 22752)	Uttarakhand, Haryana, Odisha, Bihar, Uttar Pradesh, West Bengal, Madhya Pradesh and Andhra Pradesh, Tamil Nadu, Kerala and Karnataka	Moderately resistant to leaf blast and with good cooking quality
Shobhini (IET 21260)	Bihar, Chhattisgarh, Madhya Pradesh, Gujarat, Andhra Pradesh and Rajasthan	Semi dwarf culture with strong aroma and excellent quality
VL Dhan 68 (IET 22283)	Irrigated medium hills of Uttarakhand and Meghalaya	Moderately resistant to leaf blast and neck blast
VL Dhan 157 (IET 22292)	Low elevated hills of Meghalaya and mid-hills of Uttarakhand under rainfed conditions	Moderately resistant to leaf blast
NP 107-5 (IET 22753)	Punjab, Haryana and Uttarakhand with irrigated ecology	Moderately resistant to leaf blast and brown spot

nutritional security. The focus is to develop varieties with tolerance to pests/diseases and also for different abiotic constraints (soil and water salinity, soil acidity, drought, flood and such other factors), besides matching quality attributes.

Cereals

Rice: Nineteen varieties/hybrids of rice — US 305, CSR 43 (IET 18259), JKRH 01 (IET 18181),SHIATS Dhan 1 (IET 20928), CR Dhan 300 (IET 19816), CR Dhan 303 (IET 21589), ARB 6, CR Dhan 201 (IET 21924), CR Dhan 202 (IET 21917), CR Dhan 304 (IET 22117), CR Dhan 305, CR Dhan 407 (IET 21974), CR Dhan 505, Gangavati Sona (GGV 05-01), Gontra Bindhan 3 (IET 22752), Shobhini (IET 21260), VL Dhan 68 (IET 22283), VL Dhan 157 (IET 22292), NP 107-5 (IET 22753)— have been released for cultivation in different agro-ecosystems.

Rice CR Dhan 304 is resistant to gall-midge

Heera—A high protein rice variety

A short-duration rice variety, Heera, was released in early 1990s,for rainfed uplands in the wet season and for irrigated fields in the dry season. The variety has been found to be an excellent source of vital nutrients (protein, iron and zinc), and is with long bold grains and brown hull. Its white milled kernel has 11.5% protein, 5 ppm of iron and 23 ppm of zinc. Its cooking quality is also quite good as it has intermediate amylose content. Based on its potential for commercial cultivation as nutrient-dense specialty rice, promotion of Heera in Odisha has been initiated.

Wheat: Twelve varieties of wheat — Narendra Wheat 4018, DBW 90, HD 3086, DBW 88, HD 3090, WHD 948, SHIATS-W6, K 0607, WH 1124, K 1006, Narendra Wheat 5054, MACS 6478 — have been released for cultivation in different agro-ecosystems.

Released wheat varieties

Variety	Area of adoption	Salient features
Narendra Wheat 4018	Uttar Pradesh	For rainfed/restricted timely sown conditions; resistant to brown rust and leaf blight
DBW 90	Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions) and western Uttar Pradesh (except Jhansi division), part of Jammu and Kashmir (Jammu and Kathua distt), parts of Himachal Pradesh (Una distt and Paonta valley) and Uttarakhand (*tarai* region)	For irrigated late sown conditions; resistant to stripe rust and leaf rust
Pusa Gautmi (HD 3086)	Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions) and western Uttar Pradesh (except Jhansi division), part of Jammu and Kashmir (Jammu and Kathua distt), parts of Himachal Pradesh (Una distt and Paonta valley) and Uttarakhand (*tarai* region)	For irrigated timely sown conditions; highly resistant to stripe and leaf rust
DBW 88	Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions) and western Uttar Pradesh (except Jhansi division) part of Jammu and Kashmir (Jammu and Kathua distt), parts of Himachal Pradesh (Una distt and Paonta valley) and Uttarakhand (*tarai* region)	For irrigated timely sown conditions; seedlings are resistant to most prevalent pathotypes of yellow and brown rusts, and are tolerant to Karnal bunt, and is with high biomass and high grain protein content

Variety	Area of adoption	Salient features
HD 3090 (Pusa Amulya)	Maharashtra and Karnataka	For irrigated late sown conditions; with higher yield, better disease resistance, and with good chapati quality
WHD 948	Maharashtra and Karnataka	For irrigated timely sown conditions; with high yield and resistance to major diseases, and with good pasta-making qualities
SHIATS-W6 (AAI-W6)	Uttar Pradesh	For late sown irrigated conditions; with high yield, is resistant to leaf rust and leaf blight
K 0607	Uttar Pradesh	Timely sown irrigated conditions; resistant to leaf rust, leaf blight and reported to be heat tolerant
WH 1124	Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions), western Uttar Pradesh (except Jhansi division), parts of Jammu and Kashmir (Jammu and Kathua districts), parts of Himachal Pradesh (Una and Paonta valley) and *tarai* region of Uttarakhand	For irrigated late sown conditions; resistant to stripe and leaf rust
K 1006 (Shekhar New)	North Eastern Plains Zone	For irrigated timely sown, medium to high fertility conditions; resistant to brown rust, and has high zinc and iron contents
Narendra Wheat 5054 (NW 5054)	Eastern Uttar Pradesh, Bihar, Jharkhand, Odisha, West Bengal, Asom, Manipur, Mizoram, Meghalaya, Tripura, Nagaland, Arunachal Pradesh and Sikkim	For irrigated timely sown conditions; high yield, and is resistant to brown rust
MACS 6478	Maharashtra, Karnataka, Andhra Pradesh and Tamil Nadu	For irrigated timely sown conditions; higher yield, better disease resistance, and with good chapati quality

HD 2967 wheat

This high-yielding variety of wheat with resistance to brown rust, possessing good chapati and bread-making quality and with high Zn and Fe contents has been recommended for irrigated timely sown conditions of eastern Uttar Pradesh, Bihar, Jharkhand, Odisha, West Bengal, Asom, and plains of North-eastern hill states.

Barley: Six varieties of barley, Narendra Barley 1445, VL Jau 118, DWRB 92, BH 946, Pusa Sheetal and HUB 113 have been released for cultivation.

Maize: Eleven hybrids of maize have been released for cultivation in different agro-ecosystems.

Millets and minor millets: Five varieties/hybrids of millets and four of minor millets have been released for cultivation in different agro-ecosystems.

Oilseeds: Seven varieties of oilseed crops have been released for cultivation.

Pulses: Eleven varieties/hybrids of pulses, two each of greengram, pigeonpea and fieldpea and one each of blackgram, chickpea, lentil, horsegram and cowpea have been released for different agro-ecosystems.

Released varieties of barley

Variety	Area of adoption	Salient features
Narendra Barley 1445 (NDB 1445)	Uttar Pradesh	Six-row hulled barley for saline-alkaline soils of Uttar Pradesh; with high yield and resistance to rusts and leaf blights
VL Jau 118 (VLB 118)	Jammu and Kashmir, Himachal Pradesh, Uttarakhand, Sikkim, West Bengal, Arunachal Pradesh, Asom, Manipur, Meghalaya, Mizoram, Nagaland and Tripura	Six-row hulled barley for rainfed cultivation under timely sown conditions of the North Hills Zone, and is resistant to yellow rust
DWRB 92	Punjab, Haryana, Uttar Pradesh, Delhi and Rajasthan	Two-row malt barley with good malting and brewing quality under timely sown conditions,and with resistance to stripe rust and leaf blights

Variety	Area of adoption	Salient features
BH 946	North Western Plain Zone comprising Punjab, Haryana, western Uttar Pradesh (excluding Jhansi division), Delhi, Rajasthan (excluding Kota and Udaipur divisions), *tarai* region of Uttarakhand, Jammu and Kathua districts of Jammu and Kashmir	Six- row feed barley with resistance to major diseases and is lodging tolerant
Pusa Sheetal (BHS 400)	Himachal Pradesh, Uttarakhand, Jammu and Kashmir	Six-row hulled barley for rainfed cultivation under timely sown conditions in the North Hills Zone with yellow rust resistance
HUB 113 (Mahamana)	Eastern Uttar Pradesh, Bihar, Jharkhand, Odisha, West Bengal, Asom and plains of North-eastern states	Six- row feed barley with resistance to yellow rust, leaf blight and aphids

Released maize hybrids

Hybrid	Area of adoption	Salient features
P1864 (X8F984)	Punjab, Haryana, Delhi, Uttarakhand and Uttar Pradesh	Early maturity, yellow, semi-flint
P3522 (X35A019)	Punjab, Haryana, Delhi, Uttarakhand, Uttar Pradesh, Bihar, West Bengal, Jharkhand, Odisha, Andhra Pradesh, Tamil Nadu, Maharashtra, Karnataka Gujarat, Rajasthan, Madhya Pradesh and Chhattisgarh	Late maturity, yellow-orange, semi-flint
CoH (M)7 (CMH 08-287)	Uttar Pradesh, Bihar, Jharkhand, Odisha, Andhra Pradesh, Tamil Nadu, Maharashtra, Karnataka in *kharif*	Late maturity, orange-yellow, dent, and is resistant to MLB, PR, TLB, BSDM and C. rust
CoH (M)8 (CMH 08-292)	Uttar Pradesh, Bihar, Jharkhand, Odisha, Andhra Pradesh, Tamil Nadu, Karnataka, Rajasthan, Gujarat, Madhya Pradesh, Chhattisgarh, Punjab, Haryana, Delhi and Maharashtra in *kharif*	Medium maturity, orange-yellow, semi-dent, and is resistant to MLB, TLB, RDM, DM, and is moderately resistant to PFSR and PR
CoH (M) 9 (CMH 08-350) (Single cross Hybrid Corn)	Uttar Pradesh, Bihar, Jharkhand, Odisha, Rajasthan, Gujarat, Madhya Pradesh and Chhattisgarh in *kharif*	Medium maturity, orange-yellow, semi-dent, is resistant to MLB, TLB, RDM, DM and moderately resistant to common rust, and is resistant to multiple diseases and cyst nematode
DHM 121 (BH 41009)	Odisha, Bihar, Jharkhand, West Bengal, Gujarat, Rajasthan, Chhattisgarh and Madhya Pradesh in *kharif*	Medium maturity, yellow, semi-dent, and is tolerant to moisture stress
Vivek Maize Hybrid 47 (FH 3513)	Uttarakhand, Himachal Pradesh, Jammu and Kashmir and North-eastern Hills Region	Early maturity, yellow with white cap, semi-flint, and is moderately resistant to MLB and C. rust
Vivek Maize Hybrid 53 (FH 3556)	Uttarakhand, Himachal Pradesh, Jammu and Kashmir and North-eastern Hills Region and eastern Uttar Pradesh	Extra-early maturing, yellow, semi-flint
Vivek Maize Hybrid 51 (FH 3554)	Gujarat, Rajasthan, Chhattisgarh and Madhya Pradesh	Extra-early maturing, yellow, semi-flint,and is moderately resistant to MLB, FSR, RDM and CLS
KMH 25K45 (BUMPER)	Punjab, Haryana, Delhi, Uttar Pradesh, Andhra Pradesh, Karnataka, Maharashtra, Tamil Nadu Rajasthan, Gujarat and Chhattisgarh	Late maturity, yellow, semi-dent
GH 0727 (Shrushti)	Karnataka	Late maturity, yellow, semi-flint

BSPM: Brown Stripe Downy Mildew; CLS: *Curvularia* Leaf Spot; C.Rust: Common Corn Rust; DM: Downy Mildew; MLB: Maydis Leaf Blight; PFSR: *Pythium* Stalk Rot; PR: *Polysora* Rust; RDM: Rajasthan Downy Mildew; TLB: *Turcicum* Leaf Blight

Released varieties/hybrids of millets

Crop/Variety/Hybrid	Area of adoption	Salient features
Sorghum		
HJ 541	Haryana	Improved forage sorghum variety, tall, sweet-stemmed, tolerant to stem borer; yield: 550q green fodder/ha, 125 q dry fodder/ha and 18-20q seed/ha
CSH 32 (SPH 1674/DJ 2004)	Rainfed areas of Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, south Gujarat and north Andhra Pradesh	*Kharif* hybrid, 221-cm tall; tolerant to shoot-fly, aphids and stem borer. Non-lodging and non-shattering type suitable for deep soils
Pearl millet		
KBH 108 (MH 1737)	Rajasthan, Gujarat, Haryana, Uttar Pradesh, Madhya Pradesh, Punjab and Delhi	For *kharif* season; late maturing, tall; resistant to downy mildew, blast and smut
Dhanashakti (ICTP 8203 Fe 10-2)	Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu, Gujarat, Madhya Pradesh, Rajasthan, Uttar Pradesh, Haryana and Punjab	Early-maturing variety with high iron (76–91 ppm) and zinc (39–48 ppm), and with bold, globular, shining slate grey coloured seeds; resistant to downy mildew
NBH 5061 (MH 1812)	Maharashtra, Karnataka, Andhra Pradesh and Tamil Nadu	For rainy season; late maturing, medium height, grey coloured globular bold seeds; resistant to downy mildew

Released varieties/hybrids of minor millets

Crop/Variety/Hybrid	Area of adoption	Salient features
Fingermillet		
KMR 204	Karnataka	Early maturing, blast resistant and is suitable for late sowing
Phule Nachani 1 (KOPN 235)	Maharashtra	Late maturing and is suitable for early sowing
VL Mandua 352 (VL 352)	All fingermillet-growing states, except Tamil Nadu and Maharashtra	Very early maturing
Foxtail millet		
SiA 3156	Andhra Pradesh, Karnataka, Tamil Nadu and Bihar	Medium-duration variety with very high yield potential

Released varieties/hybrids of oilseeds

Crop/Variety/Hybrid	Area of adoption	Salient features
Soybean		
JS 20-29	Madhya Pradesh, Maharashtra, Rajasthan, Uttar Pradesh	Semi-determinant growth habit, brown pods, black hilum, large seeded, average yield 2,100 kg/ha, crop duration 95 days, oil content 20.9%, protein content 41.1%; resistant to *yellow mosaic virus* (YMV) and charcoal-rot
JS 20-34	Madhya Pradesh, Maharashtra, Rajasthan, Uttar Pradesh	Determinate growth habit, glabrous, yellow pods, black hilum, medium sized seeds, average yield 2,000 kg/ha, crop duration 86 days, oil content 20.3%, protein content 40.8%; resistant to charcoal-rot; moderately resistant to girdle beetle
Raj Vijay Soybean 2001-04 (RVS 2001-4)	Madhya Pradesh	Semi-determinant growth habit, brown hilum, average yield 2,500 kg/ha, crop duration 94 days, oil content 21.5%, protein content 42%; tolerant to major leaf, pod and root diseases, girdle beetle and semi-looper

Crop/Variety/Hybrid	Area of adoption	Salient features
MAUS 2 (Pooja)	Karnataka	Semi- determinate growth habit, yellow-seeded, light-brown hilum, average yield 2,700 kg/ha, crop duration 100–105 days, oil content 20.3%, protein content 41.5%; resistant to bacterial pustule and leaf spots; moderately resistant to leafminer, stem fly and blue beetle
MAUS 162	Maharashtra	Semi-determinate growth habit, oblong, pale-yellow seeds, blackish hilum, average yield 2,100 kg/ha, crop duration 100–103 days, oil content 21.37%, protein content 41.95%; tolerant to charcoal-rot, cotyledonary spot, *Rhizoctonia* root-rot and aerial blight
DSb 21	Karnataka	Semi-determinate growth habit, yellow seed coat and brown hilum, average yield 2,700 kg/ha, crop duration 90–95 days, oil content 18.2%, protein content 38.2%; resistant to rust
Niger		
DNS 4	Karnataka	Shining black bold seeds; seed yield: 500–600 kg/ha, oil content (%): 39–41, days to maturity: 90–95 days

DNS 4 niger matures in 90–95 days and its seeds are shining black and bold

Greengram DGGV 2 is tolerant to pod shattering

Released pulses varieties/hybrids

Crop/Variety/Hybrid	Area of adoption	Salient features
Greengram		
DGGV 2	Karnataka	Large seeds, tolerant to pod shattering, is suitable for mechanical harvesting
BGS 9 (Somnath)	Karnataka	Early maturing, large shining green seeds, average yield 1,200–1,400 kg/ha, is moderately resistant to powdery mildew
Blackgram		
DBGV 5	Karnataka	Large, shining seeds with high protein and good cooking quality
Chickpea		
JG 12	Madhya Pradesh	Early maturing (110 days), medium sized seeds, average yield 2,200 kg/ha, is resistant to wilt
Lentil		
Raj Vijay Lentil 31 (JL 31)	Madhya Pradesh	Early maturing, large seeded (2.9 g/100 seeds), average yield 1,600–1,800 kg/ha; yields very good biomass, and is resistant to wilt

Crop/Variety/Hybrid	Area of adoption	Salient features
Pigeonpea		
BRG 4 (BRG 10-2)	Karnataka	Semi-determinate growth habit, suitable for normal and delayed sowing, matures in 140 150 days (mid-early), yields 1,200–1,400 kg/ha
ICPH 2671 (Hybrid)	Madhya Pradesh	Indeterminate plant type, semi determinate growth habit, matures in 180–184 days (medium-late), large brown seeds, and is resistant to wilt and sterility mosaic disease
Horsegram		
CRIDA HARSHA (CRHG 19)	Andhra Pradesh, Karnataka, Kerala and Tamil Nadu	Good biomass and dry fodder yield under moisture stress
Fieldpea		
IPFD 10-12	Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Gujarat and Rajasthan	For irrigated and rainfed conditions in *rabi* season; green seeded, dwarf type, average yield 2,200 kg/ha, and is resistant to powdery mildew
HFP 715	Himachal Pradesh, Jammu and Kashmir, Uttarakhand, Asom, Manipur, Mizoram, Meghalaya, Tripura, Nagaland, Arunachal Pradesh and Sikkim	For irrigated areas; dwarf type, average yield 1,600 kg/ha, and is resistant to powdery mildew
Cowpea		
DCS 47-1	Karnataka	Suitable for *kharif*/pre-*rabi* cultivation, and is of short duration

Cyamopsis tetragonoloba (var. HG 563) × *C. serrata* hybrids were produced successfully by manipulating pre-and post-fertilization conditions. The segregating progenies are in F_3 generation. These hybrids are considered valuable basic material for developing mapping population to initiate gene tagging and identification of quality trait loci.

Horsegram mutant—CRIDA Harsha (CRHG 19)

CRGH 19, a horsegram variety, which is a derivative from K 42, was evolved by physically induced mutation through γ irradiation. The variety yields on an average 760–1,300 kg/ha and matures in 88 days. It is a brown seeded and non-shattering type, and is tolerant to powdery mildew, anthracnose and white-fly. It has superior quality parameters with 28.3% crude protein content. The variety responds to fertilizer application up to 20 kg N+40 kg P_2O_5, and was found to record 65% higher yield over local (control) in farmers' fields.

Commercial crops

Sugarcane: Two sugarcane varieties, Sankeshwar 049 (Co Snk 05103) and Sankeshwar 814 (Co Snk 05104), have been released for cultivation.


Midlate maturing
Sankeshwar 814 sugarcane


Early maturing
Sankeshwar 049 sugarcane

Sugarcane varieties

Variety	Area of adoption	Salient features
Sankeshwar 049 (Co Snk 05103)	Andhra Pradesh, Gujarat, Maharashtra, Karnataka, Tamil Nadu, Kerala and Madhya Pradesh	Early maturing; cane yield 106 tonnes/ha; sucrose 17.20%; moderately resistant to red rot, smut and wilt; resistant to woolly aphid and tolerant to moisture stress
Sankeshwar 814 (Co Snk 05104)	Andhra Pradesh, Gujarat, Maharashtra, Karnataka, Tamil Nadu, Kerala and Madhya Pradesh	Mid-late maturing; cane yield 107 tonnes/ha; sucrose 17.50%; moderately resistant to red rot and smut and tolerant to salinity, waterlogging and moisture stress

Forage crops

Four varieties/hybrids of forage crops, including one each of berseem (Hisar Berseem 2), forage sorghum (CSV 30F), bajra napier grass (CO (BN) 5) and guinea-grass (CO (GG) 3) have been released for cultivation in different agro-ecosystems.

Varieties/hybrids of forage crops

Crop/Variety/Hybrid	Area of adoption	Salient features
Berseem		
Hisar Berseem 2 (HB 2)	Haryana	Longer duration, big head size, higher leaf : stem ratio, better regeneration, resistant to stem-rot, green fodder yield: 750–800 q/ha
Forage sorghum		
CSV 30F	Rajasthan, Gujarat, Uttarakhand, Uttar Pradesh, Haryana, Punjab, Maharashtra, Karnataka and Tamil Nadu	*Kharif* forage sorghum, 267-cm tall, tolerant to shoot fly and stem borer and foliar diseases
Bajra napier grass		
CO (BN)5 (TNCN 074)	Throughout India	Profuse tillering type, high leaf: stem ratio, high green fodder yield (1,082 q/ha/yr), dry matter yield (239 q/ha/yr) and crude protein yield (18.3 q/ha/yr)
Guinea-grass		
CO (GG) 3 (TNGG 062)	Throughout India	Profuse tillering, lush green, broader leaves, shade tolerant, more palatable, free from disease and pest infestations, non-lodging type, green fodder yield:1,082.4 q/ha, dry matter yield 229.3 q/ha, crude protein yield 20.5 q/ha

Biotechnology

Alien introgression and rust resistance in wheat: A novel *adult plant resistance* (APR) gene for leaf rust resistance was transferred from wild relative of wheat (*Aegilops markgrafii*). Cytological analysis of *Aegilops markgrafii* derived introgression line ER1 revealed 2n=42 chromosomes with most of the pollen mother cells (PMCs) showing 21 bivalents. ER1 showed high degree of resistance to both leaf and stripe rust at the adult plant stage.

Characterization of backcross of rice lines: One high-grain protein content (GPC) donor, ARC 10075, was crossed with high-yielding popular rice varieties, Naveen and Swarna. Backcross derived lines were developed by three consecutive backcrossings with the recurrent parents Naveen and Swarna, followed by a single seed descent. Some derived lines with phenotypic similarities for plant type and yielding ability to Naveen are: PLN-32 (13.1%), PLN-102 (12.5%), PLN-37 (12%) and PLN-63 (11.5%). Single grain protein content of these lines was higher (~2 mg) than Naveen. Ten lines were from the backcross derived populations, based on the phenotypic similarity with Swarna; GPC of these lines, PLS-17, PLS-156, PLS-3, PLS-114 and PLS-133, was higher both on per cent basis and single grain basis (11–13% and 1.55–1.82) as compared to Swarna.

Some physico-chemical properties of parents and introgression lines

Genotypes	Grain length (mm)	Grain breadth (mm)	Grain length: breadth ratio	Amylose content (%)	Grain type
Naveen	5.62	1.52	3.69	21.1	MS
ARC10075	6.29	1.72	3.66	25.2	MS
PLN-32	5.92	1.49	3.97	23.3	MS
PLN-37	5.98	1.61	3.71	23.6	MS
PLN-363	6.85	1.61	4.25	22.1	LS
PLN-102	6.0	1.56	3.85	20.0	MS

MS: Medium Slender; LS: Long Slender

Mapping fertility restorer (*Rf*) gene in sorghum: About 732 F_2 plants of the cross 27A × M 35-1 were used to study genetics of fertility restoration; of which, 561 were fertile and 171 were sterile giving a good fit to 3 (fertile): 1 (sterile) ratio (χ^2 value 0.96, p = 0.00), indicating that the fertility restoration is under the control of a single dominant gene. Selective genotyping of only sterile F_2 plants using several SSR markers revealed that the markers SB 2387 and SB 2388 from chromosome 4 showed co-segregation for fertility restoration. Interestingly, a *penta tricopeptide repeat* (PPR) gene (*Sb04g000550*) was found to co-exist very near to the SB 2387 locus. PPR genes, through their RNA editing ability, are known to be the candidate genes involved in fertility restoration. The SSR markers SB 2387 and SB 2388 will greatly facilitate marker-assisted breeding in cytoplasmic male sterile and restorer breeding programmes and lay foundation for map-based cloning of this *Rf* gene.

Potential donors for designing *Next Generation Rice*: Eleven possible donors of super traits (very heavy

Performance of promising rice genotypes for yield and its attributing traits

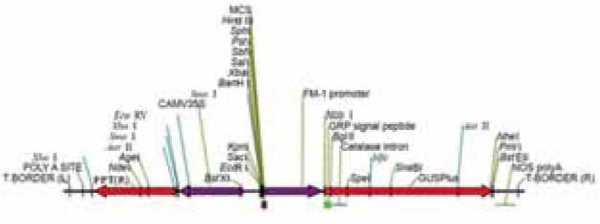
Genotype	Days to 50% flowering	Panicle length (cm)	Spikelet/ panicle	Panicle weight (g)	Grain yield (t/ha)
CR2683-7-1-2-3	135	26.5	339	7.53	7.64
CR3696-1-2-1-1-1	131	26.9	289	4.95	6.12
CR2682-7-1-1-1	132	27.5	276	8.13	8.5
CR3697-3-2-3-1-1	123	40.5	329	6.89	5.58
CR3697-3-1-1-1-1	117	37.1	241	4.69	5.99
CR2683-1-1-2-1-1	132	24.8	300	7.69	8.03
CR2683-7-1-3-1-1	135	26.5	259	7.43	6.94
CR2682-3-1-1-1	131	26.0	317	6.70	6.02
CR2683-5-2-1-1-1	135	24.5	232	6.73	6.8
CR2683-7-1-2-2	135	25.5	220	10.03	5.75
CR3697-3-1-1-4-1	115	35.0	144	3.92	5.42
Gayatri (check)	130	26.0	156	3.81	6.16
Pooja (check)	127	27.5	139	2.43	5.39

panicle, high spikelet number and very long panicle) were evaluated along with two popular check varieties in random block design with three replications with the addition of 80 : 40 : 40 NPK kg/ha and need-based plant protection measures during wet season of 2013.

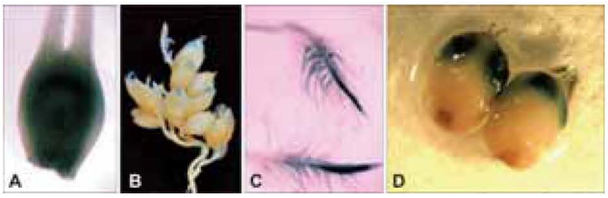
Heterologus ovule-specific promoter expression in sorghum: A megaspore mother cell-specific (MCS) promoter "FM-1" was isolated from *Arabidopsis* by PCR, confirmed by sequencing and was cloned into *pCAMBIA* 1305.2. The orientation of the promoter was verified using *BamHI*, which was located at a terminal site in the FM-1 promoter as well as in the MCS of *pCAMBIA* 1305.2.

The vector was transformed into *Agrobacterium* strain EHA 105 by freeze-thaw method, and was used for transforming sorghum *via* somatic embryogenesis pathway, deploying shoot-tip explants. A total of 3,000 explants were transformed and selection of transformants was done using Phosphinothricin (*bar* transgene that confers resistance to Phosphinothricin). In surviving batches, shoots were regenerated and advanced for root induction. A total of 95 plants were regenerated and analysed for transgene. Transgenic plants with ovule-specific promoter showed presence of promoter with *GUS* gene. Eight plants showed presence of transgenes, which were selfed, and seeds were collected.

The ovules of these transformants in T_1 generation were assayed for tissue-specific expression of the FM-1 promoter in different tissues such as root, stalk, leaves and floral parts. The plants showed GUS expression exclusively in the ovule and stigma in the early stages of flowering, thus indicating site and stage-specific activity of FM-1 promoter.

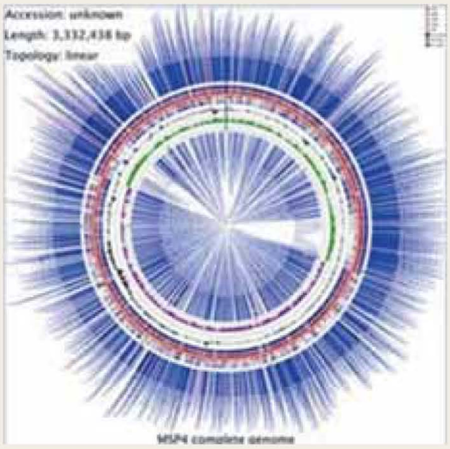


pCAMBIA 1305.2-TDNA with FM-1 promoter and PPT (R) marker



GUS expression as driven by *Arabidopsis* ovule-specific promoter FM-1 in T_1 plants. GUS expression is seen in the ovule region (A), stigma (B & C) and ovarian tissues (D)

The first complete genome of the genus *Virgibacillus*: *Virgibacillus* sp. MSP4-1, an obligate halophile, cracked



Successfully sequenced and annotated the first complete genome of the genus *Virgibacillus*. This bacterium can tolerate up to 23.5% (minimum and optimum being 8% and 10%, respectively) NaCl in the growth medium, and was isolated from a salt pan of the Rann of Kutch, Gujarat.

The annotation of the complete genome of 3,332,438 bp revealed the presence of 420 subsystems and genes for 3,459 coding sequences (CDSs), 90 RNA and 910 hypothetical proteins. Besides, there are 26 genes related to osmotic stress (osmoregulation, ecotine biosysnthesis and choline and betaine uptake) and 37 genes for oxidative stress tolerance.

Prediction of microRNA genes using computational tools: A database of castor protein sequences was generated using NCBI protein database. Castor draft genome was blasted against the castor protein database using Blast X to detect coding regions in the castor genome contigs. A database of non-coding sequences was generated out of the contigs with no hits with Blast X. This database was used for predicting 19,243 probable pre-*miRNA* genes from non-coding regions. These extracted single stranded structures were then subjected to Hierarchical Hidden Markov model.

**Blueprint of bread-wheat genome unveiled—
the last step before sequencing of full genome**

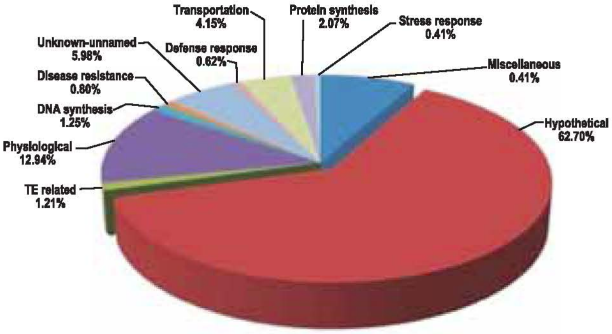
Earlier Indian scientists helped crack genetic codes of rice and tomato as part of the international consortia, and of their own in decoding of pigeonpea (*arhar*) and chickpea (*chana*) genomes. Wheat was considered as one of the hardest crop-plants to decode due to its huge genome size of 17,000 million base pairs, and three sets of highly similar chromosomes in the genome. Scientists from the ICAR's National Research Centre on Plant Biotechnology (NRCPB), New Delhi, Punjab Agricultural University (PAU), Ludhiana, and Delhi University South Campus (DU) in collaboration with the International Wheat Genome Sequencing Consortium (IWGSC) have published a chromosome-based draft sequence of the bread-wheat genome.

Technological advances made in the recent years and availability of specialized genetic stocks developed during the fifties in wheat variety 'Chinese Spring' have made it possible to isolate individual wheat chromosomes for sequencing. The decoding of the wheat genome has identified more than 125,000 genes assigned to individual wheat chromosomes. The draft sequence is a major landmark towards obtaining a complete reference sequence of hexaploid bread-wheat genome. With a chromosome-based full sequence in hand, wheat breeders would have high quality tool at their disposal to accelerate breeding programmes and to identify how genes control complex traits such as yield, grain quality, disease and pest resistance, and tolerance to drought, heat and salt stresses. The draft sequence is providing new insights into the history and evolution of the wheat genome and genes involved in grain development and disease resistance. The genetic blueprint of wheat is an invaluable resource to plant science researchers and wheat breeders. They would be able to precisely locate specific genes on individual wheat chromosomes. It would provide thousands of markers for DNA fingerprinting, diversity analysis and marker-assisted breeding in wheat. The availability of wheat genome will accelerate gene discovery efforts and fast-track development of superior wheat varieties.

The HHMMiR classified 7,188 as true putative pre-miRNAs. Further filtration with Triplet-SVM (SVM classifier) extracted 4,054 putative pre-miRNAs.

***Trichoderma*-mediated induced systemic resistance in castor against *Fusarium oxysporum ricini*:** Seeds of castor GCH 4 hybrid were sown in sterile soils either inoculated with different isolates (N13, Th4d, TV5, TaDOR 7316) of *Trichoderma* alone or of the pathogen, *Fusarium oxysporum ricini*, alone or combinations of *Trichoderma* strains and *Fusarium oxysporum ricini*. As the control, seedlings were also grown in the untreated soil. Germination percentage and wilt incidence were recorded at regular intervals. Wilt incidence was lower whenever *Trichoderma* was included in the soil along with *Fusarium* inoculum. Th4d treatment showed least wilt incidence (21%), followed by N13 (36%), TV5 (43%), TaDOR 7316 (31%). Pots with *Fusarium* inoculum alone showed 73% wilt incidence. *Trichoderma* strains also reduced the colony forming units of *Fusarium* in the soil; Th4d strain being the best in reducing the pathogen load in the soil.

Mango genome sequencing: Mango, an allotetraploid (2n= 40) fruit-tree, is with small genome of about 450 Mbp. More than 40 Gbp (~88.5X) shotgun and pair-end next generation genomic sequence data of mango genome from the popular mango variety Amrapali were generated using Roche 454 and Illumina (MiSeq, HiSeq and Mate pair) sequencing technologies. RNA sequence data using SOLiD and MISeq sequencing technology were also generated.



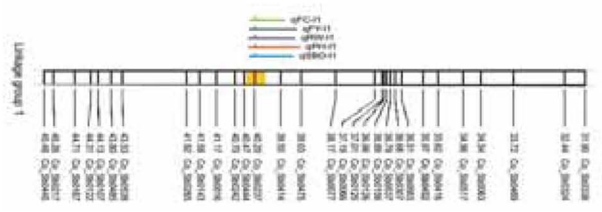
Functional categorizatoin of predicted genes from mango

As first draft assembly, a total of 211,141 (~492 Mbp) contigs were generated. A total of 11,448 unigene contigs were generated and 78,831 genes were predicted with an average gene length of 701 bps. About 185,763 SSRs have been mined in the assembled draft genome.

Analysis of co-expression network under abiotic stress tolerance in rice: Co-expression network analysis for drought and heat tolerance in rice was performed using WGCNA package in R, using transcriptome data generated and publically available microarray data, to divide stress responsive genes into tightly co-expressed module. The block-wise module function of WGCNA package in R was used to generate modules with powers 8 and 6 for drought and heat tolerance, respectively, which gave the best approximate scale-free topology (model fit >0.8) of the resultant network. The differentially expressed genes (DEG), common to drought and heat stress, were analyzed to find consensus modules showing co-expression patterns across stresses using function block-wise Consensus Modules with the following settings: powers 7 and 10, minimum module size 30 and 15 for rice drought and heat, respectively, with the merge cut height set at 0.15. Further analysis was carried to identify consensus co-expression modules by constructing a network based on co-expressed genes with high absolute correlation coefficient (r >0.8) in both drought and heat stresses. One of the top edges was between LOC_Os02g43790, an ethylene responsive TF and LOC_Os02g41510, a MYB TF with r >0.98 in both stresses. Colour coding of nodes in the network with their consensus module colour showed clear grouping of genes from the same module with high number of intra-modular edges.

Developed a high-density genetic map to detect a QTL hot-spot for bast fibre yield in jute: Using high-throughput restriction-site-associated DNA (RAD) sequencing based on Illumina HiSeq 2000 platform, the first high-resolution SNP-based genetic map of jute (*Corchorus olitorius*), with seven linkage groups, has been developed in agreement with its karyotype. This genetic map, comprising 638 SNPs, spanning 358.5 cM, with an average marker interval of 0.72 cM, covered 87.0% of the genome. The total genome of *C. olitorius* was estimated at 370.4 cM, implying that the genetic map represents 96.8% of the genome length. Comparative genomics showed that jute has maximum synteny with cacao and diploid cotton, and probably has diverged from a common ancestor about 33.7 million years ago, involving an ancestral paleo-hexaploidization event that might have shaped its seven chromosomes.

This high-resolution genetic map has been successfully used for genome-wide detection of quality trait loci (QTL) for bast fibre yield and its components in jute. A unique trait of histological fibre content that estimates the total number of fibre cell bundles in an entire stem transversal section at 90 days after sowing, has been identified as a reliable measure of retted (bast) fibre yield for jute.



A QTL hot-spot for bast fibre yield in jute on LG1, consisting of QTL for histological fibre content (FC), fibre yield (FY), plant height (PH), stem base diameter (SBD) and root weight (RW)

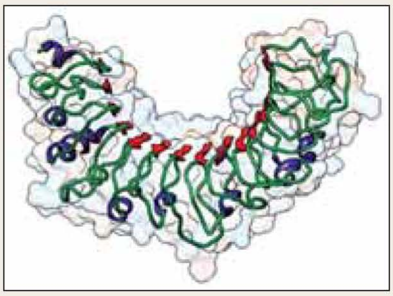
A QTL hot-spot for bast fibre yield on linkage group 1 (LG1) was detected to be co-localized with QTL for histological fibre content, fibre yield, plant height, stem base diameter and root weight. Results showed that there exists a scope for fibre yield improvement in jute through selection for transgressive segregants in the progeny of a specific cross. QTL-seq identified candidate genes within this QTL hot-spot, and this would enable development of tools for marker-assisted selection (MAS) in jute.

Safflower transformation: *In planta* transformation was attempted using reporter gene (*gus*) construct. Preliminary GUS analysis carried out with the transformed seedling explants showed intense GUS expression.

Kunitz-tryspin inhibitor-free soybean genotypes commercialized: Kunitz-tryspin inhibitor-free soybean genotypes NRC101 and NRC102 have been commercialized. License for NRC 101 and NRC102 has also been given. High oleic acid soybean IC 210, which contains double the value of oleic acid than in the regular soybean, has also been commercialized; the license for this genotype has been given too.

A new rice blast resistance gene cloned

Blast is the most devastating disease of rice, which may result up to 70–90% yield losses. An orthologue of *Pi54*, a dominant rice blast (*Magnaporthe oryzae*) resistant gene, cloned by map-based cloning approach from *indica* rice cultivar Tetep, designated as *Pi54of* has been cloned from wild relative of rice, *Oryza officinalis,* and has been reported to confer high degree of resistance to blast. Over-expression of *Pi54of* in two rice genotypes belonging to *indica* and *japonica* background imparts enhanced resistance against three highly virulent strains of *M. oryzae.*



3-D protein structure of blast resistant gene *Pi54of*

Characterization of nematode-responsive promoters: Microarray resources were used for identifying nematode-responsive and root-specific genes (5) having low expression under control conditions. In *silico* analysis revealed presence of three novel consensus motifs with respect to nematode-responsive root-specific genes.

Genetic engineering of sugarcane for drought tolerance: Transgenics (Co 86032) of sugarcane were developed with genes coding for EaDREB2, HSP70 and PDH45 (pea DNA helicase gene) driven by the Portubi 2.3 promoter. Transgenics co-expressing with DREB2 and PDH45 were also developed. Transgene integration was confirmed through PCR. All the transgenics were clonally multiplied for screening for drought. Many of the transgenic events showed an increased level of cell membrane stability.

Two plants each of control and a transgenic event with HSP70 after drought imposition

***Colletotrichum falcatum* (red-rot pathogen) genome and transcriptome data**

Predicted gene annotation of *C. falcatum* genome	Number	Whole transcriptome analysis	Number
Total genes	12,270	No of CDS	23,136
Total Annotated genes with UNIPROT	9,891	No of CDS with Blast hits	19,183
Total Unannotated genes	2,379	No of CDS with no Blast hits	3,953

Whole genome sequencing and transcriptome analysis of red-rot pathogen: Using NGS platform, whole genome and transcriptome of the fungus were sequenced. *De novo* assemblies of genomic and transcriptomic data were performed due to lack of such information in the public domain, and this is the foundation for further genomic studies in sugarcane red-rot pathogen. The new discovery of huge genomic and transcriptomic data will lead to complete understanding on the important plant pathogen, its pathogenicity and effective management of the disease through conventional or genetic engineering approach.

Introgression of diverse sterile cytoplasms from alien sources to commercial cauliflower and cabbage: Ogura CMS system was established in Indian cauliflower in 17 early and 40 mid group genetic backgrounds and exploited in hybrid combinations. For transferring sterile cytoplasms from alien species into *Brassica oleracea*, crosses were attempted with *Diplotaxis catholica*, *D. sifolia*, *D. erucoides* and *D. berthaultii*, which are being advanced through embryo culture.

Development of diagnostic marker for *Alternaria brassicicola*: Rapeseed-mustard is highly susceptible to *Alternaria brassicae* and *A. brassicicola* which lower yield in the entire mustard-growing area, and depending upon the severity, the yield losses ranged from 35 to 46%. A PCR-based protocol was developed for specific and rapid detection of the pathogen and quantifying the occurrence of this fungus for its efficient management.

Complete mitochondrial genome sequence of ladybird beetle

The complete mitochondrial genome of ladybird beetle (*Henosepilachna pusillanima*), the most beneficial among coleopterans, was sequenced, assembled and annotated. Size of the complete mitochondrial genome of *H. pusillanima* was 16,216 bp long and circular in nature. Genome analysis has revealed that there are 13 protein coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes and one control region (A+T-rich region). The size of control region is estimated to be 1,690 bp. The gene arrangement and orientations of assembled mitogenome are identical to the reported coleopteran insect species including predatory ladybird beetle *Coccinella septempunctata* L. The completely annotated genome was submitted to the NCBI (Genbank Accession Number: KJ 131489). This would be the first completely sequenced coleopteran genome from the beetle subfamily Epilachninae in the world, and also the first insect mitogenome from India.

SCAR marker for *Sclerospora graminicola* of pearl millet: Pathotype specific SCAR marker was developed for identification of pathotypes of *Sclerospora graminicola* among a mixture of isolates obtained across different pearl millet-growing regions of India. The developed marker help identifying different pathotypes and also detecting new emerging pathotypes. In *R & Avr* gene interaction, viz. polygalactronse inhibitor protein (PGIP), Map Kinase (MAPK), Chitinase and HRGP genes were characterized and transcript analyses were carried out.

Independent putative transgenic events of *Brassica juncea* developed: Fifteen independent putative transgenic events of *Brassica juncea* var. NRCDR 2 were developed with *Tv dl* gene via *Agrobacterium tumefaciens*-mediated gene transfer technique.

Molecular marker for white rust resistance in mustard: Intron polymorphic markers At5g41560 and At2g36360 were validated in two independent bi-parental F_2 populations. Markers were found tightly linked to white rust resistance loci Ac B1-A4.1 and AcB1-A5.1, respectively.

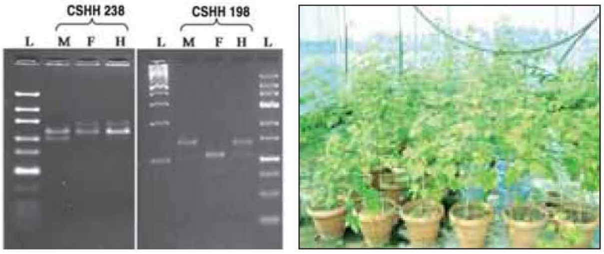
Molecular marker for high oleic acid in safflower: Molecular marker derived from *fad2* gene associated with high oleic trait in sunflower detected TSG 17 (EC699735) and CMS DOP-80 high oleic types in the exotic germplasm accessions.

DNA fingerprinting

DNA fingerprinting of 149 samples of different crops was done for public and private organizations. RAD (Restriction-site associated DNA) sequencing generated SNPs were used for haplotyping of core collections of mothbean (250), cucumber and melon (230) and grass-pea (250). LAMP (Loop-mediated isothermal amplification) assays targeting commonly employed promoters and marker genes have been developed using *Bst* DNA polymerase and ready-to-use isothermal master mix to facilitate on-site GMO screening. Whole genome sequencing of sesame using NGS (Next-Generation Sequencing) technologies generated 30.5 Gb of reads, giving a 85x coverage of the estimated genome size (~354 Mb); a pooled transcriptome deep sequencing data-set generated for anthers, flower, flower bud and shoot tip was used for joining contigs, and the full NGS data was used to mine SSR containing sequences (71,952) and many families of DNA transposons.

Seed technology

Molecular characterization of CSHH 198 cotton hybrid along with parental lines was carried out to



Molecular characterization of CSHH 198 cotton hybrid using SSR marker

assess genetic purity using 60 SSR markers; 15 markers were found polymorphic (20–33%), amplifying a total of 29 alleles, with an average of ±1.9 allelic variants per SSR locus.

Seed germination: Seeds of *Lasiurus scindicus* treated with 0.05% GA_3 showed 25% more germination than control. The phenological characters of *Sehima nervosum* var. Bundel saen Ghas 1 and *Chrysopogon fulvus* var. Bundel Dhawlu ghas 1 were studied. *In-vitro* maturation of guinea seeds supplemented with 100 ppm IAA showed more seed filling (34–41%) than control (13-18%). Pollen fertility improved in *Brachiaria* spp. with the application of brassinosteroid (10 ppm) and tryptophan 100 ppm. Application of silicon (8%) improved total seed yield and tryptophan (100 ppm) reduced seed fall before the harvest in *Brachiaria ruziziensis*.

Quality seed production

In 2013–14, 94,953 quintals of breeder seed, 144,369 quintals of foundation seed, 163,466 quintals of certified seed, 172,352 quintals of truthfully labeled seed and 73,185 quintals of planting material were produced. Further, 155.59 lakh planting material and 5.60 lakh tissue culture plantlets of field crops were also produced.

Horticulture

Fruit crops

A mango hybrid, H-12, with oval fruits, yellow peel, deep yellow pulp, 220–240 g fruit weight, 23–24° Brix and 75–77% pulp recovery was bred crossing Amrapali and Arka Anmol. This hybrid is amenable to medium-density planting (5m×5m), accommodating 400 plants/ha compared to normal spacing (10 m × 10 m) with 100 plants/ha. The fruits are borne in small bunches and have a shelf-life of 15 days.

Mango hybrid H 12 (Amrapali × Akra Anmol)

A guava hybrid (Kamsari × Purple Local), H 3-29, with 200–220 g fruits, medium soft seeds, 12-14° Brix, 4–5 mg lycopene and 235 mg ascorbic acid/100 g pulp was developed. This hybrid is suitable for table and processing.

An exotic French plantain 'NjockKon' (AAB) accession with semi-dwarf plant stature recorded higher bunch weight (25 kg) at FRS, Kannara, Kerala compared with Nendran cultivar (15 kg). In addition, a dwarf banana (NRCB Sel.-10) similar to Karpoorvalli (ABB) but early in maturity (367 DAP) with 16 fruits/hand, 12–13 hands/bunch and 18-20 kg bunch weight was identified for high-density planting and annual cropping.

Of the five acid lime varieties planted (6 m × 6 m) and evaluated under multilocational trials (11 years old), Phule Sharbati recorded high fruit yield (108.4 kg/plant) at Rahuri, Maharashtra.

Several promising hybrid grape progenies like H-80 (James × Beauty Seedless), H-181 (Concord × Cheema Sahebi), H-222 (Anab-e-Shahi × Catawba), H-307 [H-541 (Khalili × Bhokri) × Sharad Seedless] and H-384 (James × Sharad Seedless) with respect to bunch weight and berry size were identified for further evaluation.

In order to evolve downy mildew resistant grape varieties, 3,720 seeds were obtained from Seyve Villard × Thompson Seedless and Carolina Black Rose × Thompson Seedless crosses. Field and *in vitro* screening of 70 field planted progenies of Carolina Black Rose × Thompson Seedless crosses resulted in identification of 19 progenies with a UPOV rating of 1, indicating tolerance to downy mildew.

Grape genomic region corresponding to QTL *Rpv3* was analyzed and 10 new microsatellite markers identified.

Of the in 31 walnut germplasm evaluated, nut weight ranged from 16 to 23 g, kernel weight 7 to 13.5 g with kernel recovery of 45–58%. Of these, five accessions, *viz.* CITH-W-50, CITH-W-69, CITH-W-78, CITH-W-79 and CITH-W-80, were superior for nut weight (>18g), kernel weight (>9 g) and kernel recovery (>46%).

Of the 54 apricot accessions evaluated, maximum fruit yield (35.8 tonnes/ha) was recorded in CITH-AP-2 followed by Harcot (28 tonnes/ha) and Turkey (27.2 tonnes/ha), whereas highest TSS content (22°Brix) was in CITH-AP-37 followed by CITH-AP-

CITH-AP-2 is high-yielding apricot variety

24 (21.40°Brix) and CITH-AP-33 (20.93°Brix). Maximum fruit firmness index (73.8) was recorded in CITH-AP-32 followed by CITH-AP-19 (63.6) at Srinagar.

Similarly, of the 25 plum varieties evaluated, maximum fruit yield (56.6 tonnes/ha) was recorded in Mariposa followed by Tarkol (50.8 tonnes/ha), Monarch (43.8 tonnes/ha) and Black Amber (40.4 tonnes/ha), whereas maximum TSS (24.90°Brix) was in Santa Rosa followed by Burbank (23.13°Brix) and Beauty (18.95°Brix). Maximum fruit firmness index (66.5) was recorded in Black Amber followed by Santa Rosa (66.4) at Srinagar.

A promising accession of khoonphal (*Haematocarpus validus*) collected from a custodian farmer's field in Andaman and Nicobar Islands was observed to have huge potential for commercialization. The fruits turn dark red on ripening and are rich in beta carotenoids. It contains 400 GAE mg/100 g total polyphenol, 542 RE mg/100 g flavonoids, 275.56 TAE mg/100 g tannin and 203.77 C3GE mg/100 g anthocyanin.

Khoonphal fruit at different maturity stages

Vegetable crops

A number of varieties/hybrids of vegetable crops were identified for release (*see* table).

Two F_1 tomato hybrids, viz. Hybrid-369 and Hybrid-371, with triple resistance to ToLCV+BW+EB diseases, high yield (80 tonnes/ha) and firm fruits were developed.

H-369 hybrid tomato is disease resistant

Brinjal variety, CARI Brinjal 1, with green oblong fruits, 25–30 tonnes/ha yield and resistant to bacterial wilt was developed and released for cultivation for Andaman and Nicobar region.

Arka Neelachal Prabha (CHCL 92), a mid-season, (65–75 days) and high-yielding chilli variety (493 g/plant equivalent to 109 q/ha) with dark green and medium long (5–6 cm) fruits was identified for cultivation for east coast.

Arka Arjun, a French bean variety resistant to Mungbean yellow mosaic virus (MYMV) with a yield potential of 17.4 tonnes/ha was identified for summer cultivation (up to 35°C) in plateau. The pods are green, round, smooth and stringless. Arka Sharath, another French bean variety (round, fleshy and stringless pods with 20 tonnes/ha green pod yield) was recommended for release in Karnataka.

Arka Arjun provides quality pods

Two varieties of amaranth, Arka Samraksha (10–12 tonnes/ha yield) with high antioxidant activity (~500 mg/100 g fresh weigh), low nitrates (27.3 mg/100 g fresh weight) and low oxalates (1.34 g/100 g fresh weight) content, and Arka Varna (10–12 tonnes/ha yield) with high antioxidant activity (417 mg/100 g fresh weight), low nitrates (38.2 mg/100 g fresh weight) and low oxalates (1.42 g/100 g fresh weight) content were identified for release (as against normal antioxidant activity, nitrates and oxalates content ranging from 150–200 mg, 75–80 mg and 2.5 to 3.5 g/100 g fresh weight, respectively in existing amaranth cultivars). These varieties are suitable for round the year cultivation in Karnataka.

A fertile inter-specific spine gourd hybrid (*Momordica subangulata*) and teasel gourd (*Momordica dioica*) with 30–45 g fruit weight, amenable for easy propagation through stem and root cuttings, improved fruit setting (90% due to natural pollination) extended harvesting period (April–November) and higher yield (5–7 kg/plant) was identified.

CARI Poi Red, a multi-cut poi (*Basella alba* L.) variety with higher yield (50–52 tonnes/ha), glossy red leaves, better adaptability to tropical island conditions and rich in anthocyanin was identified at Port Blair. It yields 15–22 tonnes/ha in first harvest.

Potato

Kufri Lalit, a potato hybrid, resistant to late blight with red-peel, yellow flesh, round, medium deep-eyed tubers and 25.5 tonnes/ha yield (15%

Vegetable	Variety	Salient features
Pea (*Pisum sativum*)	Kashi Ageti	Early-maturing (35–37 days for 50% flowering) and 12-12.5 tonnes/ha yield
Tomato (*Lycopersicon esculentum*)	Kashi Abhay	Semi-determinate hybrid, uniform maturity and moderately tolerant to ToLCV, 60–70 tonnes/ha yield
Chilli (*Capsicum annum*)	Kashi Tez	A CMS-based early-maturing, dual purpose hybrid, tolerant to anthracnose and thrips and 14–15 tonnes/ha green fruit yield
Brinjal (*Solanum melongena*)	Kashi Uttam	Round-fruited, high-yielding (50–55 tonnes/ha), tolerant to fruit- and shoot-borer and resistant to lodging
Pointed Gourd (*Trichosanthes dioica* L.)	Kashi Suphal	Fruits contain few seeds, fleshy, attractive with 18–21.5 tonnes/ha yield
Pepo (*Cucurbita pepo*)	Kashi Shubhangi	Early-maturing, fruits are dark green, elongated, borne in 8–10 numbers/plant and yield 60–67.5 tonnes/ha
Satputia (*Luffa acutangula*)	Kashi Khushi	High-yielding (5.24–6.27 kg fruits/plant in 8–10 pickings), bearing ~140 fruits/plant in clusters (5–6 fruits/cluster)
Ivy gourd (*Coccinia indica*)	Kashi Bharpoor	High-yielding (25–28 kg/plant) and bears oval, light green fruits (3,200–3,500 fruits/plant)
Kartoli (*Momordica cochinchinensis*)	Kashi Haritika	Early-maturing and high-yielding (30–35 tonnes/ha) variety
Kakrol (*Momordica dioica*)	Kashi Gautam	Early-maturity (75-85 DAS) and bears 45–63 fruits/plant (2.5–4.5 kg/plant)
Indian Bean (*Dolichos lablab*)	Kashi Khushhaal	Semi-pole type, early-maturing. Pods 13.5 cm long, dark green, shiny, slightly curved with 4–5 coffee coloured seeds. First picking starts 107 days after sowing and yields 30–38 tonnes/ha
French Bean (*Phaseolus vulgaris*)	Kashi Sampann	Late-maturing, plants bushy, high-yielding (45–50 round, light green pods). It is tolerant to GYMV and high temperature (32–38°C) and yields 27–27.5 tonnes/ha
Watermelon (*Citrullus lanatus*)	Kashi Pitamber	Early-maturing (76–81 DAS), fruits small (2.50–3.42 kg) with yellow rind from ovary stage and yields 8.3–12.5 kg/plant

Kufri Lalit potato hybrid yields 25.5 tonnes/ha

increase over Kufri Lalima) was identified for cultivation in Indo-Gangetic plains and recommended for release.

Tuber crops

Two triploid cassava hybrids, viz. Sree Athulya (high-yielding 39 tonnes/ha) with a high starch content (34.8%) and Sree Apoorva with higher yield (37.6 tonnes/ha) and 33.3% starch content were recommended for release and cultivation in Tamil Nadu and Andhra Pradesh and Tamil Nadu and Kerala, respectively.

Similarly, two sweet potato varieties, Swarna and Aparna, with 20–25 tonnes/ha tuber yield in 110–120 days duration were released by ICAR-CIARI, Port Blair.

Flower crops

A marigold variety, Arka Bangara, with yellow gold (RHS colour chart No. 12-A) and petaloid sterile, medium size (5–6.5 cm diameter) and higher yield of flowers (45 tonnes/ha) which commences to bloom

Marigold, Arka Bangara, provides 18 tonnes/ha flowers

40–45 days after transplanting and continues up to 65–70 days was identified for release. In addition, one promising marigold hybrid for high yield, viz. IIHRMGYH-1 (30 tonnes/ha) with large (9.45 cm), golden yellow flowers for round the year cultivation and two male sterile lines, IIHRMYS-1 and IIHRMOS-1, with medium tall, apetaloid plants were identified.

Two China aster varieties namely, Arka Aradya (15 tonnes/ha, highest yield in pink types) and Arka Archana (17 tonnes/ha, highest yield in white types), suitable for loose flower and bedding, respectively, were identified. Tuberose hybrids, Arka Prajwal (18–20 tonnes/ha loose flowers) and Arka Vaibhav (200,000 spikes/ha) were recommended for release.

Orchids

Three orchid hybrids, viz. *Cymbidium* 'B. S. Basnet', *Aranda* 'Kunga Gyatso' and *Dendrobium* 'V. Nagaraju' were released. Two crosses, viz. *Cymbidium* Sleeping Nymph × *C. lowianum* and *C. lowianum* × *C.* 'Showgirl 'Coocksbridge' were registered as Darjeeling Nymph and Darjeeling's Delight, respectively with Royal Horticultural Society, UK.

Spices

Nutmeg variety, IISR-Kerala Shree, having bold nuts with whole, thick and red mace, rich in sabinene and myrcene developed through farmers' participatory breeding, was recommended for release.

IISR-Kerala Shree has bold nuts

A high-yielding (25 tonnes/ha) turmeric, variety Duggirala Red, with improved rhizome quality (curcumin 4.1%, oleoresin 8.8% and dry matter 23.5%) was identified and recommended for release and cultivation in Andhra Pradesh, Telangana, Tamil Nadu and Bihar.

Plantation crops

In coconut, among Dwarf (D) × Tall (T) hybrids evaluated, Chowghat Orange Dwarf × West African Tall (154 nuts), Chowghat Orange Dwarf × Laccadive Ordinary Tall (143 nuts) and Malayan Yellow Dwarf × Andaman Ordinary Tall (167 nuts) were superior for higher nut yield, whereas Malayan Yellow Dwarf × Tiptur Tall (MYD × TPT) was superior for higher nut yield (167 nuts/palm). Root (wilt) disease incidence was significantly lower in *inter-se* mated progenies (47%) compared to selfed ones (63%). The *inter-se* progenies recorded 35–40% higher nut yield compared to selfed ones.

Two high-yielding arecanut varieties, viz. Madhuramangala (3.54 kg dry kernel/palm/year) for Karnataka and Konkan and; Nalbari (4.15 dry kg kernel/palm/year) for Karnataka, North Bengal and North East were identified and notified for cultivation.

Four coconut varieties, viz. CARI Annapurna (240 g copra/nut), CARI Surya (104 nuts/palm/year), CARI Omkar (~100 nuts/palm/year) and CARI Chandan (~100 nuts/palm/year) were identified for dwarf stature and high yield under rainfed conditions of Andaman and recommended for release.

Medicinal plants

Vallabh Isabgol-1, a new, high-yielding Isabgol mutant of variety GI 2 with semi-erect growth, medium plant height (30–40 cm), green leaves with medium pubescence, compact spike, compact flower arrangement, high seed yield (24.5% higher) was developed. It has improved mucilage recovery (9.21 g/kg seed) than GI 2 (8.96 g/kg).

Vallabh Isabgol-1 was recommended for cultivation

Two varieties of Indian Velvet bean (*Mucuna pruriens*), viz. Arka Dhanwantari (4–4.5 tonnes/ha seed yield with 4–4.5% L-dopa) and Sel.8 (~3–3.5 tonnes/ha seed yield having 3.5–3.8% L-dopa) were recommended for release and cultivation in Karnataka.

Mushroom

A high-yielding variety of button mushroom, DMR-U3-54, was developed. Several retro-element based markers linked with fertility in *Agaricus* were identified. Presence of WRKY transcription factor (protein domain) was confirmed in *Agaricus* mushroom which might be useful in studying the evolutionary significance and stress tolerance in mushroom.

Biotechnology and tissue culture

An endochitinase gene for wilt resistance in guava was introgressed through *Agrobacterium*-mediated transformation. Crude protein extract of putative transgenic lines inhibited the growth and conidial germination of *Fusarium oxysporum* f sp. *psidii* with maximum N-acetyl glucosamine activity in transgenic guava line-22 (0.741 µM/min/µg of protein), followed by transgenic guava line-20 (0.738 µM/min/µg of protein) compared to non-transgenic one (0.0875 µM/min/µg of protein), thereby confirming the introgression of endochitinase gene in putative transgenic guava lines. In addition, QTL linkage map for seed hardiness and fruit weight in guava was developed.

Putative transgenic lines were developed for diseases like bacterial nodal blight in pomegranate and *Fusarium* wilt in banana. Whole genome sequencing of *Bee Hee Kela* and *Bhimaitia* was carried out using *HiSeq* platform in banana.

Tomato plants expressing chimeric dsRNA of four common viruses infecting tomato and chilli were developed. The structural and known silencing suppressor genes were the target of RNAi (also called gene silencing). All the control plants were showing symptoms, while transgenic lines exhibited resistance to viruses.

In addition, a vacuolar pyrophosphatase gene (PjVPl) from *Prosopis juliflora* was cloned and an overexpression construct developed. Transgenic tomato plants were developed through *Agrobacterium*-mediated transformation using *AtDREBA* gene construct to impart stress tolerance. In all, 30 acclimatized tomato plants were developed and the presence of transgene confirmed. After segregation and southern blot, 18 single copy transformants were advanced for phenotypic screening.

In order to evolve high starch cassava varieties, *glgC* gene construct was mobilized to *Agrobacterium* EHA105 and its colonies confirmed. The *gbssI* gene fragments were amplified and cloned to pGEMT vector and sequence was confirmed. The targets for cassava miRNAs in genes of cassava mosaic virus were identified.

In addition, miRNA target prediction tool for mRNA sequence was developed in R-package incorporating sequence similarity score and energy prediction and further utilized to identify plant miRNA targets in RNA seq data of elephant foot yam. A web-based interactive tool for construction of gene networks using gene expression data was developed using R-statistical environment.

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