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Conservation of Spices Germplasm in India*

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Genetic resources of crop plants include genepools of both domesticated and wild species. They are the reservoirs of useful genes, which could be of immense use for the genetic improvement of crops. During the past three decades awareness has been generated to identify, collect and conserve the fast depleting and irreplaceable crop genetic resources for use by present and future generations. According to Vavilov (1926), about 160 species of domesticated plants have originated in India. Among these, spices constitute a very important group of plants, which had its origin in India. These are high value crops with potential for large-scale export. Hence, it is imperative to collect and conserve the germplasm of spice crops.

There are many spices that are cultivated in India (Table 1). The important ones, particularly with relevance to our country are: black pepper (*Piper nigrum* L.), turmeric (*Curcuma longa* L.), ginger (*Zingiber officinale* Rosc.), cardamom (*Elettaria cardamomum* (L.) Maton), coriander (*Coriandrum sativum* L.), fenugreek (*Trigonella foenum-graecum* L.), fennel (*Foeniculum vulgare* Mill.), cumin (*Cuminum cyminum* L.), cinnamon (*Cinnamomum verum* Presl.), cassia (*Cinnamomum aromaticum* Nees), nutmeg (*Myristica fragrans* Houtt.), clove (*Syzygium aromaticum* (L.) Merr. & Perry), tamarind (*Tamarindus indicus* L.), kokam (*Garcinia indica* (Thouars) Choisy), Malabar tamarind (*Garcinia cambogia* (Gaertn.) Desr.), Mysore gamboge (*Garcinia xanthochymus* Hk. *f.* &Th.) and vanilla (*Vanilla planifolia* Jacks.). Of all the spices produced in India, chilli occupies the first place in terms of area, production and consumption. However, under the ICAR set up chilli is included under vegetables and hence, the present review does not cover this crop.

Seed spices mostly have orthodox seed, and can be easily conserved in seed genebanks. Vegetatively propagated spices and seed spices either with no seeds or with recalcitrant or intermediate seeds are conserved in field genebanks, *in vitro* genebanks and cryobanks.

Conservation of Spices in Field Genebank

Black Pepper

Black pepper (*Piper nigrum* L.) belonging to the family Piperaceae is an important spice that has its origin in the southern Western Ghats, specifically in Kerala. It is cultivated as a backyard crop as well as a commercial crop from coastal plains to elevations as high as 1500 m. The maximum cultivation in Kerala is noticed in Idukki and Wayanad districts. Two biotic factors, namely, foot rot disease and root knot nematode have greatly damaged the crop resulting in fast depletion of its genetic stock. Over 100 cultivars of black pepper have been reported from the southern Western Ghats along with 18 species distributed in the forests (Table 2). Deforestation has led to the depletion of the wild relatives of the crop. North-East, tropical and subtropical Himalaya, Eastern Ghats and northern Western Ghats need to be explored to collect more germplasm.

The Indian Institute of Spices Research (IISR), Kozhikode and National Bureau of Plant Genetic Resources (NBPGR) have given high priority for systematic collection and conservation of black pepper growing in the Western Ghats. In IISR, about 3,000 accessions of black pepper are conserved. The information about maintenance of germplasm in field genebank at various institutes is presented in Table 3.

The species-wise accessions of *Piper* L. being maintained in field genebank at NBPGR Regional Station, Thrissur and IISR, Kozhikkode are given in Table 4.

Turmeric

Turmeric (*Curcuma longa* L.) known as the 'yellow spice' is believed to have originated in India. Turmeric belongs to the family Zingiberaceae and has widespread occurrence in the tropics and subtropics of Asia. India has maximum

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Table 1. Various spice crops cultivated in India

S No.	Botanical name	Common name	Part used	Family
1.	*Acorus calamus* L.	Sweet-flag	Rhizome	Aceraceae
2.	*Allium cepa* L.	Onion	Bulb	Alliaceae
3.	*A. sativum* L.	Garlic	Bulb	Alliaceae
4.	*Alpinia galanga* Willd.	Greater galangal	Rhizome	Zingiberaceae
5.	*Amomum subulatum* Roxb.	Large cardamom, Sikkim cardamom, Nepal cardamom	Fruit, seed	Zingiberaceae
6.	*Anethum graveolens* L.	Dill	Fruit, leaf	Apiaceae
7.	*Apium graveolens* L.	Celery	Root	Apiaceae
8.	*Armoracia rusticana* Gaertn.	Horse-radish	Root	Apiaceae
9.	*Averrhoa carambola* L.	Carambola, star-fruit*	Fruit	Averrhoaceae
10.	*A. bilimbi* L.	Bilimbi, cucumber-tree*	Fruit	Averrhoaceae
11.	*Brassica juncea* (L.) Czernajev & Cosson	Indian mustard	Seed	Brassicaceae
12.	*Brassica nigra* (L.) Koch	Black mustard	Seed	Brassicaceae
13.	*Bunium persicum* (Bioss.) B. Fedtsh.	Black caraway	Seed, tuber	Apiaceae
14.	*Capparis spinosa* L.	Caper	Unopened flower bud	Capparidaceae
15.	*Capsicum frutescens* L., *C. annuum* L.	Chilli, capsicum	Fruit	Solanaceae
16.	*Carum bulbocastanum* L.	Black caraway	Fruit	Apiaceae
17.	*C. carvi* L.	Caraway	Fruit	Apiaceae
18.	*Cinnamomum bejolghota* Kosterm.	*Tejpat**	Leaf	Lauraceae
19.	*C. aromaticum* Nees	Cassia, Chinese cinnamon*	Bark, leaf	Lauraceae
20.	*C. impressinervium* Meissn.	*Tejpat**	Leaf	Lauraceae
21.	*C. tamala* (Buch-Ham.) Nees & Eberm.	Indian cassia, *tejpat**	Bark, leaf	Lauraceae
22.	*C. verum* Presl.	Cinnamon*	Bark	Lauraceae
23.	*Coriandrum sativum* L.	Coriander	Leaf, seed	Apiaceae
24.	*Crocus sativus* L.	Saffron	Stigma	Iridaceae
25.	*Cuminum cyminum* L.	Cumin	Fruit	Apiaceae
26.	*Curcuma longa* L.	Turmeric	Rhizome	Zingiberaceae
27.	*Elettaria cardamomum* (L.) Maton	Cardamom	Fruit, seed	Zingiberaceae
28.	*Foeniculum vulgare* Mill.	Fennel	Fruit	Apiaceae
29.	*Garcinia cambogia* (Gaertn.) Desr.	Malabar tamarind*	Fruit rind	Clusiaceae
30.	*Garcinia cowa* Roxb. ex DC.	Kowa*	Fruit rind	Clusiaceae
31.	*Garcinia xanthochymus* Hk. *f.* & Th.	Mysore gamboge*	Fruit rind	Clusiaceae
32.	*Garcinia indica* (Thouars) Choisy	Kokam*	Fruit rind	Clusiaceae
33.	*Hyssopus communis* L.	Hyssop	Leaf	Lamiaceae
34.	*Juniperus communis* L.	Juniper*	Berry	Cuppressaceae
35.	*Mentha arvensis* L.	Japanese mint	Leaf	Lamiaceae
36.	*Mentha spicata* L.	Spear mint, garden mint	Leaf	Lamiaceae
37.	*Mentha piperita* L.	Pepper mint	Leaf	Lamiaceae
38.	*Murraya koenigii* (L.) Sprengel	Curry leaf*	Leaf	Rutaceae
39.	*Myristica fragrans* Houtt.	Nutmeg, mace*	Kernel, aril	Myristicaceae
40.	*Nigella sativa* L.	Black cumin	Fruit	Ranunculaceae
41.	*Ocimum basilicum* L.	Sweet basil	Leaf	Lamiaceae
42.	*Origanum majorana* L.	Sweet marjoram	Leaf, flowering top	Lamiaceae
43.	*Origanum vulgare* L.	Marjoram	Leaf, flowering top	Lamiaceae
44.	*Papaver somniferum* L.	Opium poppy	Seed	Apiaceae
45.	*Petroselinum crispum* (Miller) Nyman ex A.W. Hill	Parsley	Seed	Apiaceae
46.	*Pimenta dioica* (L.) Merr.	Allspice, pimento*	Fruit, leaf	Myrtaceae
47.	*Pimpinella anisum* L	Aniseed	Fruit	Apiaceae
48.	*Piper nigrum* L.	Black pepper, white pepper	Fruit	Piperaceae
49.	*Punica granatum* L.	Pomegranate	Seed (dried with flesh)	Punicaceae
50.	*Rosmarinus officinalis* L.	Rosemary	Leaf	Lamiaceae
51.	*Salvia officinalis* L.	Sage	Leaf	Lamiaceae
52.	*Saturega hortensis* L.	Summer savory	Stem, leaf, flowering top	Lamiaceae
53.	*Syzygium aromaticum* (L.) Merr. & Perry	Clove*	Unopened flower bud	Myrtaceae
54.	*Synapsis alba* (L.) Biossier	White mustard, yellow mustard	Seed	Brassicaceae
55.	*Tamarindus indica* L.	Tamarind*	Fruit	Caesalpiniaceae
56.	*Thymus vulgaris* L.	Thyme	Leaf, flowering top	Lamiaceae
57.	*Trachyspermum ammi* (L.), Sprague ex Turrill	Bishops weed, *ajwain*	Fruit	Apiaceae
58.	*Trigonella foenum-graecum* L.	Fenugreek	Seed	Fabaceae
59.	*Vanilla planifolia* Jacks.	Vanilla	Pod	Orchidaceae
60.	*Zanthoxylum limonella* (Dennst.) Alston	Indian pepper tree*	Fruit	Rutaceae
61.	*Zingiber officinale* Rosc.	Ginger	Rhizome	Zingiberaceae

* Tree spices

Source: Modified from Ravindran *et al.* (2005)

Table 2. Species diversity of *Piper* L. in Western Ghats

S. No.	Species	Salient features
1.	*P. argyrophyllum* Miq.	Occurs at medium elevation in the peripheral areas of evergreen forests, becoming rare
2.	*P. attenuatum* Buch.-Ham. ex Miq.	A common species, occurs at low and medium elevation
3.	*P. barberi* Gamble	Included in the Red List of Threatened Vascular Plant Species as endangered, occurs in Tirunelveli forests, Tamil Nadu
4.	*P. betle* L.	Cultivated species but also occurs in forest
5.	*P. galeatum* (Miq.) C. DC.	Occurs at medium elevations, bold fruits
6.	*P. hapnium* Miq.	Very rare, endangered, occurring at low elevations, included in the Red List of Threatened Vascular Plant Species
7.	*P. hookeri* Miq.	Closely related to *P. hymenophyllum*, but less pubescent
8.	*P. hymenophyllum* Miq.	Occurs at medium to high elevations, pubescent species
9.	*P. longum* L.	Distributed all over India at low elevations, has creeping habit, medicinal value
10.	*P. pseudonigrum* Vela. & Amal.	Related to *P. nigrum* and very similar to *P. sugandhi* var. *brevipilis*
11.	*P. pykarahense* C. DC.	Reported from the Nilgiris, Tamil Nadu, included in the Red List of Threatened Vascular Plant Species
12.	*P. schmidtii* Hk. *f.*	Endangered species, occurs at high elevation above 1500 m in the Nilgiris, Tamil Nadu
13.	P. silentvalleyensis *Ravindran et al.*	New species, extremely rare, has bisexual flowers and minute fruit
14.	*P. sugandhi* Ravindran et al.	Closely related to *P. nigrum* and *P. pseudonigrum*
15.	*P. sugandhi* var. *brevipilis*	Similar to *P. sugandhi*
16.	*P. trichostachyon* (Miq.) C. DC.	A medium elevation species resembling *P. galeatum*
17.	*P. wightii* Miq.	The pepper of hill tops of Nilgiris, occurs only at high elevation around 2000 m
18.	*Piper* species (*unidentified*)	Newly discovered species from Nilgiris, related to *P. mullesua* Ham. ex D. Don, is bisexual and extremely rare

Source: Modified from Ravindran *et al.* (2000)

Table 3. Germplasm accessions of species of *Piper* L. being maintained in India

Institution	Accessions (no.)		
	Cultivated species	Wild and related species	Total
IISR, Kozhikkode, Kerala	2,079	890	2,969
NBPGR Regional Station, Thrissur, Kerala	183	67	250
Horticultural Research Station, Yercaud, Tamil Nadu	106	0	106
Pepper Research Station, Panniyur, Kerala	105	90	195
Pepper Research Station, Sirsi, Karnataka	75	21	96
Regional Agricultural Research Station, Chintapalli, Andhra Pradesh	26	29	55
All India Coordinated Research Project on Spices (AICRP) Centres	23	1	24
Total	**2,597**	**1,098**	**3,695**

area under its cultivation and the total production is around 90% of the world produce. The genetic erosion in the crop and its related species is mainly due to changes in cropping pattern in conventional areas of its cultivation and due to deforestation and habitat destruction.

Collection and conservation of turmeric germplasm are pursued actively by IISR, NBPGR and many other institutes (Table 5).

The field genebank at NBPGR Regional Station, Thrissur, has 889 accessions of *Curcuma* Roxb. germplasm including cultivated (627 accessions) and wild (262 accessions) (Tables 6 and 7, respectively). There is an urgent need for collecting and conserving the wild species reported to occur in the North-East and eastern region of the country.

Characterization and evaluation of germplasm of species of *Curcuma* were carried out at NBPGR Regional Station, Thrissur. Forty-four accessions of turmeric set seeds in Thrissur condition and these can be used in conventional breeding programmes. Additionally, several accessions of turmeric were found to be tolerant to scale insect and shoot borer under field conditions (Velayudhan and Liji 2003).

Ginger

Ginger (*Zingiber officinale* Rosc.) belongs to the family Zingiberaceae and is an important spice crop of India. It is cultivated on an area of 67,000 ha with a productivity of 3477 kg/ha. It has a good export value for its medicinal properties. The species of *Zingiber* Boeh. occurring in India are listed in Table 8. The current national holdings of ginger germplasm are given in Table 9.

Further details about the area of collection of wild species of *Zingiber* and cultivated ginger, conserved in

Table 4. Number of accessions of different species of *Piper* L. being maintained in field genebanks at NBPGR Regional Station, Thrissur and IISR, Kozhikode

S.No.	Species	Accessions (no.)		Area of Collection
		NBPGR	IISR	
1.	*P. arboreum*	1	–	Introduction from S. America
2.	*P. argyrophyllum* Miq.	11	56	Kerala, Karnataka, Tamil Nadu
3.	*P. attenuatum* Buch.-Ham. ex Miq.	5	74	Kerala, Karnataka, Tamil Nadu
4.	*P. bababudani* Rahiman et Nair	2	10	Karnataka
5.	*P. barberi* Gamble	–	2	Kerala, Tamil Nadu
6.	*P. betle* L.	9	14	Kerala, Karnataka, Tamil Nadu
7.	*P. chaba* Hunter	2	–	Kerala
8.	*P. colubrinum* Link	1	1	Introduction from S. America
9.	*P. galeatum* (Miq.) C. DC.	3	38	Kerala, Karnataka, Maharashtra
10.	*P. hapnium* Miq.	–	4	Kerala, Karnataka
11.	*P. hookeri* Miq.	–	1	Karnataka
12.	*P. hymenophyllum* Miq.	1	35	Kerala, Karnataka
13.	*P. longum* L.	21	41	Kerala, Karnataka, Tamil Nadu
14.	*P. magnificum* Trel.	1	–	Introduction from S. America
15.	*P. mullesua* Ham. ex D. Don	–	20	Kerala, Karnataka, Tamil Nadu
16.	*P. ornatum* NE Br.	–	1	Kerala
17.	P. peepuloides	–	1	West Bengal
18.	*P. pseudonigrum* Vela. and Amal.	2	–	Kerala
19.	*P. nigrum* L.	185	1237	Kerala, Karnataka, Tamil Nadu
20.	*P. sarmentosum* Roxb. ex Hunt.	–	1	Andaman and Nicobar
21.	*P. silentvalleyensis* Ravindran *et al.*	–	1	Tamil Nadu
22.	*P. sugandhi* Ravindran *et al.*	–	75	Kerala, Tamil Nadu
23.	*P. thomsonii*	–	1	West Bengal
24.	*P. trichostachyon* (Miq.) C. DC.	2	19	Kerala, Karnataka, Tamil Nadu

Table 5. Germplasm holding of turmeric and related species in the field genebanks in India

S.No.	Institution	Accessions (no.)
1.	IISR, Kozhikode, Kerala	899
2.	NBPGR Regional Station, Thrissur, Kerala	889
3.	TNAU, Coimbatore, Tamil Nadu	255
4.	Orissa University of Agriculture and Technology (OUAT), High Altitude Research Station, Pottangi, Orissa	193
5.	Regional Agriculture Research Station (RARS), Jagtial, Andhra Pradesh	189
6.	Dr Y.S. Parmar University of Horticulture and Forestry (YSPUHF), Solan, Himachal Pradesh	172
7.	Uttar Banga Krishi Vishwa Vidyalaya (UBKVV), Pundibari, West Bengal	142
8.	Tamil Nadu Agricultural University (TNAU) Horticultural Research Station, Bhavanisagar, Tamil Nadu	124
9.	Narendra Dev University of Agriculture and Technology (NDUAT), Faizabad, Uttar Pradesh	102
10.	Rajendra Agriculture University (RAU), Dholi, Bihar	76
11.	Indira Gandhi Agricultural University (IGAU) Regional Station, Raigarh, Chhattisgarh	61
	Total	**3102**

the field genebank at NBPGR Regional Station, Thrissur are presented in Tables 10 and 11, respectively.

Cardamom

In India, cardamom [*Elettaria cardamomum* (L.) Maton] occurs wild in its native state of Kerala only, but cultivated in the tropical evergreen forests of the southern Western Ghats and has common occurrence in the Silent Valley and Cardamom Hill forests. It consists of three morphologically distinct types, namely, Malabar, Mysore and *Vazhukka*. It is propagated both by seed and suckers. Variability in the natural populations is limited, probably because of it belonging to the monotypic genus in the region. Conservation of cardamom genetic resources was initiated in the 1960s and now they are being conserved at four centers (Table 12). A total of 1,419 accessions of cardamom and its wild relatives is being conserved in the field gene banks of various institutes/centers.

Tree Spices

There are many tree spices in India, some are native whereas others are introduced (Table 1). Of these, nutmeg, clove and cinnamon are widely grown in the states of Kerala, Karnataka and Tamil Nadu, and all the three are recent introductions. Allspice is also a recent introduction, but is less popular. Tamarind is a naturalized tree spice grown widely whereas, curry leaf and species of *Garcinia* L., namely, Malabar tamarind, kokam and

Table 6. Areas of collection of 627 accessions of cultivated turmeric being maintained at NBPGR Regional Station, Thrissur

State	District
Andhra Pradesh	Sreekakaulam, Visakapatnam, West Godavari, Vizianagaram
Arunachal Pradesh	Kohir
Assam	Goalpara
Himachal Pradesh	Shimla, Solan, Panchkula, Nahan, Bilaspur, Kangra, Dharmasthala
Jharkand	Ranchi, East Singbhum, Chatra
Karnataka	Shimoga, Kodagu, Dakshin Kannad, Dharwad
Kerala	Kannur, Ernakulam, Kasargod, Kottayam, Malappuram, Wayanad, Palakkad, Thrissur, Kozhikode, Thiruvananthapuram, Pathanamthitta, Idukki, Alappuzha .
Madhya Pradesh	Bilaspur
Maharashtra	Akola
Manipur	Imphal
Meghalaya	Shillong
Orissa	Kondhamal, Ganjam, Gajapati, Malkangiri, Koraput, Phulbani
Sikkim	Gangtok, East Sikkim
Tamil Nadu	Tirunelveli, Nilgiris, Erode, Pudukottai, Tiruchirappalli, Kanyakumari, Thanjavur, South Arcot, Coimbatore
Uttar Pradesh	Gorakhpur, Dehra Dun
West Bengal	Jalpaiguri

Table 7. Germplasm accessions of wild species of *Curcuma* Roxb. being maintained in the field genebank at NBPGR Regional Station, Thrissur

S. No.	Species	Accessions (no.)	Area of collection
1.	*Curcuma aeruginosa* Roxb.	4	Orissa, Sikkim
2.	*C. amada* Roxb.	48	Andhra Pradesh, Orissa, Kerala, Karnataka, Tamil Nadu, Uttar Pradesh
3.	*C. amarissima* Rosc.	1	–
4.	*C. albiflora* Thw.	3	Karnataka
5.	*C. aromatica* Salisb.	37	Andhra Pradesh, Karnataka, Kerala, Tamil Nadu, Uttar Pradesh
6.	*C. aurantiaca* Van Zijp	9	Kerala
7.	*C. brog* Val.	2	–
8.	*C. caesia* Roxb.	5	Jharkhand, Sikkim
9.	*C. cannanorensis* Ansari & Nair	1	Kerala
10.	*C. comosa* Roxb.	2	–
11.	*C. coriacea* Mangaly & Sabu	1	Kerala
12.	*C. decipiens* Dalz.	3	Karnataka, Kerala
13.	*C. ferruginea* Roxb.	2	Sikkim, West Bengal
14.	*C. harita* Sabu & Mangaly	14	Andhra Pradesh, Kerala
15.	*C. karnatakensis* Amal. *et al.*	1	Karnataka
16.	*C. kudagensis* Vela. *et al.*	5	Karnataka
17.	*C. lutea* (Ansari *et al.*) Amal. *et al.*	3	Karnataka, Kerala
18.	*C. malabarica* Vela. *et al.*	38	Karnataka, Kerala, Tamil Nadu
19.	*C. montana* Roxb.	1	Andhra Pradesh
20.	*C. neilgherensis* Wight.	4	Kerala, Tamil Nadu
21.	*C. nilamburensis* Vela. *et al.*	3	Kerala, Tamil Nadu
22.	*C. pseudomontana* Grah.	2	Kerala
23.	*C. raktakanta* Mangaly & Sabu	7	Kerala
24.	*C. soloensis* Val.	1	West Bengal
25.	*C. vamana* Sabu & Mangaly	3	Kerala
26.	*C. zedoaria* (Christm.) Rosc.	47	Orissa, Kerala, Tamil Nadu
27.	*Curcuma* species (unidentified)	15	Kerala
	Total	**262**	

Mysore gamboge are indigenous and grown to a certain extent in India.

***Nutmeg*:** Nutmeg (*Myristica fragrans* Houtt.) belongs to the family Myristicaceae, and is the only plant that produces two separate spices – nutmeg and mace. The former is the kernel of the seed and the latter, the aril covering the seed. *Myristica amygdalina* Wall., *M. andamanica* Hk., *M. attenuata* Wall. ex Hk. *f.* & Th., *M. beddomei* King., *M. fatua* Houtt. var. *magnifica* (Bedd.) Sinclaire, *M. gibbosa* Hk., *M. glabra* Bl., *M. glaucescens* Hk., *M. irya* Gaertn., *M. kingii* Hk., *M. longifolia* Wall. and *M. malabarica* Lam. occur in India. Most of these are endemic to the Indo-Malayan region including the Western Ghats. At IISR, Kozhikkode, 471 accessions are maintained in the field genebank.

Clove: Clove [*Syzygium aromaticum* (L.) Merr. & Perry] belongs to the family Myrtaceae. It is a native of Moluccas Islands (Indonesia). Under natural conditions in Moluccas

Table 8. Species of *Zingiber* Boeh. occurring in India

S.No.	Species	S. No.	Species
1.	*Z. officinale* Rosc.	10.	*Z. ligulatum* Roxb.
2.	*Z. zerumbet* (L.) Sm.	11.	*Z. spectabilis* Griff.
3.	*Z. purpureum* Rosc.	12.	*Z. clarkii* King ex Benth.
4.	*Z. roseum* (Roxb.) Rosc.	13.	*Z. marginatum* Roxb.
5.	*Z. wightianum* Thw.	14.	*Z. intermedium* Baker
6.	*Z. macrostachyum* Dalz.	15.	*Z. chrysanthum* Rosc.
7.	*Z. cernuum* Dalz.	16.	*Z. rubens* Roxb.
8.	*Z. capitatum* Roxb.	17.	*Z. squarrosum* Roxb.
9.	*Z. cylindricum* Moon	18.	*Z. elatum* R. Br.

Table 9. Conservation of germplasm of ginger in field genebanks in India

Institution	Accessions (no.)
IISR, Kozhikode, Kerala	645
YSPUHF, Solan, Himachal Pradesh	271
NBPGR Regional Station, Thrissur, Kerala	125
OUAT High Altitude Research Station, Pottangi, Orissa	172
RAU, Dholi, Bihar	103
UBKVV, Pundibari, West Bengal	31
NDUAT, Faizabad, Uttar Pradesh	29
IGKVV, Raigarh station.	35
Department of Horticulture, Sikkim	58
CARI, Port Blair	33
Total	**1502**

Table 10. Wild species of *Zingiber* being maintained in the field genebank at NBPGR Regional Station, Thrissur

S.No.	Species	Accessions (no.)	Areas of collection
1.	*Z. cernuum* Dalz.	1	Andhra Pradesh
2.	*Z. neesanum* (Grah.) Ramam.	4	Karnataka, Kerala, Tamil Nadu
3.	*Z. purpureum* Rosc.	2	Andhra Pradesh, Orissa
4.	*Z. rubens* Roxb.	2	Orissa
5.	*Z. wightianum* Thw.	1	Kerala
6.	*Z. zerumbet* (L.) J.E. Smith	14	Andhra Pradesh, Kerala, Karnataka, Tamil Nadu
	Total	**24**	

Table 11. Area of collection of 125 accessions of cultivated ginger being maintained at NBPGR Regional Station, Thrissur

State	District
Andhra Pradesh	Vishakapatnam, Vizianagaram
Himachal Pradesh	Sirmour
Jharkhand	Lohardaga, Ranchi
Karnataka	Dharwad
Kerala	Ernakulam, Idukki, Palakkad, Thrissur, Wayanad
Orissa	Koraput, Rayagada
Tamil Nadu	Namakkal
Uttaranchal	Champawat, Naini Tal, Pauri Garhwal

both clove producing (aromatic) and non-clove producing (non-aromatic) trees co-exist. Clove is grown as an intercrop in many households in Kerala and Karnataka. Some pure plantations exist in Kanyakumari district of Tamil Nadu and Thiruvananthapuram district of Kerala and are commonly planted on large scale in tea estates located at low to medium elevations. Because of the limited introductions that have taken place and self-pollinating nature of the crop, variability is very limited. A total of 215 accessions is conserved in the field genebank at IISR, Kozhikode.

***Cinnamon and Cassia*:** The true cinnamon is obtained from *Cinnamomum verum* Presl., belonging to the family Lauraceae. It is indigenous to Sri Lanka. The cassia cinnamon is obtained from various sources, the most important is *C. aromaticum* Nees (Chinese cinnamon, cassia or Chinese-cassia). The other cassia cinnamons are: Indonesian-cassia or Batavia cinnamon or Batavia-cassia [*C. burmanii* (Nees & T. Nees) Bl.], Saigon cinnamon or Saigon-cassia (*C. loureirii* Nees) and Indian-cassia or Indian-bark or *tejpat* [*C. tamala* (Buch.-Ham.) Nees & Eberm.]. Kostermans (1983) reported 13 species from South India including true cinnamon, most of them from the Western Ghats. The endemic species are *C. macrocarpum* Hk. *f.*, *C. malabathrum* (Burm. *f.*) Bl., *C. nicolsonianum* Manilal & Shylaja, *C. riparium* Gamble, *C. keralaense* Kosterm., *C. travancoricum* Gamble, *C. wightii* Meiss., *C. heyneanum* Nees, *C. gracile* (Miq.)

Table 12. Holdings of cardamom germplasm in India

Institution	Accessions (no.)		
	Cultivated	Wild relatives	Total
IISR Cardamom Research Centre, Apangala, Karnataka	326	13	339
Indian Cardamom Research Institute, Myladumpara, Kerala	673	23	696
AICRPS Centre, Pampadumpara, Kerala	104	15	119
AICRPS Centre, Mudigere, Karnataka	263	2	265
Total	**1366**	**53**	**1419**

Source: Modified from Ravindran *et al.* (2005)

Hk. *f.*, *C. chemungianum* Mohan and Henry. The non-endemic species are *C. citriodorum* Thw., *C. filipedicellatum* Kosterm., *C. goaense* Kosterem., *C. perrottetii* Meiss., *C. sulphuratum* Nees and *C. walaiwarense* Kosterm. The IISR, Kozhikkode maintains 35 accessions of cinnamon in the field genebank.

The genetic resources of cinnamon is being taken up at the Indian Institute of Spices Research, Kozhikode, Kerala Agricultural University at its Regional Research Station at Odakkali; by the Tamil Nadu Agricultural University at its Horticulture Research Station, Yercaud; by the Regional Research Laboratory, Bhubaneshwar; and by the Konkan Krishi Vidyapeeth at Vengurula. The IISR, Kozhikkode maintains in its genebank 166 cultivated types of *C. verum*, 35 related/ wild types and 14 exotic accessions. In addition, IISR, Kozhikkode also maintains a collection of Chinese cassia germplasm (*Cinnamomum aromaticum*) (Ravindran et al. 2004).

***Malabar tamarind, Kokam and Mysore gamboge*:** These crops belong to the genus *Garcinia* L. (Clusiaceae) and are found wild in evergreen or semi-evergreen forests of Western Ghats in South Maharashtra extending southwards to Karnataka, Kerala and Tamil Nadu. The genus *Garcinia* has 35 indigenous species with 3 taxonomic varieties and 3 exotic species in India. Seventeen species are endemic to India, of which seven are in Western Ghats, six in Andaman and Nicobar Islands and four in North-East India. These are less-known edible fruits, seeds of which yield fatty oils and fruit rind used as important spice in Peninsular Indian culinary preparations.

Malabar tamarind [*Garcinia cambogia* (Gaertn.) Desr.] is a multipurpose tree spice crop grown in the homesteads of Kerala for its acidic edible fruit, the rind of which is dried and used as a garnish in fish curries. It is endemic to the evergreen forests of southern Western Ghats and Sri Lanka. Dried rind lowers blood lipids and paves way for slower weight loss and supports body's natural appetite suppression mechanism. Resin of Malabar tamarind is principally used as a pigment in miniature paintings and watercolours, besides its medicinal use as a purgative. Fruit rind is hydragogue, anthelmintic and emetic, particularly in dropsy. It is employed in veterinary medicine as a rinse for diseases of mouth in cattle. Its rind possesses marked antiseptic properties (Akhtar Husain *et al.*, 1992). It is also used for polishing gold and silver ornaments and as a substitute for acetic acid for coagulation of rubber latex. The seed oil is used in medicine and the gum also makes a good varnish (Singh, 1993). The presence of HCA [(-) hydroxy citric acid] in *G.cambogia* was first reported by Lewis and Neelakandan (1965). Antony *et al.* (1998) performed quantitative analysis of HCA and HCAL [(-) hydroxy citric acid lactone] in *G.cambogia* and *G.indica* and estimated the presence of 19 to 26% of total acids in fruits. This natural HCA is a potent metabolic regulator of obesity and it also lowers blood lipids such as cholesterol and triglycerides by triggering the fatty acid oxidation in the liver via thermogenesis. It mobilizes body's fat stores and dissolves fat in the liver and also throughout the body paving way for weight management (Lowerstein, 1971; Sullivan *et al.*, 1972; Sullivan *et al.*, 1974 and Sullivan and Triscari, 1977). Administration of HCA promotes lipid oxidation and spares carbohydrate utilization in mice at rest and during running. It has antiulcerogenic effect i.e. it decreases acidity, increases the mucosal defense in the gastric areas and it prevents gastro-mucosal injury (Mahendran *et al.*, 2002a, Mahendran *et al.*, 2002b). Sarah *et al.*, 1992 studied the pattern of flowering and flower development and reported that the pattern of flower development from bud emergence to anthesis was found to be different in the case of male and female flowers. The bisexual flower bud was found to follow a sigmoid pattern, with distinct stages of development whereas the male flower bud showed a linear pattern of development. They have also reported bagging of bisexual flowers before flower opening, which gave fruit setting of only 20 per cent, thus showing that the trees are mostly cross pollinated. The seeds of *G.cambogia* are recalcitrant (Chacko and Chandrasekhara Pillai, 1997). The seed coat of Malabar tamarind is the important mechanical barrier, which delays the germination. The viability of the seeds can be retained for about one year by storing the seeds in moist sand or sawdust in open condition. The germination percentage of the seeds can be improved by treating them with gibberellic acid (Mathew and Sarah, 1995). It is increasingly becoming important industrially, commercially and medicinally, but not fully exploited. Germplasm accessions of this species are maintained at NBPGR Regional Station, Thrissur; Regional Agricultural Research Station (Kerala Agricultural Univeristy), Kumarakom, Kottayam; and District Agricultural Farm, Taliparamba, Kannur.

Kokam [*Garcinia indica* (Thouars) Choisy] is endemic to southern Western Ghats and probably originated as a crop in south Maharashtra and western Karnataka region, the fruit rind is used as a spice in south Maharashtra

and Goa. Fresh fruit rind with sugar is used in making a soft drink in Goa and western Karnataka. Edible butter obtained from the seeds is used in south Maharashtra and western Karnataka. Germplasm accessions of this species are maintained at NBPGR Regional Station, Thrissur and the Punjabrao Krishi Vidyapeeth, Dhapoli, Maharashtra.

Mysore gamboge (*Garcinia xanthochymus* Hk. *f.* & Th.) is another important but less-known tree spice, which can be commercially exploited for its fruit rind. Fruit rind is used as a spice to garnish fish curry and vegetarian preparations in coastal Karnataka. A native of India and Myanmar, it is widely distributed in the eastern Himalaya, Assam, West Bengal, Bihar, Orissa, Andhra Pradesh, Tamil Nadu, Kerala, Karnataka, Maharashtra and Andaman Islands. About 4 years old seedlings of *G.xanthochymus* are useful as rootstock for grafting and inarching mangosteen; sometimes grown in gardens as an ornamental tree for its dense foliage (Singh, 1993).

Table 13 presents the information on germplasm accessions of three species of *Garcinia* conserved in the field genebank at NBPGR Regional Station, Thrissur. Further collection of elite germplasm accessions of all the useful species of *Garcinia* is to be made from the states of Karnataka, Tamil Nadu, Kerala, Maharashtra, Goa, North-East India, Eastern India and Andaman & Nicobar Islands.

Conservation of Spices in Seed Genebank and Cryo-genebank

Seed Spices

The major seed spices grown in India are coriander, cumin, fennel, fenugreek, celery, bishops weed or *ajwain*, dill, caraway, black caraway, black cumin, white mustard, black mustard and Indian mustard. Among them, only coriander, cumin, fennel and fenugreek are grown on a commercial scale. The main seed spice growing states are Andhra Pradesh, Tamil Nadu, Gujarat, Rajasthan, Uttar Pradesh, Madhya Pradesh and Haryana. Cultivation of the remaining seed spices is limited to certain areas only.

Details of germplasm of commercially grown seed spices conserved in the seed genebanks at different centers are given in Table 14.

In addition to the above, seed spices are also conserved using the technique of cryopreservation, i.e. conservation at ultra-low temperature such as that of liquid nitrogen (-196°C). Cryopreservation offers long-term conservation. A total of 55 accessions of species of *Amomum* Roxb. (2), *Anethum* L. (3), *Cinnamomum* Schaeffer (1), *Cuminum* L. (1), *Elettaria* Maton (2), *Foeniculum* Mill. (4), *Illicium* L. (1), *Piper* L. (40) and *Trachyspermum* Link (1) are cryopreserved as seeds in the cryo-genebank at NBPGR, New Delhi.

Table 13. *Garcinia* species (Malabar tamarind, kokam and Mysore gamboge) maintained in field genebank at NBPGR Regional Station, Thrissur

Species	Accessions (no.)	Area of collection
Garcinia cambogia (Gaertn.) Desr.	136	Goa, Karnataka, Kerala, Tamil Nadu
Garcinia indica (Thouars) Choisy	38	Goa, Karnataka, Kerala, Tamil Nadu
Garcinia xanthochymus Hk. *f.* & Th.	12	Karnataka, Kerala
Total	**186**	

Table 14. Germplasm holdings of commercially grown seed spice crops

Centre	Accessions (no.)			
	Coriander	Cumin	Fennel	Fenugreek
NBPGR, New Delhi*	293	8	3	9
Rajasthan Agricultural University Agricultural Research Station, Jobner	761	323	193	337
Gujarat Agricultural University, Jagudan	101	176	141	52
TNAU, Coimbatore	410	-	-	262
Acharya NG Ranga Agricultural University, Guntur	230	-	-	124
RAU, Dholi	102	-	40	103
NDUAT, Kumarganj	29	19	15	17
Chaudhary Charan Singh Haryana Agricultural University, Hisar	-	-	40	-
IGAU, Raigarh	20	-	-	13
Total 1,946	526	431	917	

*Conserved for long-term as base collections at -20°C, other institutes maintain germplasm for medium-term storage as active collections
Adapted from Ravindran *et al.* (2005)

Conservation of Spices in *In Vitro* Genebank

With the extensive development of innovative tissue culture techniques, *in vitro* conservation of vegetatively propagated species has been proposed as a safer alternative to the field genebank. Vegetatively propagated spice crops such as ginger, turmeric, black pepper and vanilla were given priority for their *in vitro* conservation at NBPGR, as a supplementary strategy for the field genebank conservation. Simple micro-propagation and *in vitro* conservation protocols were developed for species of *Zingiber, Curcuma, Piper* (Tyagi *et al.*, 1998) and *Vanilla*. Germplasm accessions of these crops were collected from various geographical regions of the country and conserved in the *in vitro* genebank at NBPGR, New Delhi (Table 15). The methods of conservation adopted in each crop are discussed below.

Table 15. Details of germplasm of spices in *in vitro* genebank at NBPGR, New Delhi

Crops	Accessions (no.)	Area of collection
Zingiber	30	North-East India
	73*	Kerala
	6	Uttar Pradesh
	38	Himachal Pradesh
	4	Andhra Pradesh
	7	Nepal
	5	Orissa
	63	Others
Curcuma	15	Kerala
	3	Tamil Nadu
	22	North-East India
	8	Himachal Pradesh
	12	Andhra Pradesh
	3	Orissa
	28	Others
Piper	35*	Kerala
Elettaria	5	Kerala
Vanilla	4	Kerala

* Includes 53 accessions of ginger and 28 of black pepper conserved at NBPGR Regional Station, Thrissur

Ginger

In *Zingiber* species, 226 accessions belonging to *Z. casumunar, Z. cernuum, Z. montanum, Z. nimnonii, Z. officinale, Z. roseum, Z. wightianum* and *Z. zerumbet* have been conserved by sub-culturing after 8-11 months at 25°C on MS (Murashige and Skoog, 1962) + 2.5 mg/l BAP medium (Table 15) at NBPGR, New Delhi. Use of *in vitro*-induced rhizomes for extending the storage period was also explored. Although, the shoots turned yellow in 15 months, the micro-rhizomes remained green up to 14-24 months (depending upon the accession) at 25°C on MS + 0.1 mg/l NAA + 1 mg/l BAP (Bhat *et al.*, 1994). Over 30% of rhizomes were capable of sprouting in soil after 24 months of storage. This approach appears to be novel and least stressful.

Turmeric

Germplasm of 91 accessions of *Curcuma* L., including 21 morphotypes of *C. longa* L.; and those of *C. aeruginosa* Roxb., *C. amada* Roxb., *C. amarissima* Rosc., *C. angustifolia* Roxb., *C. aromatica* Salisb., *C. brog* Val., *C. caesia* Roxb., *C. latifolia* Rosc., *C. malabarica* Vela. *et al.*, *C. raktakanta* Mangaly & Sabu, *C soloensis* Val., *C. zedoaria* (Christm.) Rosc. and unidentified species of *Curcuma* are conserved in *in vitro* by sub-culturing after every 8-11 months on MS + 2.5 mg/l BAP at 25 ± 2°C.

The data on shoot regeneration and conservation period revealed that the optimum medium for shoot regeneration and conservation is not necessarily the same. Optimum media for plantlet regeneration and medium-term conservation for individual species of *Curcuma* are reported by Tyagi *et al.* (2004). The success of any *in vitro* conservation programme depends on simple and reproducible protocol. The protocol should be applicable for a large number of accessions. Simple and reproducible protocol used for conserving the s hoots of ginger germplasm on MS + 2.5 mg/l BAP, was also used for conservation of *Curcuma* species successfully.

Table 16. Conservation of spice germplasm in *in vitro* genebanks

Genera of spice crops	NBPGR, New Delhi		IISR, Kozhikkode	
	No. of accessions	Optimum subculture period (months)	No. of accessions	Optimum subculture period (months)
Zingiber	226*	8-24**	70	12
Curcuma	91	8-10	120	12
Piper	35*	12-22	26	12
Elettaria	5	8-10	35	12
Vanilla	4	8-10	215	18-19

* Includes 53 and 28 accessions of ginger and black pepper, respectively, conserved at NBPGR Regional Station, Thrissur
**Conservation period for *in vitro*-induced micro-rhizomes is from 14 to 24 months

Piper *species*

Germplasm of one accession each of black pepper (*Piper nigrum)* and related wild species, namely, *P. barberi, P. betel, P. colubrinum, P. hapnium* and *P. longum* has been maintained for 12-22 months on half-strength MS + 0.1 mg/l IAA at 25^{0}C in the *in vitro* genebank at NBPGR, New Delhi. Additionally, cultures of 28 accessions of black pepper are also conserved at NBPGR Regional Station, Thrissur. Various growth substances were tested for increasing the subculture period of *Piper* species. *Piper longum* requires sub-culturing at 12 months interval, whereas other species could be stored for up to 22 months using the axillary buds as explants cultured on 1/2 MS + 0.1 mg/l IAA.

Vanilla and Cardamom

The NBPGR presently has cultures of 4 accessions of vanilla (*Vanilla planifolia*) and 5 accessions of cardamom (*Elettaria cardamomum*) in its *in vitro* genebank at New Delhi. The multiplication medium used for vanilla is MS + TDZ (0.01 mg/l). *In vitro* conservation protocol was studied in cultures of vanilla, using two polyamines - putrescine and spermidine. The cultures of vanilla could be conserved up to 10 months on MS + 0.25 mg/l putrescine (Tyagi *et al.*, 2001). The conservation medium being used for cardamom at NBPGR, New Delhi is MS + 2.5 mg/l BAP, which is similar to that for turmeric and ginger. All the accessions of cardamom can be stored up to 7 months in this medium.

By employing slow growth methods, germplasm accessions of species of *Zingiber, Curcuma, Piper, Vanilla* and *Elettaria* are being conserved in the *in vitro* genebank by sub-culturing the suitable explants at NBPGR and IISR (Table 16). Even if the intervals between transfers are greatly extended, medium-term conservation techniques employing tissue culture poses considerable problems in management of large collections. Alternative techniques, which minimize the need for germplasm maintenance, have to be developed. Thus, cryopreservation is an obvious and preferred choice for long-term conservation. Work on cryopreservation of shoot apices, somatic embryos, buds from *in vitro*-induced rhizomes of ginger and axilliary buds of *Piper* species is in progress, using encapsulation-dehydration, vitrification and encapsulation-vitrification techniques.

Monitoring the Genetic Stability of *In vitro*-conserved Germplasm

Tissue culture system is vulnerable to genetic variation. Conservation of germplasm, maintaining genetic stability is of paramount importance in crop improvement programme. Electrophoretic analysis of isozymes has been used for detecting the variation in *in vitro*-conserved germplasm of *Curcuma* species. Isozymes of acid phosphatase, esterase, glutamine synthetase, malate dehydrogenase, polyphenol oxidase, catalase and superoxide dismutase were investigated electrophoretically to compare 19 morphotypes of *C. longa* and 5 species of *Curcuma* (*C. caesia, C. longa, C. raktakanta, C. soloensis* and an unidentified species of *Curcuma*) maintained in earthen pots (*in vivo*-conserved) and same species conserved in tissue culture (*in vitro*-conserved) for the same period. A high degree of polymorphism was observed among all 5 species and the 19 morphotypes of turmeric confirming the genetic basis of morphological variation in these accessions. However, no significant variation was observed between *in vivo*-conserved and *in vitro*- conserved plants on the basis of 7 isozymes tested (Tyagi *et al.*, 2000). Random amplified polymorphic DNA (RAPD) analysis was also done for 20 morphotypes of turmeric and 12 species of *Curcuma* with various conditions. The primers have been identified which gave good polymorphism with 3-8 bands. No significant variation was observed between *in vitro*-conserved and *in vivo*-conserved germplasm of *Curcuma*.

Future Perspectives

1. Although a large number of germplasm accessions of spices has been collected, still there is need to identify the areas and crops to fill the gaps in available collection.
2. Since genetic erosion is a continuous process, conservation of germplasm is imperative till other effective methods of evaluation and utilization are employed.
3. Long-term conservation facilities are available at NBPGR. A large number of accessions of seed spices are being maintained at various centres as active collection, which needs to be conserved on priority in the National Genebank on a long-term basis.
4. Conservation of germplasm of vegetatively propagated spices in the *in vitro* genebank is necessary as safety duplicates of field genebank. Priority crops and viruses are to be identified, and techniques for virus

indexing and elimination should be standardized for virus-free conservation of germplasm.

5. A large number of accessions of various spice crops have been conserved in the genebanks. Characterization and evaluation of these accessions are important. Molecular characterization could be very effective to determine the uniqueness of each accession.
6. It is a valid concern that spice germplasm is inadequately evaluated and consequently under-utilized. This can be addressed to some extent by identifying a set of core collections, which can ease the activities of evaluation and utilization of *ex situ* germplasm.
7. There is urgent need for phytochemical and pharmacological evaluation of spices germplasm.
8. Documentation of valuable indigenous knowledge, registration of unique germplasm and DNA fingerprinting are of paramount importance in the fast changing scenario of Intellectual Property Rights.
9. Conservation of germplasm is an expensive activity. Precise estimation of cost of conservation in genebanks may vary. The relative cost of conservation should be estimated to adopt the appropriate strategy for long-term conservation. At the same time, potential economic benefits of utilization and safety of germplasm should not be ignored. Thus, cost-effective strategies are to be adopted based on the requirement of each crop.

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Variability and Character Association Analysis in Sweet Orange (*Citrus sinensis*) Varieties

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Eighteen genotypes/varieties of sweet orange having a wide range of variability in various quantitative as well as qualitative characters are being maintained and evaluated at Regional Fruit Research Station, Abohar. A large variability in fruit yield (23-310 fruits/tree), tree height (2.7-4.6 m), tree volume (11.83-97.92 m^3), fruit weight (145-226 g/fruit), juice content (45.62-50.41 %), TSS (7.0-9.9 %), acid content (0.418-1.032 %) and ascorbic acid (18.22-26.40 mg/100 ml juice) have been recorded. The seed number ranged from 0 seeds/fruit (Declabre) to 12 seeds/fruit (Queen) in the varieties evaluated. In character association analysis, fruit weight and fruit size were positively correlated. A negative correlation was recorded between fruit size and TSS though it was non-significant. Few introductions, viz., Vainiglia Sanguigno, Olinda Valencia, Cutter Valencia and Campbell Valencia showed promise and are being evaluated for adoption on growers field. Mosambi, Jaffa, Hamlin, Pineapple, Blood Red and Valencia Late are recommended for commercial cultivation.

Key Words: Correlation analysis, Sweet orange, Variability.

In India, genetic diversity occurs in 109 species of fruits including those of *Citrus, Mangifera, Zizyphus, Musa, Syzium, Pyrus, Prunus* etc. India has a rich germplasm resource and the North-Eastern region of India is considered as home of the citrus. A large variability exists in sweet orange cultivars which can be exploited and used in breeding programmes. The improvement of any crop lies in exploring and exploiting the rich gene pool available. A breeding programme for the improvement of fruit quality along with fruit yield requires information on the nature and magnitude of heritable variability in the existing plant material, correlation of different characters among themselves, so that the desirable plants with good quality fruits and high yield can be selected. Correlation among different fruit quality characters are often helpful in understanding the behaviour of the varieties and may be useful in selecting desirable clones in a breeding programme. Various workers have tried to build up and characterize the genetic resources of citrus (Govind and Yadav, 1999, Singh *et al.*, 1999 and Verma *et al.*, 1999). As a large variability exists in sweet orange cultivars, efforts were made to maintain, characterize and evaluate the existing germplasm of sweet orange at the Regional Fruit Research Station (RFRS), Abohar.

Materials and Methods

Citrus germplasm collected at RFRS, Abohar includes 18 varieties of sweet orange introduced from various indigenous as well as exotic sources. These are being maintained in the citrus collection block. These varieties now established at RFRS, Abohar were undertaken to study their variability and character association analysis. Morphological observations of the plants as well as of the fruits were recorded. The evaluation studies were conducted when the fruits were physiologically mature. A random sample of 20 fruits was collected from each variety for this purpose. This germplasm was studied for the qualitative as well as quantitative characters and for the character association analysis of qualitative characters.

Results and Discussion

The results presented in Table 1 reveal a wide variation among the eighteen varieties of sweet orange for their various morphological characters such as tree height, tree spread (North-South and East-West) and tree volume. Tree height ranged from 2.7 m (Pineapple) to 4.6 m (Cutter Valencia). Tree spread (East-West) ranged from 2.6 m (Satgudi) to 6.4 m (Cutter Valencia) and North-East ranged from 2.8 m (Pineapple and Satgudi) to 6.6 m (Frost Valencia). Tree volume showed quite a large variation in all the sweet orange varieties under study. Tree volume ranged from 11.83 m^3 (Satgudi) to 97.92 m^3 (Cutter Valencia). The fruit yield ranged from 23 fruits/tree (Declebre) to 310 fruits/tree (Jaffa). The seed number ranged from 0-12 in the varieties evaluated. Negligible seeds (0-2 seeds/fruit) were recorded in Declabre and Vaninglia Sanguigno. Seeds were maximum (9-12 seeds/fruit) in cv. Queen, closely followed by Vanale (10-11 seeds/fruit).

Table 1. Range, Mean and coefficient of variance for vegetative characters in sweet orange germplasm collected from various sources

S.No.	Variety	Fruit Yield (No./Tree)	Tree Height (m)	East-West (m)	North-South (m)	Volume (m^3)
1.	Mosambi	215	3.6	4.3	4..3	43.18
2.	Trovita	91	3.1	4.0	4.0	30.46
3.	Queen	169	3.0	3.6	3.7	20.26
4.	Satgudi	146	2.9	2.6	2.8	11.83
5.	Teneriffe	57	3.2	2.9	3.1	15.65
6.	Jaffa	310	4.0	5.5	5.5	65.60
7.	Hamlin	185	3.7	5.4	5.4	58.00
8.	Pineapple	147	2.7	3.0	2.8	12.90
9.	Declebre	23	3.0	3.5	3.5	18.10
10.	Vaininglia Sanguigno	153	3.5	4.2	4.4	35.67
11.	Blood Red	175	3.3	3.4	3.3	19.74
12.	Vanale	82	3.0	3.7	3.5	22.02
13.	Olinda Valencia	172	4.3	4.6	4.9	53.05
14.	Frost Valencia	167	4.3	5.8	6.6	89.06
15.	Cutter Valencia	164	4.6	6.4	6.3	97.92
16.	Campbell Valencia	221	4.5	6.0	6.1	89.00
17.	Valencia late	171	4.5	5.9	6.0	85.11
18.	Tardiff	105	3.2	3.3	3.3	18.83
	Range	23	2.7	2.6	2.8	11.83
		310	4.6	6.4	6.6	97.92
	Mean	153	3.6	4.3	4.4	43.69
	C. Variance	19.8	12.0	15.6	15.5	30.92

A distinct variation was observed in all the qualitative traits, namely, fruit weight, fruit size, juice content, TSS, acid and ascorbic acid content among all the collected genotypes (Table 2). Fruit weight ranged from 145.0 g in Blood Red to 226.0 g in Trovita, fruit length from 6.3 cm in Mosambi, Hamlin and Declabre to 7.5 cm in Olinda Valencia and Frost Valencia, fruit breadth from 6.1 cm in Mosambi to 7.4 cm in Olinda Valencia, juice content from 45.62 per content in Trovita to 50.41 per cent in Pineapple, TSS from 7.0 per cent in Trovita and Vanale to 9.9 per cent in in Declabre, acid content from 0.418 per cent in Mosambi to 1.032 per cent in Olinda Valencia and ascorbic acid from 18.22 mg/100 ml juice in Trovita and Hamlin to 26.40 mg/ 100 ml juice in Pineapple.

Table 2. Range, Mean and Coefficient of Variance for 7 characters in Sweet orange germplasm collected from different sources

S.No.	Variety	Fruit Weight (g)	Length (cm)	Breadth (cm)	Juice (%)	TSS (%)	Acidity (%)	Ascorbic acid (mg/ 100ml juice)	Seed No.
1.	Mosambi	147.7	6.3	6.1	48.6	3 9.0	0.418	22.50	6-7
2.	Trovita	226.0	7.4	7.1	45.6	2 7.0	0.461	18.22	8-9
3.	Queen	181.0	6.8	6.6	49.3	5 9.1	0.717	20.29	9-12
4.	Satgudi	181.8	7.0	7.0	46.40	9.0	0.471	20.61	4-6
5.	Teneriffe	165.0	6.8	6.7	46.4	2 9.4	0.627	19.10	7-9
6.	Jaffa	162.0	6.5	6.5	49.23	8.4	0.627	21.62	4-5
7.	Hamlin	155.3	6.3	6.5	48.72	8.2	0.677	18.22	8-9
8.	Pineapple	155.0	6.9	7.1	50.41	8.7	0.677	26.40	9-10
9.	Declebre	146.8	6.3	6.5	47.93	9.9	0.537	21.48	0-2
10.	Vaininglia Sanguigno	160.7	7.0	7.1	47.97	9.2	0.435	21.05	0-2
11.	Blood Red	145.0	6.6	6.8	47.87	9.0	0.642	20.71	4-5
12.	Vanale	172.8	7.1	7.2	49.34	7.0	0.474	19.97	10-11
13.	Olinda Valencia	187.5	7.5	7.4	50.17	9.2	1.032	24.62	2-4
14.	Frost Valencia	215.0	7.5	7.2	49.57	8.5	1.012	24.38	3-4
15.	Cutter Valencia	209.0	7.4	7.1	48.56	9.0	0.931	24.12	4-5
16.	Campbell Valencia	185.7	7.1	6.9	48.34	8.0	0.976	23.94	5-8
17.	Valencia Late	180.0	7.0	6.8	49.98	8.0	0.977	22.30	3-4
18.	Tardiff	165.8	6.9	6.9	48.47	9.8	0.606	24.43	5-6
	Range	145.0	6.3	6.1	45.62	7.0	0.418	18.22	0
		226.0	7.5	7.4	50.41	9.9	1.032	26.40	12
	Mean	174.5	6.9	6.9	48.49	8.7	0.683	21.88	—
	C.V.	2.9	1.8	2.5	4.12	2.4	6.040	12.53	—

Table 3. Correlation coefficient for various qualitative characters of Sweet orange germplasm.

Character	Fruit Weight (g)	Fruit Length (cm)	Fruit Breadth (cm)	Juice (%)	TSS (%)	Acidity (%)	Ascorbic acid
Fruit weight (g)	1.000						
Fruit Length (cm)	0.821*	1.000					
Fruit Breadth (cm)	0.513*	0.873*	1.000				
Juice (%)	- 0.138	0.038	0.075	1.000			
TSS (%)	- 0.387	- 0.320	- 0.297	0.014	1.000		
Acidity (%)	0.365	0.500*	0.410	0.483*	- 0.092	1.000	
Ascorbic acid	0.055	0.336	0.332	0.605*	0.269	0.539*	1.000

critical value of 'r' at 5 % = 0.456
* Significant at 5 % level of significance

Different magnitudes of correlation coefficients were observed among the qualitative characters (Table 3). It has been observed that fruit size (fruit length and breadth) was positively and significantly correlated to fruit weight which indicates that the increase in length and the breadth of the fruit increased the fruit weight. Similar findings have also been reported in Citrus by Thamburaj and Shanmumga Subramanium (1977) and Chakrawar and Jature (1980) wherein fruit size has a positive correlation with fruit weight. There was a positive correlation of fruit size (length and breadth) with juice per cent, acidity and ascorbic acid content. A negative correlation has been observed between fruit weight and TSS and fruit size (length and breadth) and TSS.

Some Promising Collections

Mosambi: Fruit medium sized, slightly oblate to globose, areolar ring shallow, moderately seedy (6-7 seeds/fruit), colour of fruit is light yellow to pale orange at maturity, surface moderately pebbled, longitudinal grooves and ridges, flesh colour straw-yellow, juicy, acid content less, early in maturity.

Jaffa: Fruits are medium sized, globose to slightly ellipsoidal or obovate, areole absent, seeds few (4-5 seeds/fruit) and medium thick, finely pitted and moderately pebbeled, flesh colour light orange, Juicy, flavour good, mid-season maturity.

Pineapple: Fruits medium sized, spherical to slightly obovate, faint areolar ring, slightly depressed from base, moderately seedy (9-10 seeds/fruit), rind medium thick, flesh colour light orange, juicy, flavour rich though sweet, mid-season maturity, excellent for processing.

Hamlin: Fruit medium to small, globose to slightly oblate, faint areolar ring, moderately seedy (8-9 seeds/fruit), peel smooth or thin, flesh well coloured, juicy lacking in acid content, flavour sweet, earliest to mature.

Blood Red: The fruits are small, seeds few (4-5 seeds/fruit), flavour good, juicy seedy, flesh reddish at maturity, matures late during last week of December.

Vainiglia Sanguigno: Fruit small to medium, sub globose to spherical, small apical depression, Seeds negligible (0-2 seeds/fruit), rind thick, well coloured at maturity, juicy and sweet flavoured but lacking in acidity with slight bitterness, bitterness declines with age, very early in maturity, i.e., last week of November.

Queen: Mid-season variety, reddish–orange in colour, fruit much like Pineapple orange, higher in soluble solids, rich in flavour and seedy (9-12 seeds/fruit).

Olinda Valencia: Fruits medium to large, oblong to spherical, seeds few (2-4 seeds/fruit), well coloured at maturity, matures during first week of February.

Campbell Valencia: Fruit medium to large, juicy, seeds bold but few (5-8 seeds/fruit), oblong to spherical, matures during first week of February.

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Characterization of Growth and Maturity Period in *Gossypium arboreum* by the Plastochron Index

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Growth characterization of four field grown cotton genotypes was done using the plastochron index. The crop was in juvenile phase up to PI 15.48 for which 45 days were required. It required additional developmental age of PI 8.10 for expressions of flowering after completion of juvenility, whereas 4.54 more PI were required for period between flowering to its maturity. The crop exhibited simultaneous expression of vegetative as well as reproductive growth. This concurrent period was 127 days, there was a gap of 77 days from Ist boll maturity to overall maturity. During this period the developmental age was advanced by 9.82 PI. The overall maturity was achieved within 185 days during which total plastochron development was 40.95 PI. Thus, period for juvenility and the length of period for Ist maturity to overall maturity appeared to be responsible for major variation in maturity period of cotton. These two components can be employed for screening the genotypes for maturity period in cotton.

Key Words: Boll development, Concurrent phase, Cotton, *Gossypium* Sp., *Gossypium arboreum*, Plastochron index.

The growth behaviour of cotton plant is complex and unpredictable, therefore, the clear understanding of critical phases of development is a basic requirement for scheduling a research programme. This could be precisely done using the concept of plastochron index (PI) with special emphasis on detection of juvenility and identification of components of variation in maturity period among the genotypes. To express plant age on developmental basis rather than chronological age, Erickson and Michelini (1957) proposed a concept of PI which is based on simple non-destructive measures of leaf length. The PI has been used for studies on morphology and physiology of leaf development in various plant species (Lamoreaux *et al.*, 1978). Vendeland *et al.* (1982) evaluated the PI on soybean and suggested changing the formula to a more sensitive indicator under field drought conditions. Jamadagni and Birari (1992) used PI to detect juvenility and to decide the components of maturity in cowpea, Mehetre and Jamadagni (1997) and Fehr *et al.* (1971) characterized growth and maturity period in soybean. In cotton, production of new branches, formation of squares, new bolls, staggered maturity of boll along with emergence and expansion of leaves are nebulously related with each other. Resorting these growth attributes from each other a precise scale is required, use of PI could be such a precise scale for evaluating the genotypes for this nebulous growth behaviour period in cotton. This investigation was aimed for characterization of growth and components of the maturity period in four field grown cotton (*Gossypium arboreum*) genotypes during a rainy season.

Materials and Methods

A field experiment conducted during rainy season of 2002 consisted of four varieties Y-1, Turab, Sawata and G-27 of the cotton *G. arboreum*. They were grown in randomized block design with four replications. Each genotype was grown in four-row-plot of 7.20 m length keeping intra- and inter-row spacing of 90 X 30 cm. Three randomly selected plants of each genotype from each replication were marked for recording the appearance of first branching, square initiation, flowering, boll bursting, as well as over all maturity and boll development period. The same plants were also regularly monitored for the time of emergence of every leaf on the main shoot. The length of each central leaflet was recorded with clear plastic rule from the day of emergence until the attainment of final length. The PI was estimated by the formula of Erickson and Michelini (1957).

$$PI = n + \frac{(\log Ln - \log 10)}{(\log Ln - \log Ln+1)}$$

where, n is the serial number of the youngest leaf that exceeds 10 mm in length, Ln and Ln+1 are the lengths of leaves n and n+1, respectively.

Results and Discussion

The data on duration of various phenological phases and developmental age in terms of PI are given in Table 1. The overall maturity of cotton comprises following component phases:

Table 1. Plastochron index for various stages of growth and duration of various phenological phases in four cotton genotypes.

Genotypes	Final PI	Time for Final PI [d]	PI at Ist Branch	Time for Branch [d]	PI at Ist Sq. initiation	Time for Ist Sq. initiation [d]	PI at Ist Flow	Time for Ist Flow [d]	PI at Ist Burst	Time for Ist Boll Burst [d]
Y-1	37.19	176	13.252	40	14.84	42	21.91	63	32.27	102
Turab	37.29	183	9.165	28	12.84	43	21.98	66	31.09	104
Sawata	43.18	189	14.197	37	17.16	47	26.13	71	32.04	111
G-27	46.15	193	9.151	34	17.09	52	24.34	72	29.05	113
Mean	**40.95**	**185.25**	**11.44**	**34.75**	**15.48**	**46**	**23.59**	**68**	**31.13**	**107.5**
S.E.	1.92	3.21	1.15	2.22	0.89	1.97	0.88	1.84	0.63	2.0
C.D.	6.14	10.26	3.67	7.09	2.84	6.29	2.81	5.88	2.01	6.39
C.V.(%)	9.40	3.46	20.10	12.77	11.56	8.55	7.46	5.40	4.72	4.29

S.E. =Standard Error; C.V. = Coefficient of Variation; C.D.= Critical Difference d=days

Maturity period = juvenile period + period from Ist square to Ist flowering + Ist flowering to Ist boll maturity + Ist boll maturity to overall maturity.

In general, the crop had the juvenile period of 45 days. It expressed flowering after 22 days from the date of spell of Ist Square. The period for Ist flowering to Ist boll maturity was 39.5 days (Table 2 and 3).

The data on components of vegetative phases are given in Table 2. The crop exhibited branch initiation from 35th day and the branching was continuous till 162 days from sowing. This clearly indicated that though the crop completed juvenility within 45 days it exhibited simultaneous expression of vegetative and reproductive growth in further period. This period is of about 127 days. In other words, this phase can be considered as concurrent period of vegetative and reproductive growth, which can be a characteristic feature of this crop.

Expression of the developmental age in terms of PI is perhaps the more appropriate way for characterization of growth behaviour (Jamadagni and Birari, 1992, Jamadagni *et al.*, 1995). The data on chronological age PI for various phenophases of four cotton genotypes are given in Table 3. It is based on emergence of new leaves on the main stem of plant. The crop attained 40.95 PI age till overall maturity. During juvenile phase the crop reached 15.48 PI. It required additional developmental age of 8.10 PI for expression of flowing after completion of juvenility where as 4.54 more PI were required for the period between flowering to Ist maturity. It is to mention that though there was uniform number of PI from square to flowering and flowering to Ist maturity, there was variation in chronological period for these two phases. This clearly indicates that the chronological period and developmental age do not advance at the same rate. Further, total 77 days were required for overall maturity

Table 2. Components of vegetative phases and corresponding PI in four cotton genotypes.

Phases	No of days [d]					Age in PI				
	Y-1	Turab	Sawata	G-27	Mean	Y-1	Turab	Sawata	G-27	Mean
Juvenile	41	42	46	51	**45**	14.84	12.84	17.16	12.09	**15.48**
Ist Branching	40	28	37	34	**34.75**	13.25	9.16	14.18	9.15	**11.44**
Last Branching	157	161	163	168	**162.25**	28.20	27.95	32.40	33.15	**30.43**

PI= Plastochron Index; d=days

Table 3. Chronological duration (days) and Plastochron index for various phenophase of four cotton genotypes.

Phases	No of days [d]					Age in PI					PI during specific phase				
	Y-1	Turab	Sawata	G-27	Mean	Y-1	Turab	Sawata	G-27	Mean	Y-1	Turab	Sawata	G-27	Mean
Sowing to Juvenility	41	42	46	51	45	14.84	12.84	17.16	17.09	15.48	7.07	9.14	8.93	7.25	8.10
Ist Sq. to Ist Flowering	21	23	24	20	22	21.91	21.98	26.13	24.34	23.59	7.07	9.14	8.93	7.25	8.10
Ist Flowering to Ist Maturity	39	38	40	41	39.5	32.27	31.09	32.04	29.05	31.13	10.36	9.11	5.91	4.71	4.54
Ist Maturity to Overall maturity	74	79	78	80	77.75	37.19	37.29	43.26	46.15	40.95	4.92	6.72	11.24	17.10	9.82

from the date of Ist maturity to overall maturity. During this period the developmental age was advanced by only 9.82 PI. This again indicates that the chronological period and PI do not match with each other. It is to mention that the period between Ist maturity to overall maturity was characterized by production of newer branches and appearance of new bolls, which are nebulously related with each other. The plastochron development for this period was only 9.82 PI. Leaves are the sites of the production of signals like florigen, other hormones and metabolic activities (Sestak, *et al.*, 1985; Jamadagni and Sengupta, 1992) for expression of vegetative and reproductive phases. On this background continuous production of leaves up to the economic harvest of cotton warrants the supportive role of plastochron development for the indeterminate developmental behaviour of the crop.

Table 4 indicates the components of maturity period (days) in *G. arboreum* genotypes. The cotton genotypes individually showed variation for total maturity period in the range of 176-193 days with an average of 185.25 days. G-27 had longest duration whereas Y-1 had shortest maturity period. In Y-1 the juvenility was shorter by 4 days in comparison of average juvenility period, whereas it was 10 days shorter than that in G-27. There was no remarkable variation in the period from Ist flowering with an exception of Sawata that had 4 days longer period for this phase than in G-27. The period from Ist flowering to Ist maturity also did not vary remarkably. The period for Ist maturity to overall maturity was 6 days shorter in Y-1 in comparison with G-27. The difference of 17 days period for overall maturity in Y-1 in comparison with G-27 was thus due to shorter juvenility by 10 and 6 days shorter period for phase of Ist maturity to overall maturity. The periods for Ist Square to Ist flowering, Ist flowering to period of overall maturity is more or less equal. Thus period for juvenility and the length of period for Ist maturity to overall maturity appeared to be responsible for major variation in maturity period of cotton. These two components can be employed for screening the genotypes for maturity period in cotton.

Table 4. Components of maturity period (days) in *G. arboreum* genotypes

Genotypes	Juvenility period [d]	Time for Ist Bursting [d]	Boll development Period [d]	Time for over all maturity [d]	Ist boll Bursting To overall maturity [d]
Y-1	41	102	60	176	74
Turab	42	104	61	183	79
Sawata	46	111	64	189	78
G-27	51	113	61	193	80
Mean	45	107.5	61.5	185.25	77.75

d=days

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Genotypic Variation for Quantitative and Qualititative Traits in Asiatic Carrot (*Daucus carota* L. var. *sativa*)

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Thirty two diverse genotypes of Asiatic carrot were evaluated at the Research Farm, Indian Institute of Vegetable Research, Varanasi during winter 2001 and 2002 for estimating the variability for eleven quantitative and qualititative traits of horticultural importance. The analysis of variance was highly significant for all the traits indicating the presence of wide variability in the genotypes. High heritability estimates were recorded for carotene content, average fresh root weight with leaves, plant height, TSS and leave length. High estimates of genetic advance were recorded for root weight with leaves and average fresh root weight. The high heritability was associated with high genetic advance as per cent of mean for average fresh root weight, root weight with leaves, carotene content and TSS, and found to be the most reliable selection parameters. HCP-191, Barwal-2, HC-155, HCP-183, HC-4-2, VN-11550-K and HC-2-A were recorded to be superior genotypes for yield and its components, which can be used in further breeding programme.

Key Words: Carotene, Carrot, *Daucus carota* L. var. *sativa*, Genetic Variability, Genotypes, TSS.

Carrot (*Daucus carota* L. var. *sativa* Hoffm.) is an important vegetable because of high yield and high carotene and vitamin-A content (Huang *et al.*, 1994). Many cultivars, some indigenous but mostly introduced from Europe and America, are being cultivated in India. â-carotene, the predominant and active carotenoid found in carrot, makes a significant contribution to its nutritional value (Yamaguchi and Sugiyama, 1960). Parameters of genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection (Robinson *et al.*, 1949). Thus, the present studies aim to evaluate the available genotypes and to quantify and document the varietal variation in terms of yield attributes and qualitative traits like total soluble solids (TSS) and carotene content of some exotic as well as indigenous carrot genotypes/ cultivars selected from gene pool of the carrot germplasm at the Indian Institute of Vegetable Research (IIVR), Varanasi.

Materials and Methods

The experimental material included 32 entries (HCP-1, HCP-191, HCY-2, Barwala-2, HCP-183, HCY-17, Barwala Red, HC-155, HC-119, Medium Long Nantes, HC-2-A, VN-11550, HC-4-2, HC-112, HC-191, Shahabad, HC-3, HC-5, HC-4, HCP-11, HC-197, Barwala, Rewari Red, HC-11, HC-118, No.10, HCP-195, HC-165, No.-5, HC-122, HCJ-109 and HCP-2-2) belonging to yellow, red, black and orange colour root types. These were grown in Randomized Block Design with three replications. The trial was conducted under network on hybrid vegetable production technology in Uttar Pradesh at the Research Farm, Indian Institute of Vegetable Research, Varanasi, during winter 2001 and 2002. All the genotypes were sown on ridges in a single row of 3 m length in each replication with 60 cm spacing between rows and 8 cm between plants, respectively. All the recommended package of practices were followed during the course of investigation for raising a good crop. The observations were recorded on yield attributing traits viz; plant height (cm), root length (cm), root diameter (cm), root weight with leaves (g), flesh thickness (cm), core thickness (cm), number of leaves/plant, leave length (cm) and average fresh root weight (g) as well as on qualitative traits, viz; Total Soluble Solids (TSS) (%), exterior root colour, core colour and carotene content. Five roots from each replication were selected randomly, pooled and composite samples were analyzed in triplicate. Total soluble solids (%) were determined using a hand refractometer. The visual color of carrot roots was determined by the level of total carotenoids present, the accumulation of other specific pigments as well as the distribution of pigments between phloem and xylem. Carotenoids were extracted in acetone and portioned in petroleum ether and quantified by measuring the absorbance at 452 nm in an UV-visible double beam spectrophotometer as per the standard procedure (Ranganna, 1986). The specific absorbance values (specific extinction coefficient) tabulated by Davies

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(1976), was used for the calculation of carotene. Total carotene was expressed as mg/100 g fresh weight of carrot. Analysis of variance was calculated as the method suggested by Panse and Sukhatme (1985). The phenotypic and genotypic coefficients of variation (PCV and GCV) were estimated as per Burton (1953). Heritability in a broad sense suggested by Allard (1960) and genetic advance (in terms of percentage of mean) were computed according to Johnson *et al.* (1955).

Results and Discussion

Range, mean and analysis of variance for different quantitative and qualitative traits are presented in Table 1. The mean sum of squares were highly significant for all traits, indicating the presence of wide variability in the genotypes studied. Root weight with leaves showed a wide range (20.07-194.30 g), the minimum and maximum root weight with leaves was recorded in accessions Shahabad and Barwala-2, respectively. Plant height ranged from 48.00 (HC-3) to 78.40 cm (HCP-191), with a mean of 65.82 cm. Root length and root diameter also registered considerable variability, which ranged from 15.60 (HC-3) to 23.60 cm (Barwala-2) and 3.04 (HC-4) to 4.92 cm (Barawala-2), respectively. Maximum flesh thickness (1.42 cm) was recorded in HC-3 and minimum (0.66 cm) in HCJ-109, whereas maximum (1.69 cm) and minimum (0.88 cm) pith thickness were recorded in HCP-1 and HC-165, respectively. The present set of genotypes possessed an average of 8.41 leaves/plant, which ranged from 6.40 (HC-4) to 11.00 (HCP-191). Leaf length varied from 32.80 to 58.50 cm, Shahabad registering the lowest and HCP-191 the highest. HCP-195 exhibited maximum TSS (8.04 %) whereas a minimum TSS was exhibited by HCP-191 (3.83%). Maximum carotene (8.95%) was recorded in HC-2-A and minimum (1.44%) in HCP-183. Average fresh root weight showed a wide range (21.80-108.90 g), the minimum and maximum yield was recorded in genotype HCP-116 and HCP-191, respectively.

In general, the phenotypic variance and phenotypic coefficients of variation were higher than the respective genotypic variance and genotypic coefficients of variation for all the traits (Table 2) indicating a considerable influence of environment on their expression. Average fresh root weight had highest coefficient of variation at the genotypic and phenotypic level followed by root weight with leaves. Brar and Sukhija (1981) and Tweatia et al. (1990) also studied the coefficient of variation in carrot, which was highest for root and leave weight. Sizable coefficient of variation at genotypic and phenotypic (12-25 %) level was observed for carotene content, TSS, core thickness, leave length and root diameter at phenotypic and genotypic level indicating high level of variability in these characters and ample scope for effective improvement, whereas plant height and root length showed less coefficient of variation at both the level (phenotypic

Table 1. Range, mean and analysis of variance for different qualitative and quantitative traits

Characters	Range		Mean	Standard error	CV (%)	CD at	
	Min.	Max.				5%	1%
Plant height (cm)	48.00 (HC-3)	78.40 (HCP-191)	65.82	1.29	2.40	2.58	3.43
Root length (cm)	15.60 (HC-3)	23.60 (Barwala-2)	18.74	0.70	4.59	1.40	1.86
Root diameter (cm)	3.04 (HC-4)	4.92 (Barwala-2)	3.75	0.24	7.79	0.48	0.64
Root weight with leaves (g)	20.07 (Shahabad)	194.30 (Barwala-2)	88.36	2.48	3.43	4.96	6.60
Flesh thickness (cm)	0.66 (HCJ-109)	1.42 (HC-3)	1.003	0.057	7.00	0.114	0.152
Core thickness (cm)	0.88 (HC-165)	1.68 (HCP-1)	1.27	0.100	9.65	2.00	0.266
No. of leaves/plant	6.40 (HC-4)	11.00 (HCP-191)	8.41	0.56	8.11	1.12	1.49
Leaf length (cm)	32.80 (Shahabad)	58.50 (HCP-191)	46.67	1.55	4.06	3.10	4.12
TSS (%)	3.83 (HCP-191)	8.04 (HCP-195)	5.72	0.28	5.96	0.56	0.75
Carotene content (%)	1.44 (HCP-183)	8.95 (HC-2-A)	6.03	0.092	1.87	0.184	0.25
Average fresh root weight (g)	21.80 (HCP-11)	104.90 (HCP-191)	45.32	1.59	4.29	3.18	4.23

*, ** Significant at 5% and 1% level of probability, respectively

Table 2. Components of variance, coefficient of variation, heritability, genetic advance and genetic advance as % of mean for different qualitative and quantitative traits

Characters	Variance		Coefficient of variation		Heritability (Broad sense)	Genetic advance	Genetic advance as % of mean
	Genotypic	Phenotypic	Genotypic	Phenotypic			
Plant height (cm)	36.92	39.41	9.23	9.54	93.70	12.12	18.41
Root length (cm)	2.52	3.26	8.48	9.64	77.30	2.88	15.37
Root diameter (cm)	0.21	0.30	12.13	14.42	70.80	0.79	21.07
Root weight with leaves (g)	924.43	933.62	34.41	34.58	99.00	62.32	70.53
Flesh thickness (cm)	0.017	0.022	13.13	14.88	77.90	0.24	23.93
Core thickness (cm)	0.037	0.052	15.12	17.93	71.10	0.33	25.98
No. of leaves/plant	1.41	1.88	14.12	16.88	75.20	2.12	25.21
Leave length (cm)	32.44	36.02	12.20	12.86	90.10	11.13	23.85
TSS (%)	1.31	1.43	19.99	20.86	91.80	2.26	39.51
Carotene content (%)	2.309	2.322	25.21	25.28	99.50	3.12	51.74
Average fresh root weight (g)	390.76	394.53	43.63	43.83	99.00	40.53	88.99

and genotypic). Genotypic coefficient of variation would be more useful for assessing the variability.

Burton (1953) has suggested that genotypic coefficient of variation together with heritability estimate would give the best option expected for selection. Heritability estimates were high (> 90%) for carotene content, average fresh root weight, root weight with leaves, plant height, TSS and leave length. High estimates of heritability were reported for leaf length, leaf weight and root weight (Brar and Sukhija, 1981 and Tweatia *et al.*, 1990). High heritability for the characters controlled by polygene might be useful to plant breeder for making effective selection. Moderate heritability (70-80%) for flesh thickness, root length, number of leaves/plant, core thickness and root diameter, suggested that the environmental effects constitute a major portion of the total phenotypic variation and hence, direct selection for these traits will be less effective. Johnson *et al.* (1955) reported that the heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect for selecting the best genotype as it suggests the presence of additive gene effect (Panse, 1957). High estimates of genetic advance were recorded for root weight with leaves (62.32) and average fresh root weight (40.53). Results of similar trend were also reported by Brar and Sukhija (1981) and Tweatia *et al.* (1990). The high heritability was associated with high genetic advance as percent of mean (>39%) for average fresh root weight, root weight with leaves, carotene content and TSS. The parallelism between the magnitude of heritability and degree of genetic gain has been due to the additive genes playing a predominant role. Presence of high and moderate heritability for plant height and root length with low genetic gain suggested that high heritability did not necessarily lead to increased genetic gain unless sufficient genetic variability existed in the genotypes.

Occurrence of sufficient genetic variability for yield *per se* and its contributing traits, in the present set of genotypes can be exploited for carrot improvement. Average fresh root weight, carotene content, TSS and root weight with leaves were observed to be most reliable selection parameters. On the basis of above finding, HCP-191, Barwala-2, HC-155, HCP-183, HC-4-2, VN-11550

Table 3. Best seven genotypes for various morphological and qualitative traits

Characters	Accessions						
	HCP-191	**Barwala-2**	**HC-155**	**HCP-183**	HC-4-2	**VN-11550K**	**HC-2-A**
Plant height (cm)	78.40	67.80	71.20	74.00	67.60	71.40	65.40
Root length (cm)	20.00	23.60	19.50	20.80	18.20	20.20	18.60
Root diameter (cm)	4.34	4.92	4.80	3.90	4.04	3.26	3.38
Root weight with leaves (g)	110.00	194.00	132.00	102.00	118.00	86.00	80.20
Flesh thickness (cm)	1.08	1.14	1.04	0.92	1.12	0.86	0.92
Core thickness (cm)	1.68	1.66	1.64	1.46	1.56	1.32	1.14
No. of leaves/plant	11.00	10.00	10.20	9.80	8.60	9.60	7.80
Leave length (cm)	58.50	45.00	49.00	53.20	49.60	51.20	46.80
TSS (%)	3.85	6.06	5.99	4.15	3.93	5.99	6.19
Carotene content (%)	4.79	5.50	6.31	1.43	3.99	5.11	8.95
Average fresh root weight (g)	104.90	82.30	82.30	78.60	70.70	62.20	56.80
Inner core color	Yellow	Yellow	Yellow	Light Black	Light Yellow	Yellow	Yellow

K and HC-2-A were recorded to be superior genotypes (Table 3) for yield *per se* and its component traits, which can be used in future breeding programme.

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Isozyme and Protein Polymorphism in Groundnut (*Arachis hypogaea* L.) Germplasm

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Forty-one groundnut germplasm accessions with multiple stress resistance were characterized using proteins (hypocotyl and seed) and glutamate oxaloacetate transaminase (GOT) isozyme. GOT and seed proteins showed less variation but differentiated botanical types. Hypocotyl proteins exhibited more variation and identified five genotypes. Isozyme and proteins together revealed a total of 22 electrophoretic phenotypes and differentiated fifteen genotypes. A large number of related germplasm exhibited the same electrophoretic phenotype but morphologically similar mutants could be differentiated.

Key Words: Germplasm, Groundnut, Isozyme, Proteins, Resistance

Groundnut is one of the important oilseed crops of India but productivity (<1000 kg/ha) is lower than the world average (1300 kg/ha). Biotic and abiotic stresses are the major constraints in achieving higher productivity. Though a large number of resistant germplasm is available, only two accessions (NC Ac 17090 and PI 259747) appear in the parentage of released cultivars in India (Nigam, 2000). One of the reasons for limited germplasm utility could be lack of proper understanding of germplasm. The characterization of germplasm could help in proper maintenance besides better utilization in breeding programmes. Though, many morphological descriptors are available for characterization, due to their overlapping nature, instability and vulnerability to environment, they are not very much useful. Under the circumstances, biochemical markers would be of great help.

Gel electrophoresis of proteins has become a standard and powerful tool for application in a multitude of biological disciplines. Isozymes and seed proteins, because of their stability and reproducibility, have potential to serve as tools for fingerprinting genotypes. Present study was carried out in forty-one groundnut genotypes consisting of interspecific derivatives, advanced breeding lines, induced mutants and released cultivars with resistance to various biotic/abiotic stresses to know the biochemical relatedness/variation with the help of isozyme and protein polymorphism.

The analysis of variation for total proteins and the isozyme glutamate oxaloacetate transaminase (GOT) was performed by polyacrylamide gel electrophoresis (PAGE) technique. The hypocotyls of six-day-old seedlings in each genotype were chopped into small pieces and ground well using pestle and mortar by adding chilled phosphate buffer (0.2M; pH 8.0). Filtered homogenate was centrifuged at 10,000 rpm for 15 minutes and supernatant was used as source of protein and GOT isozyme. Protein content was estimated following the procedure of Lowry *et al.* (1951). Gels were prepared according to the method of Hames and Rickwood (1984). Protein sample (100 μg) was loaded with micropipette along with 10 μl sample buffer containing bromophenol blue in each well. The electrophoresis was carried out at constant voltage (70 V) till the dye front reached the bottom of the gel. Proteins were visualized by staining with Coomassie Brilliant blue and Fast Blue BB salt was used for GOT isozyme. Relative mobility (Rm) of the protein band was determined. In case of GOT isozyme, gels were incubated in dark at 30°C, till blue bands appeared. The gels were fixed in 7 per cent acetic acid and bands were scored.

In case of seed proteins, seeds were pressed under the folds of Whatman No.1 filter paper to defat the seeds and 40 mg of seed material was extracted for 1 hour at room temperature with 1 ml of Tris-HCl extraction buffer (65mM; pH 6.8). Samples were then boiled for 3 min and cooled for 30 min after which they were centrifuged briefly to remove particulate material and used for electrophoresis. One-dimensional SDS-PAGE (12.5 % separating gel and 2.5 % stacking gel) was carried out in a vertical gel system. Staining was done using Coomassie Brilliant blue and bands were scored. The protein and GOT data were analysed using NTSYS PC (2.0) software to calculate the similarity (using Dice coefficient) between different accessions.

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Glutamate Oxaloacetate Transaminase (GOT): A total of four bands with Rm values 0.338, 0.385, 0.431 and 0.492 were resolved. First three bands displayed four banding patterns through their presence or absence (Table 1). Pattern I was characterized by presence of bands of Rm value 0.338, 0.385 and 0.431 while pattern II had all the four bands. Both these patterns had genotypes belonging to Virginia or Valencia botanical types with some Spanish genotypes. Pattern III with only two bands (Rm values 0.431 and 0.492) was specific to Spanish type. Pattern IV had only one band (Rm 0.492) with only one genotype TG 49 which belonged to Spanish Bunch category. Some Spanish genotypes displaying pattern I and II had Virginia genotypes in their ancestry. Lacks and Stalker (1993) reported the usefulness of GOT to categorize botanical types of groundnut and use of isozymes as markers to follow the introgression pattern especially in interspecific hybridization.

Hypocotyl proteins: As many as 14 bands with Rm values ranging from 0.218 to 0.945 were resolved. Of these, 10 bands were polymorphic. Based on the presence or absence of these bands, 14 electrophoretic phenotypes were identified (Table 1). The genotypes ICGV 86590, ICGV 93020, ICGV 93028, ICGV 96262, ICGV 96266 showed unique banding patterns.

Seed proteins: A total of 17 bands were resolved among genotypes with Rm values ranging from 0.300 to 0.970.

Table 1. Banding pattern for polymorphic bands of GOT, hypocotyl and seed proteins in groundnut germplasm

Genotype	GOT				Total Proteins										Seed Proteins				
	.338	.385	.431	.492	.218	.436	.545	.600	.625	.636	.800	.900	.925	.945	.529	.567	.735	.895	.962
ICGV 86699	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 87165	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 88256	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 93023	+	+	+	+	—	+	+	—	—	+	—	+	+	+	—	+	—	—	+
A 30b	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
B 37c	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
GPBD 4	—	—	+	+	—	+	+	—	+	+	+	+	+	+	—	+	—	—	+
ICGV 86031	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	+	+	—
ICGV 87264	—	+	+	+	+	+	+	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 87807	+	+	+	+	—	—	—	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 90266	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 91173	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	+	+	+
ICGV 91177	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 91180	—	+	+	+	—	+	+	+	—	+	+	+	+	+	—	+	—	—	+
ICGV 92188	—	+	+	+	+	+	+	—	—	+	+	+	+	—	—	+	—	—	+
ICGV 93008	—	+	+	+	+	+	+	—	—	+	+	+	+	—	—	+	—	—	+
ICGV 93020	—	+	+	+	—	+	+	—	—	+	+	+	+	—	—	+	—	—	+
ICGV 93021	—	+	+	+	—	—	+	—	—	+	+	+	+	+	+	—	+	+	—
ICG 2271	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	—
ICG 1697	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 96262	—	+	+	+	+	+	—	—	—	+	+	+	+	+	—	+	—	—	+
ICGV 96266	—	+	+	+	—	+	+	—	—	—	+	+	+	+	—	+	—	—	+
Dh 73	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
R 8972	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
R 9214	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
R 9227	+	+	+	+	+	+	+	—	—	+	+	+	+	+	+	—	+	+	—
VL 1	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	—
28—2	—	+	+	+	—	+	+	—	—	+	+	+	+	+	+	—	+	+	—
45	—	+	+	+	—	+	+	—	—	+	+	+	+	+	+	—	+	+	+
110	—	+	+	+	—	+	+	—	—	+	+	+	+	+	+	—	+	+	+
ICGV 86590	—	+	+	+	—	+	+	—	—	+	+	—	—	—	—	+	+	+	+
K 134	—	—	+	+	—	+	—	+	+	+	+	+	+	+	—	+	—	—	+
KRG 1	—	—	+	+	—	+	+	—	+	+	+	+	+	+	—	+	—	—	+
JL 24	—	—	+	+	—	+	+	+	+	+	+	+	+	+	—	+	—	—	—
TMV 2	—	—	+	+	—	+	+	+	+	+	+	+	+	+	—	+	—	—	—
Dh 8	—	—	+	+	—	+	+	—	—	+	+	+	+	+	—	+	+	—	—
Dh 40	—	—	+	+	—	+	—	+	+	+	+	+	+	+	—	+	—	—	+
R 8808	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	—	—	+
TAG 24	—	+	+	+	—	+	+	—	—	+	+	+	+	+	—	+	+	+	—
TG 26	—	—	+	+	+	+	+	—	—	+	+	+	+	+	—	+	—	—	+
TG 49	—	—	—	+	+	+	+	—	—	+	+	+	+	+	+	—	+	+	—

+: Present —: Absent

Of these, only five bands with Rm values of 0.529, 0.567, 0.739, 0.895 and 0.962 were polymorphic. Based on the presence or absence of these polymorphic bands, seven electrophoretic phenotypes were identified (Table 1). This could help in unique identification of Dh 8 genotype only. Chandran *et al.* (2002) reported higher polymorphism with seed proteins in released cultivars. Hartzook et al. (1969) obtained highly repeatable clear resolutions showing differences in total seed protein content among three botanical types (Virginia Bunch, Valencia and Spanish Bunch) and concluded that PAGE of seed proteins could be used as a tool in establishing cultivar identification.

GOT and seed proteins individually did not show much variation among the germplasm but helped in differentiation of the botanical types while hypocotyl proteins gave more variation among the germplasm.

Combination of Isozyme and Proteins: Individual isozyme and proteins (hypocotyl and seed) uniquely identified only a few genotypes. But when isozyme and protein data were considered together, a total of 22 different electrophoretic phenotypes were formed (Fig 1). Fifteen genotypes were differentiated unambiguously with cultivar-specific protein profile. It is interesting to note that one of the 22 electrophoretic phenotypes comprised 12 genotypes, all of which had North Carolina accession in their pedigree. GPBD 4 which has KRG 1 as female parent, as expected, clustered with the later. The induced mutants 28-2, 45 and 110 derived from the genotype VL 1 shown morphological similarity with respect to number of branches, colour and shape of leaves, pod shape and length. But, at biochemical level there was variability with mutants 45 and 110 clustering together, while 28-2 and VL 1 forming separate solitary clusters. Gorman *et al.* (1982) suggested the use of multiple enzyme system for complete cultivar fingerprinting. Chandran and Pandya (1999) established relation between accessions of *Arachis* and identified

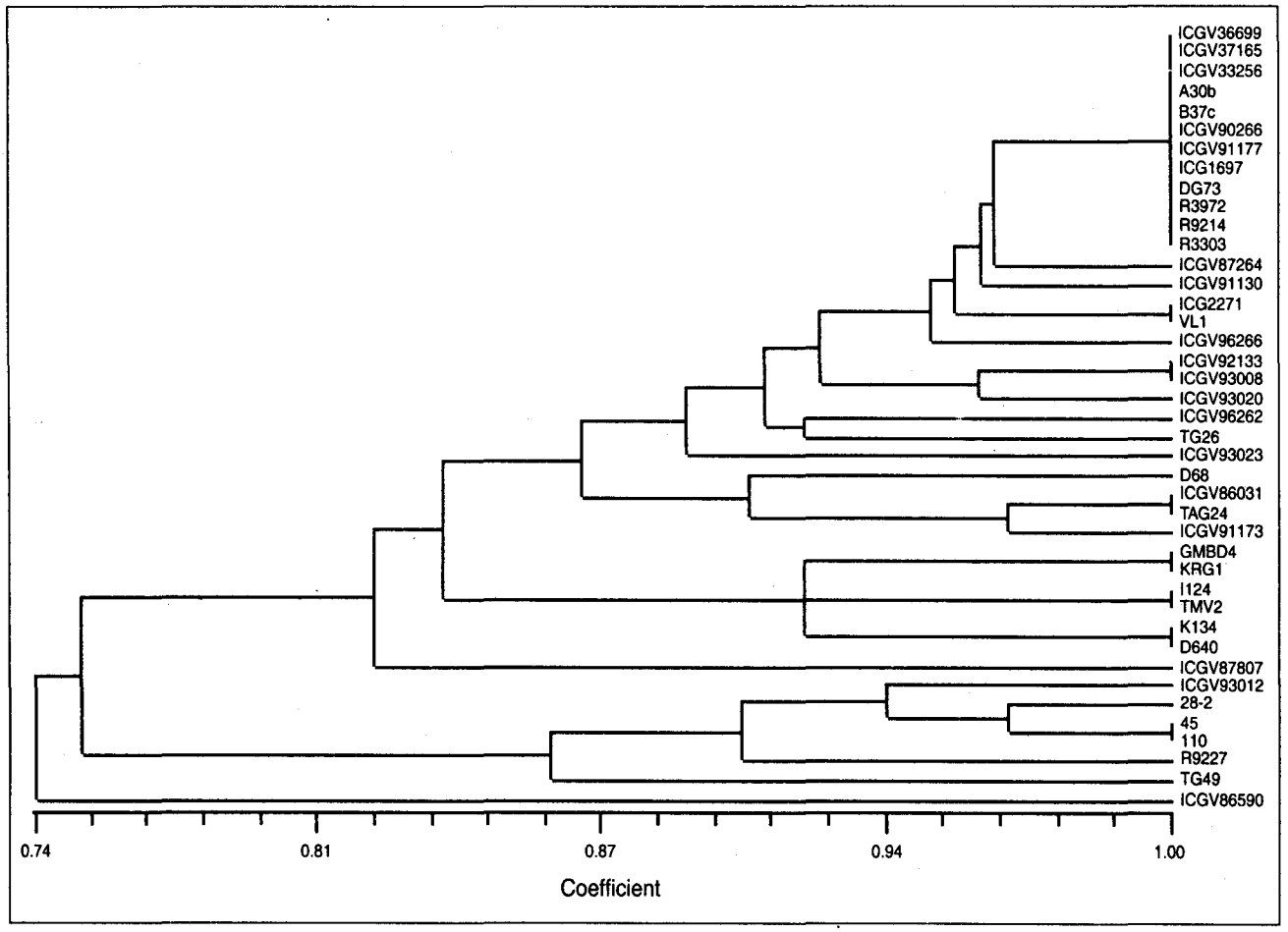

Fig. 1: Dendrogram of groundnut germplasm based on proteins (hypocotyl and seed) and GOT isozyme

duplications of the accessions with isozyme and protein polymorphism.

The biochemical markers differentiated the resistant germplasm and found suitable for grouping the genotypes with common ancestry. They were also useful in differentiating morphologically similar disease resistant mutants. However, the extent of variation was limited for developing fingerprints for all the genotypes. The limited polymorphism with biochemical markers underscores the need for employing DNA based markers. An integrated approach utilizing both morphological and biochemical/molecular markers could help in proper characterization of the genetic resources of the groundnut crop.

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Characterization and Evaluation of Some Exotic Guava Accessions under Bangalore Conditions

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Six exotic accessions and two popular varieties of guava (*Psidium guajava* L.) were evaluated and characterized for morphological, yield and quality traits under Bangalore conditions. Considerable variability was recorded for morphological, yield and quality parameters. All the exotic accessions possessed attractive red flesh with high acidity and hence are suitable for the preparation of several processed products. The accession 7-39 EC 147034 was the high yielder combined with good processing qualities and high vigour hence could be exploited in crop improvement programme. The accessions 9-35 EC 147036 and EC 162904 were also found to be next best promising types.

Key Words: Characterization, Evaluation, Exotic Germplasm, Morphological Traits, *Psidium guajava* L., Yield and Quality.

Guava (*Psidium guajava* L.) the 'apple of tropics' reported to be originated in tropical America is now well adopted and widely grown throughout our country and became a crop of commercial significance. Due to its hardy nature, it is highly remunerative without much care. The fruits are not only delicious but also rich in nutrition especially vitamin 'C'.

As a part of crop improvement programme, germplasm introduction has been undertaken through National Bureau of Plant Genetic Resources and the exotic types collected are conserved under field gene bank (FGB). Since a precise knowledge on various morphological, yield and quality parameters of these accessions is lacking an attempt was made to evaluate and characterize them systematically, which will be of immense use in selection of suitable accessions for specific traits in crop improvement programme.

Materials and Methods

The materials used for the study consisted of six exotic collections *viz.*, EC 14039, 7-39- EC 147034, 7-12- EC 147036, 9-35- EC 147036, EC 147037, EC 162904 and two popular varieties viz., Allahabad Safeda and Lucknow 49, maintained in the FGB at IIHR, Bangalore. The plants were spaced at 6x6 m with four plants per accession and each tree constituted one replication. The observations were recorded from the trees of about 15-18 years old for a period of three years from 2000 to 2002.The accessions were evaluated and characterized for various parameters viz., growth, leaf, inflorescence, fruit, seed and fruit bio-chemical constituents as per the standard descriptor. The fruit chemical constituents were analysed by the methods of AOAC (1984). The colour chart developed by Royal Horticultural Society London was used for describing the colour.

Results and Discussion

The genotypes evaluated showed considerable degree of variation in respect to their growth, leaf, flower, fruit and biochemical attributes (Table 1 to 5). As regards growth parameters the exotic collections are semi tall to tall growing with high to medium in vigour and branching density. And the crown diameter and tree volume were also more. Positive correlation of fruit yield/ tree with the spread, stem girth and tree volume in guava has been reported by Rakesh *et al.* (2002). Thus these traits could be made useful in selection of parents for higher yield based on their general combining ability

With respect to leaf parameters, the shapes are elliptic to broadly elliptic with acute tip and obtuse base and are intermediate to dense in nature. The young leaf colour varied from shades of grayed orange in exotic collection to yellow green in popular cultivar, Allahabad safeda. The density of leaves plays a major role in photosynthesis. Higher the number of leaves more is the photosynthesis and hence higher yield.

Flowering commenced from first week of March and extended for 42 to 67 days in different accessions. The accession with longer duration of flowering helps in extending the fruit availability in the market and enables the producer to get higher price. The flower bud shape was sub-globose to sub ovate. The length and breadth ranged from 1.45 to 2.47 cm and 0.7 to 1.1 cm respectively. The variations with respect to

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Table1. Growth descriptors of guava germplasm

Accession	Tree vigour	Tree height (m)	Trunk circum-ference (cm)	Trunk surface	Trunk/bark colour	Crown diameter (m) E-W: N-S	Tree volume (m^3)	Crown shape	Tree girth habit	Branching density	Branching pattern
EC 14039	Medium	3.58	49.4	Smooth	Grey group 201C	5.45:6.05	245.61	Broadly pyramid	Semi Erect	Medium	Irregular
7-39 EC 147034	High	4.9	56.7	Smooth	Grey group 201 A	6.4:6.5	426.72	Broadly pyramid	Semi Erect	Dense	Horizontal
7-12 EC 147036	Medium	4.95	57.5	Rough	Grey group 221 B	5.58:6.15	357.75	Pyramid	Erect	Medium	Irregular
9-35 EC 147036	High	4.55	54.5	Rough	Greyed Brown 199 A	6.2:6.4	378.02	Broadly pyramid	Spreading	Medium	Irregular
EC 147037	High	4.3	58	Smooth	Greyed green 197 B	5.10:5.85	272.28	Broadly pyramid	Erect	Dense	Opposite
EC 162904	High	4.97	90.6	Rough	Greyed group 201B	5.86:5.5	321.1	Pyramid	Erect	Dense	Irregular
Allahabad safeda	Medium	2.9	44	Smooth	Light grey 201 B	4.20:4.15	106.07	Broadly pyramid	Spreading	Dense	Horizontal
Lucknow-49	High	2.65	39	Smooth	Light grey 201A	4.25:4.50	106.17	Broadly pyramid	Spreading	Dense	Opposite

Table 2. Leaf descriptors of guava germplasm

Accession	Leaf density	Colour of young leaf	Mature leaf colour	Leaf blade length (cm)	Leaf blade width (cm)	Leaf blade shape	Leaf apex shape	Leaf base shape	Leaf upper surface pubsc-ence	Leaf linerv-surface pubsc-ence	Petiole length (cm)	Leaf thickness
EC 14039	Intermediate	Greyed orange 166B	Dark green	9.68	5.7	Broadly	Acute	Rounded	Present	Present	0.48	Medium
7-39 EC 147034	Dense	Greyed orange 164A	Green	9.1	4.1	Elliptic	Acute	Rounded	Present	Present	0.39	Medium
7-12 EC 147036	Intermediate	Greyed orange 176A	Green	10.96	4.8	Elliptic	Acute	Rounded	Present	Present	0.33	Medium
9-35 EC 147036	Dense	Greyed orange 176 A	Dark green	10.4	5.1	Elliptic	Acute	Rounded	Present	Present	0.47	Thick
EC 147037	Dense	Greyed orange 176 A	Dark green	8.5	4.1	Broadly Elliptic	Acute	Rounded	Present	Present	0.62	Thick
EC 162904	Intermediate	Greyed orange 166 B	Green	9.85	4.3	Elliptic	Acute	Rounded	Present	Present	0.5	Thick
Allahabad Safeda	Intermediate	Yellow green 152 D	Green	10.8	4.9	Elliptic	Acute	Narrowly rounded	Present	Present	0.56	Medium
Lucknow - 49	Dense	Yellow green 152 B	Green	10.9	5.3	Broadly Elliptic	Acute	Rounded	Present	Present	0.53	Medium

Table 3. Floral descriptors of guava germplasm

Accession	FBL (cm)	FBW (cm)	FBS	CMS (cm)	Pedicel Length (cm)	Corolla Shape	Style Len. (cm)	Date of flowering	Time taken for 50% of flowering	Completion of flowering
EC 14039	1.76	0.7	Sub globose	4	1.4	Broadly Elliptic	1.2	5-Mar	22	45
7-39 EC 147034	2.16	0.8	Sub Ovate	4.2	1.9	Elliptic	1.2	4-Mar	27	61
7-12 EC 147036	2.35	0.9	Sub globose	4.1	2.27	Broadly Elliptic	1.4	8-Mar	25	48
9-35 EC 147036	2.35	0.9	Sub globose	4.4	1.92	Elliptic	1.4	15-Mar	30	67
EC 147037	2.5	0.8	Sub globose	4.2	22	Broadly Elliptic	1.3	1-Apr	28	48
EC 162904	2.35	0.8	Sub Ovate	4.2	1.8	Broadly Elliptic	1.2	6-Mar	23	42
Allahabad Safeda	1.45	0.9	Sub globose	4.5	2	Elliptic	1.5	20-Mar	30	61
Sardar	2.47	1.1	Sub globose	4.3	2.8	Broadly Elliptic	1.8	15-Mar	21	58

FBL- Flower bud length FBW- Flower bud width
FBS- Flower bud shape CMS-Corolla maximum spread

Table 4a. Fruit descriptor (external) of guava germplasm

Accession	Mature skin colour	Fruit shape	Average Fruit weight (g)	Fr.surface	Fr.base	Fr. apex	Fr.style	Fr.stylar scar	Yield/ plant(kg)	Frint attractiveness
EC 14039	Light yellow	Sub-globose	88.5	Smooth glossy	Convex	Acute	Deciduous	Protruded	75.6	Good
7-39 EC 147034	Dark yellow	Oblong	109	Smooth glossy	Necked	Rounded	Persistant	Protruded	146	Intermediate
7-12 EC 147036	Yellow	Sub-globose	102	Smooth	Convex	Rounded	Deciduous	Protruded	42.3	Intermediate
9-35 EC 147036	Dark yellow	Sub-globose	107.6	Smooth glossy	Necked	Rounded	Deciduous	Protruded	118.4	Intermediate
EC-147037	Yellow	Globose	98	Smooth	Convex	Rounded	Deciduous	Protruded	46.5	Intermediate
EC 162904	Dark yellow	Sub-globose	136.14	Smooth glossy	Slightly necked	Rounded	Deciduous	Even	103.6	Intermediate
Allahabad safeda	Yellow	Globose	115.12	Smooth glossy	Convex	Rounded	Deciduous	Depressed	54	Excellent
Sardar guava (L.49)	Yellow	Sub-globose	126.3	Rough and dull	Convex	Rounded	Deciduous	Protruded	62.4	Intermediate

Table 4b. Fruit descriptor (internal) of guava germplasm

Accession	Flesh colour	Flesh texture	Flesh flavour	Flesh taste	Fruit length (L.S) cm	Fruit width (C.S.) cm	Fruit Volume (ml)	Size of of seeds	Texture of seeds	No. of seeds/ fruit
EC 14039	Red (38B)	Firm	Weak	Acidic	5.8	4.9	125.56	Medium	Medium	127
EC 147034 (7-39)	Red (37A)	Firm	Intermediate	Acidic	6.9	5	102.22	Medium	Hard	242
EC 147036 (7-12)	Red (37B)	Firm	Strong	Acidic	5.6	5.9	80	Medium	Hard	164.28
EC 147036 (9-35)	Red (38C)	Firm	Intermediate	Acidic	6.4	5.8	98	Medium	Hard	313.21
EC-147037	Red (37C)	Firm	Weak	Acidic	5.3	5.4	95	Medium	Medium	135.3
EC 162904	Red (37B)	Firm	Intermediate	Acidic	7.13	6.34	136	Medium	Hard	242.7
Allahabad Safeda	White	Firm	Strong	Sweet	5.39	5.87	107.11	Small	Soft	149.07
Sardar guava (L.49)	White	Firm	Intermediate	Sweet	5.88	5.45	110.5	Medium	Medium	217

Table 5. Fruit chemical constituents of guava germplasm

Accession	TSS° B(%)	Dry matter(%)	Vit 'C' mg/g	Titrable acidity (as citric acid)	Reducing sugar (g)	Non reducing sugar (g)	Total sugar (g)
EC 14039	7.3	15.72	158.37	2.16	7.05	0.81	7.86
9-35 EC 147036	9.35	17.36	196.33	1.6	5.69	1.37	7.06
7-39 EC 147034	9.2	16.69	194.98	3.12	4.01	0.93	4.94
7-12 EC 147036	10.06	16.59	198.54	2.2	3.19	1.8	4.98
EC 147037	8.4	16.05	169.51	1.82	4.14	1.24	5.38
EC 162904	8.87	18.34	226.87	3.25	8.03	0.85	8.88
Allahabad safeda	9.8	19.8	195	0.58	6.73	1.77	8.5
L.49 (Sardar)	10.6	21.65	205	0.61	6.95	1.86	8.8

quantitative parameters are more prominent than qualitative parameters.

The fruit shapes recorded were globose, sub-globose and oblong with yellow to dark yellow pericarp. The fruit bases were met with necked to convex and the apex were of acute to rounded. The average fruit weight ranged from 88.5 in EC 14039 to 136.14 g in EC 162904. The seeds were of medium to hard in nature.

The fruit yield per plant varied from 42 kg in 7-12 EC 147036 to 146 kg in 7-39 EC 147034 compared to the popular cultivars of Allahabad safeda (54 kg) and Lucknow 49 (62 kg). The accession EC 14039 also recorded higher yield of 72.28 kg. Hence, the exotic collections 7-39 EC 147034, 9-35 EC 147036 and EC 162904 could be exploited for obtaining higher yield.

The fruit quality and pulp colour are the desirable factors in selection of guava varieties for processing or fresh consumption. Interestingly all the exotic collections possessed attractive red flesh (grades ranged from 37A to 38 B) with intermediate to strong flavour and acidic taste coupled with firm flesh which is highly preferred for the preparation of several processed products. The processed products of guava are an important part of international trade (Campbell, 1984; Menzel, 1985). The quality parameters recorded showed wide variability among the accessions, which could be used to make selections in guava. The collection EC 162904 recorded higher Vit 'C' (226.87 mg/100g), sugar (8.88g), acidity (3.25%) and dry matter (21.65%). The accessions 7-39 EC 147034 and 7-12 EC 147036 were also found to be promising. Hence, these accessions could be used as parents for incorporating specific trait in the crop improvement programme. High acidity helps in better storability. Studies on ascorbic acid content and acidity of different guava varieties and varietal suitability for processing was studied by Taeotia and Awasthi (1967), Singh and Dhawan (1983) and Murali and Verma (1989).

The accessions evaluated showed considerable variability for morphological, yield and quality parameters. The attractive red flesh combined with good processing qualities and high yield could be exploited in crop improvement programme.

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Characterization of Some Macromutations Induced by Single and Combination Treatments of Gamma Rays, EMS and SA in Urdbean (*Vigna Mungo* L. Hepper)

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Two improved cultivars of urdbean (*Vigna mungo* L. Hepper), namely, PDU1 and T9 were treated with single and combination doses/concentrations of gamma rays, ethyl methane sulphonate (EMS) and sodium azide (SA). A number of various types of morphological macromutations were induced in M_2 generation. Out of these, fourteen mutants from PDU1 and thirteen from T9 were identified as true breeding for plant morphology, pod- and seed characters and early maturity in M_3 generation. Many macromutants showed significant improvement in yield and other yield components as compared to their parents.

Key Words: Ethyl methane sulphonate (EMS), Gamma rays, Macromutations, Sodium azide (SA), Urdbean (*Vigna mungo*)

Urdbean (*Vigna mungo* L. Hepper) is an important pulse crop of India grown on an area of about 3.15 m ha with a production of 1.49 mt. But the productivity is only 473 kg/ha in the country. The productivity of this crop is very low, particularly when compared with the pigeonpea and chickpea. Since urdbean is a highly self-pollinated crop, the natural variability available is far less to make selections for its improvement. Induced mutagenesis has immense potential in creating genetic variability among naturally exhausted population which is utilized in selection programme for obtaining desirable improvement. The present study was conducted to induce and isolate useful macromutants which could be utilized for genetic improvement of this crop.

Material and Methods

Two improved cultivars of urdbean (*Vigna mungo* L. Hepper), namely, PDU1 and T9 were employed as experimental materials. Three hundred pure, healthy and dry seeds of each cultivar were used for each treatment. The seeds were irradiated with gamma rays at 15, 30, 45 and 60 kR doses from Gamma Cell-200 having a 2000 Curie ^{60}Co source available at the Division of Genetics, IARI, New Delhi in 1996. For chemical mutagenic treatments, the seeds were presoaked in distilled water for 6 hr and then treated with ethyl methane sulphonate (0.02, 0.04, 0.06 and 0.08 M concentrations) in freshly prepared phosphate buffer (pH 7.0) or sodium azide (2, 4, 6 and 8mM concentrations) in phosphate buffer (pH 3.0). For combination treatment, the gamma irradiated seeds at 15-60 kR doses were presoaked in distilled water for 6 hr and then treated with 0.02 M EMS or 4mM SA in the manner described earlier. The mutagen treated seeds were thoroughly washed in running water for an hour to avoid traces of the chemicals, if any.

The mutagen treated seeds along with the untreated control seeds were sown in five rows each measuring 5 m with 30 x 10 cm spacing to raise M_1 generation. The surviving plants were harvested separately and individual plant progenies were raised in M_2 generation. A number of macromutations were induced in various treatments in M_2 generation. The macromutants having sufficient seeds were grown in M_3 generation in RBD with three replications and they were characterized and also confirmed for their breeding behaviour. The observations were recorded on ten competitive plants from each replication for various yield and yield components in M_3 generation.

Results and Discussion

Several types of macromutations were induced by different mutagenic treatment in M_2 generation with respect to growth habit, leaf structure, maturity period and flower, pod and seed characteristics in both the cultivars, viz., PDU1 and T9. A dose dependent increase in the frequency and spectrum of macromutations was recorded in M_2 generation. A total of 31 and 34 types of macromutants were induced in cvs. PDU1 and T9, respectively. A wide spectrum of viable mutations can be expected in a mutation experiment. The probable causes of these macromutations may be chromosomal changes and most probably point

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Table 1: Mean values of yield and yield attributing traits of macromutants in cv. PDU1 in M_3 generation

S. No.	Macromutant	Mutagen treatment	Plant height (cm)	Days to maturity	Number of branches/ plant	Number of pods/ plant	Pod length (cm)	Number of seeds/ pod	Seed yield/ plant (g)	100-seed weight (g)
1.	Tall	30 kR + 4mM SA	52.50**	79.20	5.36**	36.40**	4.25	5.85	7.50**	4.50
2.	Bushy	45 kR	42.82	81.50	6.90**	34.86**	4.36	5.60	7.30**	4.25
3.	Spreading	30 kR + 4mM SA	40.24	85.50**	7.58**	27.60**	4.35	5.85	7.10**	4.40
4.	Dwarf	30 kR + 4mM SA	31.10**	75.60**	3.15*	20.15**	4.10	5.58	6.15	4.25
5.	Broad leaved	0.08 M EMS	38.63*	85.25**	4.50	20.58**	3.90**	5.15**	5.90	4.05
6.	Anthocyanin pigmented	30 kR	44.52	81.36	4.16	22.60	4.05**	5.35**	5.75*	4.20
7.	Hairy	45 kR + 0.02 M EMS	38.36**	82.37	4.52	18.22**	4.40	5.86	5.35**	3.90**
8.	Bold podded	0.02 M EMS	39.52	82.50	3.92	32.86**	5.05**	6.80**	7.32**	4.82**
9.	Short podded	0.08 M EMS	44.50	81.85	4.35	35.68**	3.25**	4.90**	6.10	3.85**
10.	Bold seeded	8 mM SA	45.50**	80.68	4.55	32.87**	4.75**	6.25**	7.25**	5.45**
11.	Small seeded	45 kR	42.56	82.86	4.55	30.50**	3.90**	4.80**	4.85**	3.05**
12.	Round seeded	15 kR +0.02 M EMS	41.96	84.85**	3.90	30.80**	3.95**	4.95**	5.05**	3.50**
13.	Brown seeded	4 mM SA	46.80**	82.90	4.35	32.80**	4.35	5.70	6.90**	4.50
14.	Early maturing	15 kR + 0.02 M EMS	35.50**	65.00	4.05	20.15**	4.15	5.56	5.15**	4.15
		Control	42.00	80.50	4.25	25.50	4.30	5.75	6.25	4.30
		SE ±	1.29	1.30	0.296	1.64	0.105	0.136	0.237	0.147

* Significant at 5 per cent level
** Significant at 1 per cent level

or gene mutations. Most of these macromutations are reported to be polygenic in nature (Yadav and Singh, 1988; Saini and Mahana, 1989 and Thakur and Sethi, 1993).

Fourteen and thirteen true breeding macromutants for plant morphology, pod and seed characters and early maturity derived from cultivars PDU1 and T9, respectively were isolated in M_3 generation. These macromutants showed distinct morphological features as compared to their parents (Tables 1 and 2). Eleven macromutants derived each from both the cultivars showed significantly higher seed yield than their parents. In case of the remaining macromutants, the performance was either equal or even less than the parents. The characteristic features of these macromutants are described below:

Growth habit mutants: The *dwarf, tall, bushy, spreading, tendriller* and *long peduncled* mutants were isolated in M_3 generation. The *dwarf* mutants were characterized by condensed nodes, shorter internodes and low yield as compared to the control. The plants exceeding the height of the respective controls by at least 10 cm were placed in tall category. The *bushy* mutants were also induced in both the cultivars which were characterized by shorter internodes, compact stature and with higher number of pods. The *spreading* mutant exhibited branching parallel to the ground and covered more area than the normal plants. In the *tendriller* mutant, the leaflets were modified into tendrils. The *long peduncled* mutant had the characteristic of increased *peduncle* length joining the pods. Similar mutants have been reported by Pande and Raghuvanshi (1988) and Singh and Yadav (1991) in greengram and Thakur and Sethi (1993) and Gautam and Mittal (1998) in blackgram.

Leaf mutants: The two true breeding leaf mutants, namely, *narrow* leaved from T9 and *broad* leaved from PDU1 were isolated in M_3 generation. The *broad* leaved mutant exhibited increased leaf area and with significantly reduced plant height and number of pods per plant. The *narrow* leaved mutant showed reduced leaf area with decreased seed yield as compared to the parents. Many types of leaf mutants have been reported in urdbean following mutagenesis (Singh and Raghuvanshi, 1985; Thakur and Sethi, 1993 and Gautam and Mittal, 1998).

Early maturing mutants: The *early* maturing mutants were isolated from both the cultivars in M_3 generation. These mutants matured 10 to 15 days earlier than the normal period of the control and yielded lower than the respective controls. The *early* maturing mutants have been reported in urd (Singh, 1988 and Gautam and Mittal, 1998) and mung (Singh and Yadav, 1991).

Hairy and anthocyanin pigmented mutants: These included the *hairy* and *anthocyanin* pigmented mutants. The *hairy* mutants had the characteristic of hairy growth all over the above ground parts, particularly on stem and pods. These mutants showed significantly reduced number of pods per plant and low seed yield than the control. This kind of mutants has been reported by Gautam and Mittal (1998) in urdbean. The presence of anthocyanin pigment, particularly on stem and branches of the plant was the characteristic feature of *anthocyanin* pigmented

mutant. This amount also yielded significantly lower seed yield than its parent. Such mutants have been reported by Tickoo (1987) and Singh and Yadav (1991) in mungbean.

Pod mutants: The *short, bold* and *long* podded mutants were induced by different mutagenic treatments in both the cultivars in M_3 generation. The *short* podded mutants had relatively less number of seeds per pod with lower yield than the control. Such mutants have been reported by Thakur and Sethi (1993) and Gautam and Mittal (1998) in urdbean. The *bold* and *long* podded mutants had significantly increased pod length, greater number of seeds per pod and more seed yield over their parents. Gautam and Mittal (1998) observed such mutants in urdbean.

Seed mutants: The *brown* and *chocolate* testa colour mutants were isolated in M_3 generation as compared to the black testa colour of the parent varieties. Both the mutants exhibited a significant increase in the seed yield over the respective parents. The *bold* seeded mutants were induced in both the cultivars which showed significantly increased pod length, number of seeds per pod, 100 seed weight and seed yield as compared to the controls. The *small* and *round* seeded mutants were also induced which showed significantly lower yield than the parents. The seed mutants for varied testa colours, shapes and sizes have been reported by Ali Khan and Veeraswamy (1974) in redgram and Singh *et al.* (1982) in greengram. These coloured testa mutants are likely to involve single genes.

Increasing mutation frequency is very important aspect for improvement of mutation breeding programme. Gamma rays, EMS and SA have been demonstrated to induce mutations by different mechanisms. The combination of these mutagens in appropriate sequences has been shown to cause a synergistic increase in mutation frequency as observed during the present study as well as in the past (Cheng, 1987 and Cheng and Gao, 1988). The combined treatments induced a higher mutation frequency, resulting in a higher mutation efficiency and an expansion of the spectrum of morphological mutations, thus offering more opportunities for selection in mutation breeding practice.

Many mutants such as *tall, bushy, early* maturing, *long-* and *bold* podded, *bold* seeded, *hairy,* etc. induced during the present study show the desirable characteristics from the breeders' point of view and hold promise for isolation of improved types from their progenies in the later generations.

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Important Crop Germplasm Introduced into India during the Year 2004

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The information about the promising introductions made during the year 2004 for various biotic, abiotic stresses including value added traits has been presented in this paper. A total of 28,437 accessions of germplasm in 89 crops were introduced from 51 countries/International Agricultural Research Institutes and supplied to various user scientists in country for their further utilization in various crop improvement programmes.

Key Words: Introduction, Promising, Stresses, Traits, Value

Germplasm introduction has resulted in establishment of large number of crops and development of high yielding varieties. Not only India, almost all countries are inter-dependent with respect to plant genetic resources required for their crop improvement programmes. The plant breeder needs more diverse germplasm to develop better varieties. Hence the acquisition of diverse and superior germplasm from exotic sources is of prime importance. In the past large number of diverse genotypes were imported in various crop plants from different ecological areas of the world. These germplasm resources were utilised in various crop improvement programmes throughout the country. Some introductions have been used directly as new varieties, and have became popular as commercial cultivars like Laxmi, Suwan in maize; Rumsun, Record, Vinimik in sunflower, Asiriya, Mwituvde in groundnut; Lincoln, Little Marvel, Meteor in pea; Aleppo-4, Aleppo-3311 in cotton; El Savador in subabool. Many superior varieties were also used directly in fruit crops, like apple, pear, peach, apricot, almond, walnut, plum etc., while others were used as a donor/parents and then released as new varieties after several selection cycles, like varieties Rohini, Mangala of wheat; Barakat in rice; Sona, Himani in barley; Chandan makka in maize; Vijay in pearlmillet; UF-70-103 in groundnut and many others in different crops. Introduction of plant genetic resources is extremely important as large numbers of cultivated crops in India are of exotic origin. Some well known new crops are soybean, sunflower, kiwifruit, macadamia nut, pecannut, paradise tree, rambuttan, pawpaw, mangosteen, persimmon etc. The continuing needs of crop improvement necessitate more concerted efforts towards introduction of targeted germplasm with specific traits. In this process specific introductions having desired traits for various biotic, abiotic stresses and value added traits were made during 2004. In all 28,437 accessions of germplasm in 89 crops were introduced from 51 countries/ International Agricultural Research Institutes.

In last two decades with the enforcement of Convention on Biological Diversity (CBD) and provisions of the Trade Related Aspects of Intellectual Property Rights (TRIPs) under World Trade Organization (WTO), there is a general apprehension that free exchange of germplasm would be adversely affected because of issues related to sovereign rights of countries and IPR. An analysis of the introduced germplasm in 2004 from other national genebanks (NGB) and Consultative Group (CG) centres showed that 44.3 per cent of the total germplasm received from CG centres followed by 42 per cent from USDA, other national genebanks contributed 8 per cent. Four per cent of the germplasm was from AVRDC, Taiwan; other private seed companies a meagre 1.7 per cent. If we consider only CG centres and other national genebanks (NGB), the share of NGB is 55.7 per cent. The major germplasm was introduced from USDA, USA. Apart from USA the major source countries were Australia, UK, Japan, Russia, Canada, Sri Lanka, Sweden, Switzerland and China. The data also indicates that national gene banks are major providers of millets, oilseeds, forages, vegetables and fruits, as CG centres do not maintain these crops. In cereals and grain legumes the germplasm received in the form of international nurseries/ trials which are received from CG centres are not included in this data; the indents placed are not considered. Germplasm of Indian origin which was repatriated from CG centres was also not included.

The details of some important introductions, for the information of the user scientists so that these valuable germplasm may be utilized in the ongoing crop improvement in the country, are presented in Table 1.

Table 1. Promising introduction made in different crops.

Crop	EC No.	Traits	Distribution
Germplasm resistant to biotic stress			
Oryza sp. (Rice)	EC 539103-10	Brown Plant Hopper resistant lines	Directorate of Rice Research,
	EC 539111-118	Bacterial blight resistant lines	Hyderabad,
	EC 539131-38	Tungro virus resistant lines	Andhra Pradesh
	IRRI, Philippines		
	EC 56738-39	Blast resistant lines	CRURRS Hazaribagh
	EC 546740	Brown Plant Hopper resistant lines	Jharkhand
	IRRI, Philippines		
Var MR 219,	EC 548000-001	Multiple disease resistant	Directorate of Rice Research,
MR 220	Malaysia		Hyderabad, Andhra Pradesh
	EC 549239	Sheath blight resistant	Tamil Nadu Agricultural University,
	IRRI, Philippines		Coimbatore, Tamil Nadu
Var. Boliviar	EC 550177	Resistant to blast, narrow brown	Directorate of Rice Research
	USA	leaf spot (*Cercospora janseana*)	Hyderabad, Andhra Pradesh
Var. Saber	EC 550175	Resistant to blast (*Pyricularia grisea*) and	Directorate of Rice Research,
	USA	sheath blight (*Rhizoctonia solani*), brown	Hyderabad, Andhra Pradesh
		leaf spot (*Cercospora janseana*) leaf smut	
		(*Entyloma oryzae*) and panicle blight	
Triticum aestivum	EC 538958	Resistant to stem rust	Directorate of Wheat Research,
(Wheat)	USA		Karnal, Haryana
Var. Bigsky			NBPGR, New Delhi
Var. Outlook	EC 541189	Resistant to wheat aphid (*Diuraphis noxia*)	Directorate of Wheat Research,
	USA	due to presence of resistance gene Dn4,	Karnal, Haryana
		stem rust (*Puccinia graminis*) and moderately	NBPGR, New Delhi
		resistant to stagonospora blotch	
		(*Stagonospora nodurum*)	
Var. Deloris	EC 552125	Resistant to dwarf bunt	Directorate of Wheat Research,
	USA	(*Tilletia controversa*)	Karnal, Haryana
			NBPGR, New Delhi
Var OK 101	EC 5438493	Resistant to wheat soil borne	Directorate of Wheat Research,
	USA	mosaic virus	Karnal, Haryana
			NBPGR, New Delhi
Var. Caledonia	EC 550175	Resistant to loose smut (*Ustilago tritci*),	Directorate of Wheat Research,
Var. Richland	EC 550176	USAwheat spindle streak Mosaic virus and	Karnal, Haryana
		soil borne wheat mosaic virus	NBPGR, New Delhi
GP 97L9521	EC 550180	Resistant to stem rust (*Puccinia graminis*)	Directorate of Wheat Research,
GP N 95 L 11881	EC 550181		Karnal, Haryana
	USA		NBPGR, New Delhi
Var. OK-102	EC 550632	Resistant to leaf rust (*Puccinia triticina*),	Directorate of Wheat Research,
	USA	tan spot (*Pyrenophiera tritici-repentis*)	Karnal, Haryana
		powdery mildew (*Blumeria graimines*) and	NBPGR, New Delhi
		wheat soil borne mosaic virus	
Zea mays (Maize)	EC 54687	Downey mildew resistant	Directorate of Maize Research,
	Indonesia		IARI, New Delhi
			NBPGR, New Delhi
Hordeum vulgare	EC 538157	Resistant to stripe rust, barley yellow	Directorate of Wheat Research,
(Barley)	USA	dwarf virus, leaf rust, powdery mildew	Karnal, Haryana
Var. UC 933		net blotch and scald	NBPGR, New Delhi
Var. UC 969	EC 538158USA	Resistant to barley yellow dwarf virus,	Directorate of Wheat Research,
		leaf rust, net blotch and scald	Karnal, Haryana
			NBPGR, New Delhi

Crop	EC No.	Traits	Distribution
Var. UC 960	EC 538159USA	Resistant to Barley Yellow Dwarf Yirus, leaf rust, Powdery Mildew, net blotch and scald	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Var. UC 937	EC 538160USA	Resistant to stripe rust, Barley Yellow Dwarf Virus, leaf rust, Powdery mildew, net blotch and scald	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Var. Vivan	EC 540807	Resistant to covered smut, false loose smut, common root rot	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Var. Niobe	EC 548499 Canada	Resistant to surface borne smuts, spot form of net blotch and scald	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Panicum miliaceum Var. Horizon	EC 552153USA	Resistant to russian wheat aphid (*Diuraphis noxia*), head rot associated with stem maggot (Meromyza sp.) and euopean corn borer (*Ostrinia nunbilalis*)	Project Coordinator (Small Millets), University of Agricultural Sciences, GKK, Bangalore
Glycine max (soybean) Var.Washita	EC 537946USA	Resistant to root knot nematodes (*Meloidogyne incognita*)	NRC soybean, Indore, Madhya Pradesh
Var. Catoosa	EC 537947USA	Resistant to soybean cyst nematode (*Heterodero glycines*) and root knot nematode (*Meloidogyne incognita*)	NRC soybean, Indore, Madhya Pradesh
	EC 538800	Rust resistant lines	NRC soybean, Indore, Madhya Pradesh
	EC 538829	Root knot nematode resistant	NRC soybean, Indore, Madhya Pradesh
	EC 538834	Resistant to soybean scab	NRC soybean, Indore, Madhya Pradesh
	EC 538841	Resistant to soybean cyst nematode	NRC soybean, Indore, Madhya Pradesh
GP- D98- 1216	EC539008	Resistant to phytophthora rot (*Phytophthora sojae*) and races 3 and 14 of soybean cyst nematode (SCN-*Heterodera glycines ichinohe*)	NRC soybean, Indore, Madhya Pradesh
Carthamus Tinctorius (Safflower)	EC 548822USA	Resistant to alternaria, pseudomonas bacterial blight and head rot	Directorate of Oilseeds Research, Hyderabad, Andhra Pradesh
	EC 548825-29USA	Resistant to verticillium wilt	Directorate of Oilseeds Research, Hyderabad, Andhra Pradesh
	EC 548830-46USA	Resistant to phytophthora root rot	Directorate of Oilseeds Research, Hyderabad, Andhra Pradesh
	EC 548847-48USA	Resistant to verticillium wilt, striped hull	Directorate of Oilseeds Research, Hyderabad, Andhra Pradesh
	EC 548849USA	Thrip resistant line	Directorate of Oilseeds Research, Hyderabad, Andhra Pradesh
Linum Usitatissimum (Linseed)	*EC 541217-223* EC 541218, 541226 Russia	Rust resistant Fusarium wilt resistant	Project Coordinator (Linseed), AICRP, CSUAT, Kanpur NBPGR, New Delhi
Cicer arietinum (Chickpea)	EC 539009 Spain	Resistant to Ascochyta blight (*Ascochyta rabie*)	Indian Institute of Pulses Research, Kanpur, Uttar Pradesh Genetics Division, IARI, New Delhi
Cicer echinospermum (Wild chickpea)	EC 539329 ICARDA, Syria	Resistant to Fusarium wilt	Indian Institute of Pulses Research, Kanpur, Uttar Pradesh

Crop	EC No.	Traits	Distribution
Cicer bijugum (Wild chickpea)	EC 541549-50 ICARDA, Syria	Resistant to leaf minor, bruchids and ascochyta blight	Punjab Agricultural University, Ludhiana Indian Institute of Pulses Research, Kanpur
Cicer Echinospermum (Wild chickpea)	EC 541555-556 ICARDA, Syria	Fusarium wilt resistant	Punjab Agricultural University, Ludhiana Indian Institute of Pulses Research, Kanpur
Cicer judaicum (Wild chickpea)	EC 541557-558 ICARDA, Syria	Resistant to leaf minor, bruchids and ascochyta blight	Punjab Agricultural University, Ludhiana Indian Institute of Pulses Research, Kanpur
Cicer pinnatifidum (Wild chickpea)	EC 541559 ICARDA, Syria	Fusarium wilt resistant	Punjab Agricultural University, Ludhiana Indian Institute of Pulses Research, Kanpur
Cicer judaicum (Wild chickpea)	EC 541561-62 ICARDA, Syria	Resistant to bruchids and cyst nematode	Punjab Agricultural University, Ludhiana Indian Institute of Pulses Research, Kanpur
Phaseolus vulgaris (French bean) Var. AC Pintoba	EC 537955Canada	Resistant to Bean Common Mosaic Virus (BCMV) and Fusarium wilt (*Fusarium oxysporum*)	NBPGR Regional Station, Shimla
Var. ORCA	EC 538843USA	Dominant I gene for for resistance to Bean Common Mosaic Virus (BCMV), Curly Top Virus (CTV), root rot complex caused by *Fusarium solanii*, *Rhizoctonia solani* and *Pythium* sp.	NBPGR Regional Station, Shimla
GP-USPT-Ant-1	EC 539010USA	Resistant to rust race-53, endemic to Michigan which infers presence of the UR-3 rust resistance gene and hypersensitive necrosis response to the NL-3 strain which infers presence of the I gene for resistance to BCMV	NBPGR Regional Station, Shimla
Var. EMGOPA 201-OURO	EC 541908Brazil	Resistant to Bean Common Mosaic virus (BCMV), Poty virus and angular leaf spot (*Phaeoidariopsis griseola*)	NBPGR Regional Station, Shimla
	EC 540793-794 CIAT, Columbia	Resistant to angular leaf spot, caused by *Phaeoidariopsis griseola* and anthracnose (*Colletotrichum lendemothionum* and resistant to BCMV)	NBPGR Regional Station, Shimla
Pisum sativum (Pea)Var. Accord.	EC 538177USA	Resistant to fusarium wilt race 1, 2 and 5	Indian Institute of Horticultural Research, Bangalore, Karnataka
Var. Barok	EC 538178USA	Resistant to fusarium wilt race 1, 2 and 5	Indian Institute of Horticultural Research, Bangalore, Karnataka
Var. Bridger.	EC 538179USA	Resistant to common pea mosaic virus and common wilt virus	Indian Institute of Horticultural Research, Bangalore, Karnataka
Var. Duke	EC 538180USA	Resistant to fusarium race-1, powdery mildew and common pea mosaic virus	Indian Institute of Horticultural Research, Bangalore, Karnataka
Var. Early frosty	EC 538181USA	Resistant to fusarium wilt, yellow bean mosaic virus	Indian Institute of Horticultural Research, Bangalore, Karnataka

Crop	EC No.	Traits	Distribution
Cucumis melo (Musk melon) Var. TGR 1551	EC 541901Spain	Resistant cucumber mosaic virus	Punjab Agricultural University, Ludhiana Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Cucumis melo ssp. melo (Muskmelon)	EC 539195-219USA	Tolerant to cucumber mosaic virus (CMV) and fusarium wilt	Punjab Agricultural University, Ludhiana Indian Institute of Vegetable Research, Varanasi
Lycopersicon esculentum (Tomato)	EC 538398-400 AVRDC, Taiwan	Resistant to bacterial wilt, tobacco mosaic virus	Indian Institute of Vegetable Research, Varanasi NBPGR, New Delhi
Lycopersicon esculentum Tomato	EC 538415-16 AVRDC, Taiwan	Resistant to white fly transmitted gemini virus (WTG) bacterial wilt (BW), tobacco mosaic virus (TMV), Fusarium wilt race 1 (F1)	Indian Institute of Vegetable Research, Varanasi NBPGR, New Delhi
Lycopersicon esculentum Tomato	EC 538429-31 AVRDC, Taiwan	Fruit worm resistant lines	Indian Institute of Vegetable Research, Varanasi NBPGR, New Delhi
	EC 538432-435 AVRDC, Taiwan	Resistant to Bacterial wilt, (BW) tobacco mosaic virus (TMV), leaf blight (LB) and fusarium wilt	Indian Institute of Vegetable Research, Varanasi NBPGR, New Delhi
	EC 552129-2137 AVRDC, Taiwan	Resistant to white fly transmitted gemini virus conditioned by TY-2 gene, bacterial wilt, fusarium wilt race 1	Indian Institute of Vegetable Research, Varanasi NBPGR, New Delhi
	EC 552143-2148 AVRDC, Taiwan	Resistant to tomato mosaic virus conditioned by the TM 2a allele	Indian Institute of Vegetable Research, VaranasiNBPGR, New Delhi
	EC 542063 AVRDC, Taiwan	Homozgous for SW-Sallele resistant to tomato spotted wilt virus	Southern Petrochemicals Industries Corporation, Hosur, Karnataka
	EC 542064 AVRDC, Taiwan	White fly-transmitted gemini virus conditioned by TY-2 gene from H 24 (WTG), Bacterial wilt (BW), tobacco mosaic virus conditioned by the TM29 allele (TMV), fusarium wilt race 1 (F1), gray leaf spot pathogen (*Stemphyllium* sp.)	Southern Petrochemicals Industries Corporation, Hosur, Karnataka
	EC 548605-13 AVRDC, Taiwan	Resistant to white fly transmitted gemini virus conditioned by the Ty-2 gene from H 24 (WTG), bacterial wilt, tomato mosaic virus conditioned by the TM2a allele (TMV), gray leaf spot pathogen (*Stemphyllium* sp.) and fusarium wilt race 1 (F1)	Horticultural College and Research Institute Periyakulam, Kerala
Capsicum sp.	EC 538331-32 AVRDC, Taiwan	Resistant to anthracnose, tolerant to aphids	Indian Institute of Vegetable Research, VaranasiNBPGR, New Delhi
	EC 538333-34, 538351 AVRDC, Taiwan	Resistant to bacterial wilt, bacterial black spot and potato virus Y	Indian Institute of Vegetable Research, Varanasi NBPGR, New Delhi
	EC 538335-339 AVRDC, Taiwan	Resistant to pepper venial mottle virus (PVMV), Chilli veinal mottle virus (CVMV), Potato virus Y (PVY) and potato virus V (PVV)	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Solanum melongena (brinjal)	EC 550890 Philippines	Tolerant to fruit and shoot borer, resistant to bacterial wilt and leaf hoppers	MAHYCO Life Sciences Research Centre, Maharashtra

Crop	EC No.	Traits	Distribution
Germplasm resistant to abiotic stress			
Oryza sp. (Rice)	EC 39139-44IRRI, Philippines	Iron toxicity tolerant lines	Directorate of Rice Research, Hyderabad, Andhra Pradesh
	EC 541909-916 EC 541917-928 EC 541929-939 IRRI, Philippines	Submergence tolerant lines Salinity tolerant lines Zinc deficiency tolerant lines	Narendra Dev University of Agriculture and Technology, Faizabad, Uttar Pradesh
	EC 546319-340 EC 546341-50,52, 53,56,57,59 EC 546354,60,61 IRRI, Philippines	Phosphorus deficiency tolerant lines Iron toxicity tolerant lines Aluminium toxicity tolerant lines	Indira Gandhi Agricultural University Raipur, Chattisgarh
	EC 548158-81 IRRI, Philippines	Salinity tolerant lines	Anbil Dharmlingam Agricultural College and Research Institute, Tamil Nadu
	EC 550863-71 EC 550872-81	Restorer lines TGMS lines	Sympenta India Ltd. Pune, Maharashtra
Triticum aestivum (Wheat)	EC 538234-35 EC 538236-56 EC548493 EC 550180,181USA	Salinity tolerant lines Salinity tolerant lines Acidic soil tolerant Lodging resistant	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Zea mays (Maize)	EC 552705-08 CIAT, Columbia	Acid soil tolerant	Directorate of Maize Research, IARI, New Delhi
Hordeum vulgare (Barley) Var. Vivan	EC 540807 Canada	Drought tolerant	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Panicuin miliaceum Var. NE-1	EC 552154 USA	Lodging tolerant	Project Coordinator (Small Millets), University of Agricultural Sciences, GKK, Bangalore
Glycine max (Soybean)	EC 537946 EC 538805, 538811-12 EC 538823-30 USA	Lodging tolerant Drought tolerant lines Drought and heat tolerant lines	NRC Soybean Indore
Linum usitatissimum (Linseed)	EC 541198 EC 541204 EC 541206 Russia	Lodging resistant	Project Coordinator (Linseed), AICRP, CSUAT, Kanpur NBPGR, New Delhi
Pisum sp. (Pea)	EC 548807-13 Russia	Genotypes with stiff stem, lodging resistance	Project Coordinator (MULLaRP), Indian Institute of Pulses Research, Kanpur, Uttar Pradesh
Gossypium Hirsutum (Cotton)	EC 541867-76 USA	Upland cotton resistant to adverse conditions	Central Instutute for Cotton Research, Nagpur, Maharashtra
Lycopersicon esculentum (Tomato)	EC 538417-28 AVRDC, Taiwan	Heat tolerant lines	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
	EC 550834, 836. Srilanka		
Brassica oleracea var *botrytis* (Cauliflower)	EC 548146-49 USA	Cold tolerant lines	Indian Institute of Horticultural Research, Bangalore, Karnataka

Crop	EC No.	Traits	Distribution
Traits for Value Addition			
Oryza sativa (Rice) GP KBNT Lpa 1-1	EC 552817 USA	Low phytic acid (39%)	Directorate of Rice Research, Hyderabad
GP GLPA	EC 552822 USA	Gold hull, low phytic acid germplasm	Directorate of Rice Research, Hyderabad
	EC 546247-79	New Plant Types	Central Rice Research Institute, Cuttack
	EC 541940-972 EC540540-781	New plant types (reduced number of litters, all tillers are fertile, increased no. of grains per panicle and larger parcels size)	Syngenta India Ltd, Pune, Maharashtra
	EC 541907 IRRI, Philippines	High iron content	Indira Gandhi Agricultural University, Raipur, Chattisgarh
	EC 549244 IRRI, Philippines	Iron rich line	Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu
GP Aromatic se.	EC 550889 USA	Good aroma and cooking quality of Basmati 370	Directorate of Rice Research, Hyderabad
Var. Boliviar Var. Saber	EC 550177 EC 550178 USA	Long grained, superior parboiling and canning quality	Directorate of Rice Research, Hyderabad
Triticum astivum (wheat) Var. Big sky	EC 538958 USA	High grain protein content Var. Nusky	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
	EC 538959 USA	Excellent and use qualities for bread and noodle production	Directorate of Wheat Research, Karnal NBPGR, New Delhi
GP 97L9521 GP N 95 L11 881	EC 550180 EC 550181 USA	Strong gluten	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Zea mays (Maize)	EC 539005-007 USA	High amylose content, high lysine content and waxy germplasm	Directorate Maize Research , IARI, New DelhiNBPGR, New Delhi
Sorghum bicolor (Sorghum)	EC 538162-76 USA	Sweet types	Punjab Agricultural University, Ludhiana, Punjab NRC Sorghum
Glycine max (Soybean)	EC 538824 USA	Low lipoxygenase	NRC Soybean, Indore, Madhya Pradesh
	EC 538833 USA	Less than 5.5% linoleric acid	NRC Soybean, Indore, Madhya Pradesh
Carthamus tinctorius (Safflower)	EC548814-15, 548818-21 USA	High oleic acid content lines	Directorate of Oilseeds Research, Hyderabad, Andhra Pradesh
	EC548816-17, 548833-36USA	High oil content	Directorate of Oilseeds Research, Hyderabad, Andhra Pradesh
Lens culinaris (Lentil)Var. Merit	EC 550084 USA	Large seeded	PC (MULLaRP), IIPR Genetics Division, IARI, New Delhi NBPGR, New Delhi
Capsicum annuum (Pepper)	EC 538330 AVRDC, Taiwan	Cayenne type large thick red	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Cucumis melo ssp. Melo (musk melon)	EC 539195-9219 USA	High TSS content, orange fleshed, netted exterior	Punjab Agricultural University, Ludhiana, Punjab Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh

Crop	EC No.	Traits	Distribution
Other Agronomic Traits			
Oryza sativa (Rice) GP LGRU ef	EC 552825 USA	Early flowering	Directorate of Rice Research, Hyderabad
GP Aromatic se	EC 550889 USA	Early maturing	Directorate of Rice Research, Hyderabad
	EC 546752-71 IRRI, Philippines	Weed competitive lines	CRURRS, Hazaribagh, Jharkhand
Var. Boliviar	EC 550177	Early maturing	Directorate of Rice Research,
Var. Saber	EC 550178 USA	Early maturing	Hyderabad, Andhra Pradesh
Triticum aestivum (Wheat)	EC 537952-54 USA	High yielding	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Var. Big sky	EC 538958 USA	High yielding	Directorate of Wheat Research, Karnal,
Var. Nusky	EC 538959 USA	Superior adaptation	Haryana
Var. Caledonia	EC 550175 USA	High yielding	NBPGR, New Delhi
Var. Richland	EC 550176 USA	High yielding	
Var. Deloris	EC 550180,181 EC 552125USA	High grain yielding (3554 kg/ha) High yielding	Directorate of Wheat Research, Karnal, Haryana NBPGR, New Delhi
Zea mays (Maize)	EC 546871 Indonesia	Early maturing	Directorate of Maize Research, IARI, New Delhi NBPGR, New Delhi
Hordeum vulgare (Barley)			
Var. UC-933	EC 538157	Early maturing	Directorate of Wheat Research, Karnal,
Var. UC-969	EC 538158	Early maturing	Haryana
Var. UC-937	EC 538160	High yielding	NBPGR, New Delhi
Var. Vivan	EC 540807	High grain yielding and shattering resistant	Directorate of Wheat Research, Karnal,
Var. Niobe	EC 548499 Canada	High yielding and early maturing	Haryana NBPGR, New Delhi
Panicum miliaceum (Proso millet)			
Var. Horizon	EC 552153	Broadly adapted	Project Coordinator (Small Millets),
Var. NE-1	EC 552154 USA	High yielding	University of Agricultural Sciences, GKK, Bangalore
Cicer arietinum (Chickpea)	EC 539009 Spain	Early flowering	Indian Institute of Pulses Research, Kanpur, Uttar Pradesh Genetics Division, IARI, New Delhi
Elymus haffmanii GP RS-H	EC 538230 USA	High yielding	IGFRI, Jhansi NBPGR, Reg. Stn. Bhowali
Glycine max (Soybean)			
Var Washita	EC 537946	High yielding resistant to shattering	NRC, Soybean Indore
Var. catoosa	EC 537947 USA	High yielding	
Lycopersicon esculentum (Tomato)	EC 538398-400 AVRDC, Taiwan	Early maturing	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh

Crop	EC No.	Traits	Distribution
Linum usitatissimum (Linseed)	EC 541202 EC 541226 Russia	Early maturing	PC (Linseed), AICRP, CSAUAT, Kanpur NBPGR, New Delhi
Phaseolus vulgaris French bean Var. EMGOPA 201-OURO	EC 541908 Brazil	High yielding excellent cooking qualities	NBPGR, RS, .Shimla
Lens culinaris (Lentil) Var. Merit	EC 550084 USA	High yielding	PC MULLaRP, IIPR, Kanpur Genetics Division, IARI, New Delhi
Vicia faba Var. UN 56	EC 550179 Spain	Unifoliate genetic stock significantly higher branching from basal nodes	IIPR, Kanpur
Lines for heterosis exploitation			
Oryza sativa (Rice)	EC 546287-318 EC 546362-73 IRRI, Philippines	Monogenic lines Introgression lines	Indira Gandhi Agricultural University, Raipur, Madhya Pradesh
	EC 546374-87 EC 546388-487 EC 546488-90 IRRI, Philippines	CMS and maintainers RestorersTGMS lines	Maharastra Hybrids Seeds Co. Ltd, Andhra Pradesh
	EC 539085-94 EC 539095-02 IRRI, Philippines	Isogenic linesPyramided lines	Directorate of Rice Research, Hyderabad, Andhra Pradesh
	EC 546243-6246 IRRI, Philippines	Mutant lines	Centre for Plant Molecular Biology Tamil Nadu Agricultural University, Tamil Nadu
	EC 550863-71 EC550872-81 IRRI, Philippines	Restorer lines and TGMS lines	Syngenta India Ltd., Pune, Maharashtra
	EC 552826-856 IRRI, Philippines	CMS, Maintainer, TGMS and Restorer lines	Directorate of Rice Research, Hyderabad
	EC 541514-517 EC 541518-31 IRRI, Philippines	TGMS linesRestorer lines	Nuzi veedu Seeds Ltd. Secunderabad, AP
	EC 546232-6242 IRRI, Philippines	Introgression lines	Centre for Plant Biology NAU
	EC 1973-542056 IRRI Philippines	Introgression lines	Department of Plant Molecular Biology, PAU, Ludhiana
Sorghum bicolor (sorghum)	EC 538941-46 EC 558947-55 USA	Maintainers of the A1, cytoplasmic genetic male sterility system Restorers of the A1, cytoplasmic genetic male sterility system	NRC Sorghum, Hyderabad, Andhra Pradesh
Lycopersicon esculentum	EC 550834, 836 Sri Lanka	Heat tolerant	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Brassica oleracea var. *botrytis* (Tomato)	EC 548146-56 EC 548157 USA	CMS Lines Male fertile line	Indian Institute of Horticultural Research, Bangalore, Karnataka

Crop	EC No.	Traits	Distribution
New Crops			
Monarada sp.	EC 538844 Canada	Dwarf type, good writer hardiness and resistant to powdery mildew	Division of Floriculture and landscaping, IARI, New Delhi
Brachiaria hybrid Cv. Mulato	EC 549024-25 USA	Stoloniferous growth, excellent forage production, vigorous regrowth excellent palatability, resists burning and drought, tolerant to spilt be bug and produces forage round the year	IGFRI RRS, UAS Campus Dharwad, Karnataka.

The NBPGR is continuing its efforts to identify promising germplasm through literature search and personal contacts; and to introduce the same for utilization by Indian plant breeders.

Evaluation of Okra Germplasm for Fruit Yield, Quality and Field Resistance to Yellow Vein Mosaic Virus

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Field experiments were conducted with 941 indigenous and exotic germplasm of okra [*Abelmoschus esculentus* (L.) Moench] at the Regional station of National Bureau of Plant Genetic Resources, Thrissur, Kerala from 1999-2001 to identify high yielding okra germplasm coupled with acceptable fruit quality and field resistance to yellow vein mosaic virus (*YVMV*). During the preliminary germplasm evaluation, 62 high yielding accessions were identified and were subjected to further evaluation in order to confirm the stability of desired traits for which they were selected. As regard to fruit yield per plant, indigenous accession IC 265147 collected from Thrissur district of Kerala performed better than all others did. Fruit colour, pubescence, shape, thickness, mucilage content and taste of fruits were considered together for assessing fruit quality. Based on 1 to 9 point quality score chart the accessions were grouped into four quality groups viz. low, medium, good and excellent. Accessions IC 43735, 43736, 43720, 128088, 39137A, 111500 and 265147 recorded high fruit yield per plant coupled with better fruit quality hence qualifying themselves for entry into breeding programme. Screening of these germplasm for *YVMV* field resistance under natural epiphytotic condition revealed that none of the accession was 'immune' or 'highly resistant,' 43 were 'moderately resistant', three accessions viz., IC 218887, IC 69286 and EC 305619 were 'resistant' and the rest were susceptible. The results also revealed that none of the yellow vein mosaic virus disease resistant accessions were exceptionally high yielding or *vice versa.*

Key Words: *Abelmoschus esculentus*, Field resistance, Fruit quality, Okra, Yield, *YVMV*

Among the diseases of okra [*Abelmoschus esculentus* (L.) Moench], bhendi yellow vein mosaic bigeminivirus (*YVMV*) happens to be the most devastating one. This disease considerably reduces fruit yield and fruit quality (Bhagabati *et al.*, 1998). Since cultivation of disease resistant lines is more economical and environmentally safe, screening germplasm for inbuilt resistance coupled with high yield and acceptable fruit quality becomes imperative. Many workers (Sharma and Sharma, 1984; Salehuzzaman, 1985; Bisht *et al.*, 1988; Arora *et al.*, 1992) have screened okra germplasm and have reported the presence of genotypic differences for *YVMV* field resistance. The National Bureau of Plant Genetic Resources has also screened as many as 1400 indigenous and exotic okra germplasm for field resistance to *YVMV* (Thomas *et al.*, 1990 & 1991; Bisht *et al.*, 1993). Wherever resistant source to *YVMV* have been identified, it could not be directly exploited due to their poor yield or other undesirable characters associated with resistance. It is, therefore, necessary to screen genetically divergent germplasm to identify high yielding okra lines that posses not only resistance to the virus but also bear quality fruits. The present study was planned and conducted in this direction.

The experiments were carried out in a phased manner at the Regional Station of National Bureau of Plant Genetic Resources, Thrissur, Kerala from 1999-2001. In a preliminary study on characterisation and evaluation involving 941 okra accessions raised in augmented design, 62 lines exhibiting high fruit yield (over the check, yielding 7.60 fruits/plant), fruit quality and field resistance to *YVMV* were selected. During 2001, these accessions were evaluated in a completely randomized block design in two replications, under natural epiphytotic condition, to screen them for field resistance to *YVMV* and assess their fruit yield and quality. One row of susceptible check (IC 248257) was raised at every fifth row among the lines of test genotypes to ensure generation of adequate virus inoculums and insect vector in order to promote better chance of infection. Observation on fruit yield per plant, fruit quality and field resistance to *YVMV* were recorded.

For assessing physical fruit quality, freshly harvested tender fruits from each accession were taken and based on fruit colour, pubescence, shape, thickness, mucilage and taste comparative quality score were recorded in 1 to 9 point scale. The accessions were then grouped into four classes of fruit quality namely, low (score 1 to 3), average (4 to 5), good (6 to 7) and excellent (8 to 9).

YVMV disease severity was scored using 0 to 5 point scale. Based on the score, percent disease severity (PDS) and percent disease incidence (PDI) was calculated. From

PDS & PDI, coefficient of infection (CI) was arrived (Deo *et al.*, 2000). Based on CI, the accessions were categorized into six groups viz., 'highly resistant' (CI = 0 to 5),' resistant' (5 to 10), 'moderately resistant' (10 to 20), 'moderately susceptible' (20 to 40), 'susceptible' (40 to 70) and 'highly susceptible' (70 to 100).

Analysis of variance among 62 lines for fruit yield, fruit quality and coefficient of infection for *YVMV* indicated significant differences due to genotypes (Table 1), hence substantial variability in the germplasm collection for these traits exist. Fruit yield varied from 3.63 fruits/plant in IC 248257 to 17.50 fruits/plant in IC 265147. Twenty-three accessions recorded significantly higher yield as compared to check variety (Table 2). IC 265147, a collection from Thrissur district of Kerala, outperformed all others for number of fruits per plant followed by IC 39137-A, IC 43750-B and IC 43720. Fruit quality of these accessions was good. Four accessions viz., IC Nos. 128088, 140926, 43720 and EC 329422 showed better vigour with few fruit bearing branches. In homestead cultivation, with unlimited input supply, these accessions may serve as ideal genotypes.

From 941 active germplasm accessions, eleven accessions bearing more palatable and sweet fruits were identified. On further testing, most of them were found susceptible to red ant; black ant and fruit rot (*Choanephora cucurbitarum*). However, three exotic collections viz., EC 329424, EC 329361, EC 329359 remained free from fruit rot infection. Two accessions IC 140907 and IC 282252 had long fruits (> 25 cm) with less mucilage and slow fibre formation. Therefore, delay in harvest for one or two days may not affect the fruit quality drastically. However, these two accessions secured minimum fruit quality score due to their unattractive yellowish fruit colour. In North India, where short fruits are preferred IC 43736 may serve as the best choice.

Table1. ANOVA for number of fruits per plant, fruit quality scoring index (FQSI) and coefficient of infection (CI) for *YVMV* in 63 okra germplasm accessions

Source of Variation	Degrees of freedom	Mean squares		
		No. of fruits/plant	FQSI	CI
Replication	1	1.63	3.84	405414.93 *
Treatment	62	8.35 **	6.69 **	100698.31 **
Error	62	1.61	1.76	10110.98

*, ** refers to significant at P= 0.05 and 0.01 respectively.

Table 2. Merits and demerits associated with 24 (out of 63) selected high yielding okra germplasm

Sl. No.	IC / EC Nos.	Fruit No/ plant	Fruit quality score	Desirable features	Undesirable features
1	IC 33332	9.22	5.67	Early flowering	Poor keeping quality
2	IC 43720	10.26	5.33	Suitable for kitchen garden	Fruit quality and susceptible to YVMV
3	IC 43750 B	10.19	7.00	Earliness	-
4	IC 43735	9.65	8.67	Earliness and quality fruits	-
5	IC 43736	9.73	3.67	Short fruit	-
6	IC 43741	7.60	7.00	Fruit quality	-
7	IC 45799	8.63	1.33	-	Hairy fruits and susceptible to YVMV
8	IC 282236	7.69	6.00	Earliness	-
9	IC 282241	9.16	6.67	-	Susceptible to fruit rot
10	IC 128076	7.81	6.67	-	-
11	IC 128088	8.10	4.67	Branched, suitable for kitchen garden	-
12	EC 329422	9.57	5.33	Branched, suitable for kitchen garden	Susceptible to YVMV
13	IC 282268	8.11	6.00	Attractive fruits	Susceptible to fruit rot
14	EC 169331	8.32	7.33	Long slender fruits	-
15	IC 34190	9.05	7.00	-	-
16	IC 34190 A	8.32	7.00	Earliness	Twisted fruits and susceptible to fruit rot
17	IC 39137 A	10.10	6.00	Dark green fruits	-
18	IC 42485 B	8.93	6.67	Early	-
19	IC 90251	8.07	8.00	-	Susceptible to YVMV and fruit borer
20	IC 111488	8.87	5.00	-	-
21	IC 111500	9.64	5.67	Ideal plant type	Light green fruits
22	IC 265648	8.50	2.33	-	Photosensitive
23	IC 265147	17.50	8.00	-	-
24	IC 218895	8.24	7.67	Long fruits	Spiny fruits and susceptible to YVMV
Check (Pusa Sawani)		**7.60**	**6.67**		
Grand mean for 63 accessions		**7.42**	**5.87**		
CD	**2.60**	**0.37**			
CV (%)	**17.26**	**22.59**			

Another indigenous collection IC 218887 exhibited deep purple fruit with high quality score. However, it remained poor yielder throughout the study period. Pubescence on fruits varied from downy to prickly. Introgressed hybrid derivative (naturalized) between *Abelmoschus manihot* ssp. *tetraphyllus* (L.) and *A. esculentus*, namely IC 43745, IC 45799 and EC 305745 had spiny fruits which were difficult to harvest and not consumable.

The study also indicates that more than 50 per cent of the accessions identified for high yield were associated with undesirable traits like poor fruit quality, susceptibility to *YVMV*, fruit rot, etc. Only few accessions *viz.*, IC Nos. 43735, 43736, 43720, 128088, 39137A, 111500 and 265147 possessed good quality fruits with high yield hence, recommended for inclusion in okra improvement programme.

Reaction of 62 germplasm accessions and check variety Pusa Sawani to *YVMV* is presented in Table 3. The result showed that the virus infected all accessions under study. However, the degree of severity varied from accession to accession. None of the germplasm accession was 'immune' or 'highly resistant' to this disease. Nath *et al.* (1999) also reported that no cultivated variety is immune to this disease. Based on coefficient of infection, three accessions viz., IC 218887, IC 69286 and EC 305619 were grouped under 'resistant' category, 43 under 'moderately resistant', five as 'moderately susceptible' and 12 as 'highly susceptible' categories. Of the three accessions under field resistance category, one (IC 218887) was a poor yielder and the other two (IC 69286 and EC 305619) had poor fruit quality.

To sum up, none of the indigenous and exotic germplasm of *A. esculentus* was 'immune' or 'highly resistant' to *YVMV* under field condition. Even germplasm exhibiting moderate degree of field resistance to *YVMV* did not record high yield or bear quality fruits. Under such circumstances, screening of lines showing field resistance to *YVMV* with high yield and quality in the cultivated species may not yield the desired results whereas that for lines having any one of these quality appears to be a rational approach in order to introgress the desired genes. Perhaps, transfer of gene(s) for resistance available from related wild species to the high yielding cultivars with better fruit qualities may be rewarding as reported by Nerkar and Jambhale (1985).

Table 3. Grouping of okra genotypes based on their field resistance to YVMV

S.No.	IC / EC Nos.	CI	Resistant category
1	IC 69286	5.6	Resistant
2	IC 218887	7.2	Resistant
3	EC 305619	7.2	Resistant
1	IC 43720	70	Highly susceptible
2	IC 45799	74	Highly susceptible
3	IC 218894	72	Highly susceptible
4	IC 282240	70	Highly susceptible
5	EC 329359	88	Highly susceptible
6	EC 329422	76	Highly susceptible
7	IC 90234	100	Highly susceptible
8	IC 90251	73	Highly susceptible
9	IC 93777	73	Highly susceptible
10	IC 282270	71	Highly susceptible
11	IC 248257	100	Highly susceptible
12	IC 265626	71	Highly susceptible
1	IC 282252	21.60	Moderately susceptible
2	IC 90230	22.40	Moderately susceptible
3	IC 265648	23.00	Moderately susceptible
4	IC 140906	22.40	Moderately susceptible
5	IC 18540	23.50	Moderately susceptible
1-43	IC Nos.-33340, 128076, 45803, 113904, 282241, 218889, 882272, 128072, 128088, 282268, 169331, 34190, 39137-A, 52322, 90295, 99724, 111488, 111500, 111507, 117221-A, 117308, 256154, 265147, 43741, 43744, 43750, 33332, 43733, 43735, 43736, 782236, 15435, 34190-A, 42485-B, 429424, 329361, 282285, 218870, 140926, 140907, 182232, and Pusa Sawani	10-19.5	Moderately resistant

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SHORT COMMUNICATION

Comparison of the Storage Potential of French bean (*Phaseolus vulgaris* L.) and Cowpea (*Vigna unguiculata* L walp) Genotypes after Natural and Artificial Ageing

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Variation in the longevity of French bean and cowpea seeds under ambient (20-43°C) and accelerated ageing conditions were studied in ten French bean and five cowpea lines differing in seed size and seed coat colour. Significant differences in the storability among the genotypes, storage periods and the interaction genotype and storage periods were observed. Germination%age in the various French bean genotypes ranged from 0-67 % after 15 months of storage under ambient conditions and by 30 months most genotypes were dead. In cowpea all genotypes, except IC 45409, retained germination values ranging from 66 to 96% after 3 years of storage under ambient conditions. Seed germination after accelerated aging was positively correlated with that after natural ageing under ambient conditions and negatively with seed weight. Under ambient storage conditions French beans are poor storers as compared to cowpeas.

Key Words: Accelerated ageing, Cowpea, French bean, Longevity, Natural ageing.

French bean (*Phaseolus vulgaris* L.) and cowpea (*Vigna unguiculata* L. Walp) are important grain legumes of India. These are used both as pulses and green vegetables. While cowpeas are recognized as distinctly tropical in adaptation, common beans are better adapted to sub-tropical or temperate climate.

Ageing during storage is a major cause of poor seed quality, particularly in tropical countries where high relative humidity of storage leads to an increase in seed moisture content. This combined with high ambient temperature results in rapid seed deterioration leading to a decline in seed vigour and ultimately reduced germination. Information related to the optimal storage conditions and periods for the safe storage of French bean and cowpea seeds is scant. Variable periods of longevity under different ambient conditions have been reported (Paiva *et al.*, 1972, Vieira and Fonseca, 1986; Aguirre and Peske, 1991). Pandey (1989) observed a decline in vigour and viability of French bean after second year of storage at 24-32^0 C and 10.0± 0.8% moisture content. Under the subtropical climatic conditions of Brazil, French bean seeds with 12-14% moisture content could maintain over 80% germination for 2 years (Aguirre and Peske, 1991). Planning for the safe storage of seeds can be efficiently done if information on relative storability of genotypes is also available. Further, for a rational improvement of seed storability and vigour, knowledge of the variability present in the germplasm and the inter-relationships among various seed characteristics is also important. However, relatively few storage studies have evaluated differences among genotypes in French bean and cowpea (Aguirre and Peske, 1991).

The objective of the present work was to study the variability between French bean and cowpea genotypes with respect to seed storability and the inter-relationship with some seed characteristics.

Seeds of ten French bean and five cowpea genotypes grown and harvested at Bhowali and Thrissur respectively, in 1995, were used for the experiment starting in the same year. These were selected for differences in their seed weights and seed coat colors. The details of accessions are given in Table 1. The initial seed moisture content was 8.7-10.3%. Seed moisture content was determined by drying ground seeds for one hour at 130°C, and was expressed on dry weight basis (ISTA 1985). Seeds were stored in paper envelops at ambient temperature (20-43°C) and in laminated aluminum foil packets at 5^{0}C. At 5°C seed moisture was 7.5-8.0% for all seed lots. Seed moisture during unsealed storage at ambient temperature varied from 8.4 -10.7% in French bean and 7.0-10.3% in cowpea. One lot of each genotype was accelerated aged at 42°C and 100% RH for 4 days.

Germination and vigour of seeds stored at ambient temperature was evaluated at periodic interval of 5 months in French bean and 6 months in cowpea and only once in 3 years for seed stored at 5°C. For the accelerated aged lots, germination was done once at the end of ageing period. Germination test was conducted following the ISTA guidelines (ISTA, 1985). Three replicates were used with 100 seeds in each replicate. Vigour was measured

Table 1. Initial germination and other seed characteristics of french bean and cowpea genotypes

Accession no.	Initial seed germination (%)	Germination after accelerated ageing (AA) %	MC after AA%	Wt increase after imbibition (%)	100 Seed weight (G)	Germination after ambient storage (%)	Germination after 3 years of storage at 5°C (%)	EC umhos/cm/ gdw	Seed coat colour
French bean						**After 15 months**			
IC 16903	91	8	23.3	21.2	41.6	16	90	0.336	Violet
IC 37846	100	18	18.7	9.8	21.5	58	100	0.342	Fawn
IC 84548	90	2	21.6	17.6	33.2	0	90	0.257	White specks on purple
IC 84549	92	6	19.0	23.1	34.2	0	90	0.393	White specks on purple
IC 84564	95	33	19.5	8.4	19.8	67	94	0.291	Fawn
IC 145918	100	10	18.2	6.2	21.7	22	98	0.238	Black
IC145919	99	24	18.4	7.4	22.5	62	98	0.253	Black
IC 145923	95	0	23.2	19.0	29.0	0	95	0.692	Yellowish brown
IC 145924	90	6	22.6	20.4	30.0	4	92	0.892	Orange
IC 196464	99	4	23.2	12.6	36.0	40	98	0.376	Violet mottled
Cowpea						**After 3 years**			
IC32865	98	75	19.5	9.40	6.67	66	96	0.309	White
IC44646	96	77	18.6	7.6	6.05	82	95	0.234	Black
IC44723	94	89	17.8	8.4	8.76	96	92	0.264	Red
IC44792	96	86	17.5	8.3	7.93	94	96	0.243	Black
IC45368A	98	64	20.4	12.0	9.63	82	98	0.247	Red
IC45409	98	14	23.2	12.5	10.00	16	98	0.324	White

as radical length of 20 seeds at 25°C after 120 hours. Electrical conductivity of leakage from seeds was measured for three replicates of 10 seeds each placed overnight in 25 ml of distilled water at 20°C. Rate of water uptake was measured by immersing 10 seeds in 10 ml of distilled water at 25°C. Seeds were removed from water after 8 hours, blotted dry and weighed. Changes in weight due to imbibition were expressed in terms of% weight increase as compared to air-dry weight of seeds. For studying the storability of ten French bean and five cowpea genotypes over seven storage periods, the design adopted was Factorial Completely Randomized Design with three replicates for each of the crops.

The initial germination of various genotypes varied from 90-100% and the 100 seed weight varied from 19.8 to 41.6 g in French bean and 6.0 to 10.0 g in cowpea (Table 1). Large variability among genotypes was observed in seed germination, seedling vigor and storability during both long-term storage (ambient temperature) and accelerated ageing (42°C and 100% RH). Statistical analysis of the germination data of both French bean and cowpea revealed significant differences between genotypes, storage periods at ambient temperature and the interaction genotypes and storage periods.

At five months after storage statistical analysis of germination data revealed no significant difference among French bean genotypes. At this time ageing effect was still not detected in most genotypes though a decline in vigour was observed in others (Figs 1 and 2). At

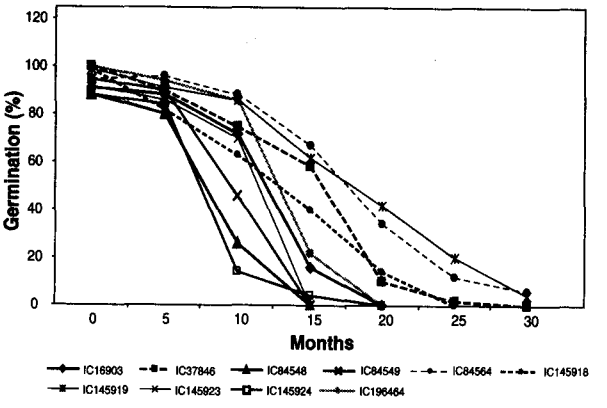

Fig. 1 Seed germination in different genotypes of french bean during ambient storage

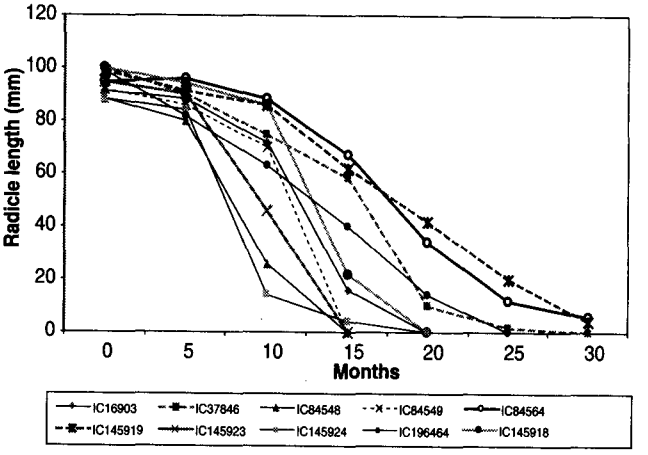

Fig. 2 Seedling vigour in different genotypes of french bean during ambient storage

10 months after storage significant difference (p=0.05) in the maintenance of viability among most genotypes was observed and these differences became marked as the storage duration progressed. At ambient temperature germination was maintained at a high level for most genotype for five months it then declined rapidly for some cultivars viz. for IC 84548, IC 84549, IC 145923 and IC145924 germination dropped to 0 by 15 months of storage (Fig. 1). For others the decline was gradual. The germination%age of various genotypes varied from 0–67% at 15 months of storage. By 30 months all accessions except IC 84564 and IC145919 were dead.

In cowpea germination started to decline after one year in IC 45409 and was only 16 per cent after 3 years of storage whereas the other accessions maintained high germination values of 66-96% (Fig. 3), however, vigour started to decline after 12 months of storage in the various genotypes. Thus, genotypes such as IC 37846, IC 145919 and IC 145918 of French bean and IC45409 and IC 44792 of cowpea had similar germination before storage but showed large difference in storability during ambient storage as well as accelerated ageing (Table 1 & Fig 1, 3).

A loss in vigour of French bean after 3 weeks and in germination after 9 weeks has been reported by Kueneman (1983) under high temperature (32°C) and high RH (90%). Pandey (1989) observed a 38% reduction in germination after 3 years of storage at 24-32°C and 10± 0.8% moisture content. Various other reports have indicated storability of French bean varying from 8-53 months after harvest under ambient laboratory conditions (Deakin 1974, Vieira and Fonseca 1986, Aguirre and Peske 1991). Aguirre and Peske (1991) have reported that bean seeds with moisture content below 11.5% can be hermetically stored up to 8 months at 30°C without significant loss in their germination, although cultivar differences in storability of French bean have been observed with some cultivars maintaining 80% germination for 15 months after harvest whereas others maintaining this level of germination for longer period (20 months) under ambient conditions of Brazil. Further, it was observed that the decline in germination started at 6.1 – 16.2 months depending on the cultivars; however, viability was lost for all cultivars at approximately 38 months after harvest at 12% moisture under ambient conditions. Similarly, variability in the longevity of cowpea genotypes was observed by Vieira and Fonseca (1986), where 80% germination was maintained for

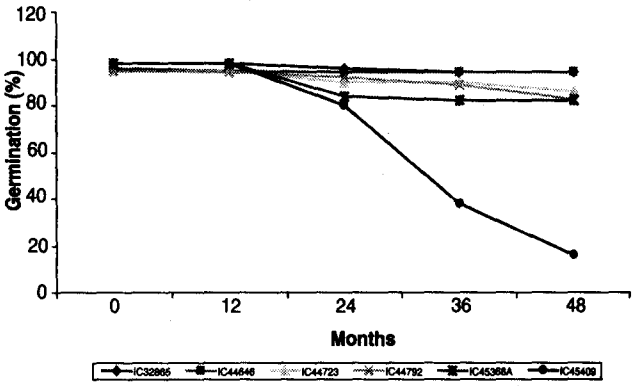

Fig. 3: Germination percentage of different cowpea genotypes during ambient storage

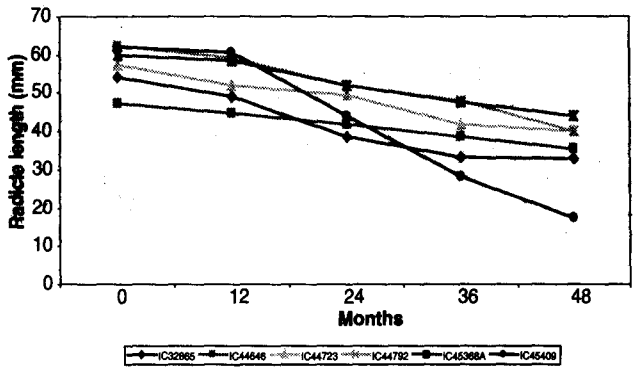

Fig. 4: Seedling vigour in different cowpea genotypes during ambient storage

periods varying from 27 – 35.2 months in the various cultivars. Under the ambient conditions of Brazil viability was lost after 18 months to 56 months after harvest (Aguirre and Peske, 1991). % germination after accelerated ageing was positively (p=0.01) correlated with germination after natural ageing at ambient temperature and negatively with 100 seed weight (Table 2). After accelerated ageing germination varied from 0-33% among French bean genotypes and from 14-89% among cowpea genotypes (Table 1). Genotypes which maintained higher germination during accelerated ageing also retained higher germination at ambient temperature after 15 months of storage in French bean and 3 years in cowpea. Measurements of seed moisture content (mc) revealed an increase during accelerated ageing from a mean of 10.1% to 17.5-23.2% for the various genotypes (Table 1). Decline in germination after both accelerated and natural ageing was negatively correlated with the seed moisture (Table 2). The differences in equilibrium seed moisture of various genotypes could be one of the explanations for differences in deterioration. Seeds which showed a rapid fall in germination after ageing absorbed moisture rapidly from the high humidity

Table 2. Correlation Coefficients between various seed traits

Traits	Moisture content after accelerated aging	Initial moisture content	100 seed weight	Germination after ambient ageing	EC
French bean					
Initial moisture content	0.611				
100 seed weight	0.729*	0.787**			
Germination (%) after ambient aging	-0.484	-0.803**	-0.611		
EC	0.578	0.565	0.222	-0.522	
Germination (%) after accelerated aging	-0.618	-0.670*	-0.692	0.871**	-0.440
Vigor (radical length, mm)	-0.524	-0.560	0.489	0.727*	0.632
Cowpea					
Initial moisture content	0.594				
100 seed weight	0.711*	0.783**			
Germination (%) after ambient aging	-0.402	-0.781**	-0.584		
EC	0.498	0.423	-0.188	-0.511	
Germination (%) after accelerated aging	-0.590	-0.695	-0.676*	0.836**	-0.384
Vigour (radical length, mm)	-0.512	-0.424	0.472	0.701*	0.586

conditions of accelerated ageing reaching moisture content of over 20%. In contrast seed lots which retained a high germination imbibed slowly and equilibrated at lower moisture content. Increase in weight of seeds after eight hours of imbibition at 25°C revealed that some genotypes are poor imbibers (less than 10% increase) as compared to others (more than 17% increase) (Table 1).

Seed moisture and storage temperature are the most important factors influencing seed survival during storage (Roberts, 1972). For every 1% reduction in moisture content from 14.0-10.5% storage potential of French bean seeds has been reported to increase 1.6-1.7 fold (Aguirre and Peske, 1991). In both French bean and cowpea there was no significant change in the germination in any of the genotypes at 5°C (Table 1).

Difference in the storage potential of cultivars within species of grain legumes have been found to be associated with various other seed characteristics like seed size (Singh *et al.*, 1972, Tiwari and Gupta, 1981) and seed coat pigmentation (Deakin, 1974). Large seeded French bean cultivars lost viability faster than cultivars of small seeds (Aguirre and Peske, 1991). Although a negative correlation between seed weight and% germination after accelerated ageing has been observed in both French bean and cowpea but germination at ambient temperature was not associated with 100 seed weight (Table 2). Vieira and Fonseca (1986) have shown that cultivars with white seed coats and/ or large seeds lost germination faster than cultivars of other colours and/ or small seeds. Such an association between seed coat colour and loss of germination was not observed in this study although seeds with black coat colour had lesser leachate conductivity than seeds having relatively lighter coats (Table 1).

Differences in tolerance to ageing treatment have also been reported in cultivars of cotton by Bourland and Ibrahim (1982). Similarly, Burris (1980) found significant genotypic effects for germination and vigour in storability of soybean seeds, which were correlated with vigour. He suggested that selection for vigour might be used for improving storability. Also such genetic variability may have potential for incorporating resistance to viability loss especially when seeds are stored under adverse conditions.

The correlation observed between seed germination after accelerated ageing and after natural ageing under ambient conditions in both French bean and cowpea indicate that differences in seed storage potential among cultivars can be identified by carrying out an accelerated ageing test before storage as has been shown for a number of other species (Tekrony, 1995). Use of accelerated ageing in selection of genotypes tolerant to the adverse storage conditions may alleviate problems of low seed quality and poor storability.

Results show that the two grain legume species *viz.* French bean and cowpea differ greatly in their loss of germination during storage. Under adverse storage conditions French beans are poor storers as compared to cowpeas. Results also highlight the differences in storability of seeds among various genotypes. In French bean IC 84564 and IC 145919 and in cowpea IC 32865 and IC 44646 were better storers than the other accessions studied.

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SHORT COMMUNICATION

Enhancing Seed Germination in Wild Medicinal Germplasm of Cold Arid Deserts

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Key Words: Dormancy, Germination, Medicinal Plants.

Unrestricted exploitation of the wild medicinal plants with no attention to their cultivation has placed them on the verge of extinction. Propagation and cultivation studies are among the most important tools for *ex situ* conservation and sustainable utilization of medicinal and aromatic biodiversity. Propagation through seeds is a slow process as seeds exhibit dormancy. International Seed Testing Rules does not include these medicinal species because most of these are of Indian origin. Therefore, present work was undertaken to develop dormancy breaking protocols for better propagation and *in-situ* conservation of some medicinal plant species through cultivation technology. The seeds of twenty-six medicinally important species were received from NBPGR, Shimla station (jointly collected by Forest Research Laboratory, Leh and NBPGR) for long-term conservation at National Genebank. On testing their viability, six species showed poor germination because of dormancy. Three of the species viz. *Physachlaina preatle* (Decne) Miers (IC 394042, Solanaceae), *Cicer microphyllum* (IC 394064, Fabaceae) and *Sophora macrophora* (IC394052, Fabaceae) showed thick glossy hard seed coat and were subjected to acid scarification with concentrated Sulphuric acid for varying time periods. Rest of the three species viz. *Urtica hyperborea* Jacq. ex Wedd. (IC394066), *Aconogogum tartiosum* (IC394067), *Hippophae rhamnoides* ssp. *turkstenica* Rousi (IC394073) were given chilling treatment at 5°C for 7 days and 15 days as per Tables 1 and 2. After the treatment the seeds were subjected to germination tests using two replicates of 25 seeds each per treatment. Seeds were placed in sterilised plastic petriplates with double layer Whatmann No. 1 filter paper moistened with 5 ml of distilled water. The germination test was carried out in dark at 20°C.

The percentage of normal seedlings and hard seeds were calculated from the total number of seeds placed. Emergence of radicle was used as indicative of germination. Data thus generated was subjected to analysis of variance.

The results indicated that in *Physachlaina praeatle* concentrated sulphuric acid treatment given for 10 minutes increased the germination to 96% while shorter duration (one and five minutes) were not effective. Longer duration of 20, 30 and 60 minutes resulted in increased number of dead seeds and were thus lethal. In case of *Sophora macrophora*, acid scarification for 10 and 20 minutes resulted in 50-55 percent increase in germination against control where dormancy was 100%. The most successful treatment was found to be the exposures for 30 minutes and 60 minutes but number of dead seeds increased in 60 minutes. The wild chickpea (*Cicer microphyllum*) showed 100% dormancy in control. Acid scarification for 10 and 20 minutes partially successful in breaking the hardseededness. Thirty and sixty minutes of seed treatment with concentrated sulphuric acid resulted in 94-100% germination. The seeds of *Urtica hyperborea* showed near complete dormancy and were given chilling treatment. Chilling for 7 days resulted in 64% increase in the germination whereas longer exposures of 15 days

Table 1. Effect of Acid Scarification on seed germination

Sulphuric Acid Treatment	Species					
	Physachlaina preatle		*Sophora macrophora*		*Cicer microphyllum*	
	Normal seed	Hard seed	Normal seed	Hard seed	Normal seed	Hard seed
10 min.	96	4	44	56	34	72
20 min.	44	8	52	48	44	54
30 min.	4	8	88	4	94	6
60 min.	4	8	88	4	100	–
Control	12	88	4	92	6	92

CD at 5%= 6.73

Table2. Effect of Cold stratification on seed germination

Chilling Treatment	Species					
	Urtica hyperborea		*Aconogogum tartiosum*		*Hippophae rhamnoides*	
	Normal seed	Hard seed	Normal seed	Hard seed	Normal seed	Hard seed
7 days	64	30	64	26	90	6
15 days	90	8	90	6	96	-
Control	10	82	6	90	6	90

CD at 5%= 6.88

resulted in 90% germination. In *Aconogogum tartiosum* (IC-394067) only 6% germination was recorded in control. Chilling for 7 days increased the germination by 64% while for 15 days resuluted in 90% germination. In *Hippophae rhamnoides* spp. *turkstenica* the control showed only 6% germination whereas chilling for 7 and 15 days resulted in above 90 and 96% germination, respectively.

The purpose of giving any physical/chemical treatment to any hard seed is to soften the seed coat and facilitate the germination by easy imbibition of water. A standard set of rules for uniform germination and dormancy breaking technique for most of the agricultural and horticultural crops have been devised by International Seed Testing Association (ISTA). For gene bank purposes, International Bureau of Plant Genetic Resources (IBPGR), Advisory Board on Seed Storage had also formulated a set of rules which are basically ISTA Rules with slight modifications. Most of the medicinal plants, being wild in nature, exhibit dormancy and pose problems during conservation programmes. Information on standard procedures for their germination and breaking dormancy is lacking. Among the presently investigated species, three species showed coat imposed dormancy in which the hard seed coat acts as a barrier to uptake of water thereby restricting the germination. Any physical or chemical scarification can abrase the seed surface for easy imbibition of water, thereby facilitating the onset of germination (Bewlay and Black, 1985). Such work has been reported in *Plantago ovata* (Stebbins and Day, 1967), in *Commiphora mukul* (Dalal *et al.*, 1989). Ahmed *et al.* (1990) had also reported the beneficial effect of concentrated sulphuric acid scarification in different species of *Indigofera.*

Chilling the horticultural crop seeds is a common practice. Bewlay and Black (1985) reported that chilling induced build up of gibberellic acid in hazelnut seeds which is essential for dormancy breaking, as dormant non-chilled hazelnut embryos germinate only when exogenous supply of gibberellic acid is ensured in the medium. ISTA (1985) recommends it for many temperate species like *Silybum marianum*, *Papaver rhoes* and *Apium graveolens*. Raina *et al.* (1994) had shown that chilling at 3°C for 15 days enhanced the germination by 70% in *Swertia chirata*. In the present study, a 100% increase was observed in *Urtica hyperborea*, *Aconogogum tartiosum* and *Hippophae rhamnoides* ssp. *turkestenica*.

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SHORT COMMUNICATION

Identification of Resistant Sources Against *Alternaria* Blight Disease of *Rabi* Pigeon pea (*Cajanus cajan* (L.) Millsp)

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Key Words: ***Alternaria* blight, *Alternaria tenuissima*, *Cajanus cajan*, Pigeopnea, Resistant.**

Pigeon pea (*Cajanus cajan* (L.) Millsp.) is an important pulse crop grown extensively throughout the country under varied cropping systems. When the crop is sown in *rabi* season under high plant density, it remains short in height and exhibits very high yield potential, which is 2 to 3 times more than the *kharif* sown crop. However, prevalence of *Alternaria* blight caused by *Alternaria tenuissima* (Fr.) Wiltsh posses serious threat to wide spread adoption of *rabi* pigeon pea in potential areas particularly in Bihar, Uttar Pradesh and West Bengal. *Alternaria* blight is of little or no importance in the main pigeon pea crop planted during *kharif* season.

Alternaria blight of pigeon pea in epiphytotic form was first reported in 1971 from North India (Patwardhan and Singh, 1971). Due to change in the cropping system severe outbreak of *Alternaria* blight was seen in September planted pigeon pea especially in the cultivars Bahar and Basant in the states of Uttar Pradesh and Bihar (Venkateshwaralu *et al.*, 1981, Narula, 1983, Mahmood *et al.*, 1984). The symptoms of this disease first appear in the second fortnight of November and attain maximum inoculum build up in the late maturing genotypes. The disease caused extensive damage to the aerial parts of plants resulting in complete brightening and great reduction in yield. Under severe condition of infection, 80 to 100 per cent yield losses have been reported in *rabi* pigeon pea (Lal, 1997). Genetic amelioration for disease resistance is considered to be the most effective and economic method of protecting the crops to ensure their productivity.

Considering the limited information available on the sources of resistance and the genetic control of resistance to *Alternaria* blight in pigeon pea grown under *rabi* cropping system, identification of sources of resistance is the first and most important task.

A total of 109 germplasm collections comprising released varieties, local collections, advanced lines and germplasm accessions received from International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India were planted in three replications of 3 m length at 30 cm distance between rows. The crop was artificially inoculated by spraying spore suspension obtained from 7-days old culture at 2 days intervals at flowering stage. To maintain a high humidity to create favourable conditions for maximum disease development, water was sprayed twice a day for seven days. A susceptible check entry, Bahar, was planted on borders all around the screening plots.

Observations were recorded on randomly selected ten plants from each genotype. Screening was rigorously carried out at modified 0-5 point scale (Singh *et al.*, 1986). Each plant was critically observed for the presence of concentric rings and water soaked translucent areas. Thereafter numerical rating grade was given on the basis of percentage area covered by the pathogen on the plant. Pathogen reaction was categorized considering rating scale and disease intensity as follows:

Rating scale	Disease intensity	Pathogen reaction
0	0	Near immune/highly resistant (I)
1	1-10	Resistant (R)
2	11-25	Moderately resistant (MR)
3	26-50	Moderately susceptible (MS)
4	51-75	Susceptible (S)
5	76-100	Highly susceptible (HS)

On the basis of disease intensity, genotypes were classified into different groups i.e. near immune (I), Resistant (R), moderately resistant (MR), Moderately susceptible (MS), Susceptible (S) and highly susceptible (HS).

None of the genotype was found to be completely free from visible symptoms of the disease. Two entries namely RAUP-32 (DA 11 x Bahar) and RAUP-34 (ICP-5455 x Bahar) were found to be resistant (1-10% intensity)

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Table.1. Reaction of Pigeon pea germplasm to *Alternaria* blight disease in Rabi 2002-2003

Reaction	Scale	No. of entries	Name of entries
Highly resistant	0	0	Nil
Resistant reaction	1	2	RAUP-32, RAUP-34
Moderately resistant	2	65	7-14, 7-16, BS-3, IC-285558, IC-315861, IC-315862, IC-315863, ICP-10900, ICP-10901, ICP-10909, ICP-10926, ICP-10928, ICP-11298, ICP-11892, ICP-13253, ICP-14282, ICP-15027, ICP-3679, ICP-5124, ICP-6344, ICP-6917, ICP-7182, ICP-7185, ICP-7186, ICP-7234, ICP-7239, ICP-7252, Muzaffarpur Local, Pant-A-3, Pusa-9, RAUP- 12, RAUP-1, RAUP-13, RAUP-14, RAUP-19, RAUP-2, RAUP-20, RAUP-22, RAUP-26, RAUP-27, RAUP-3, RAUP-30, RAUP-31, RAUP-4, RAUP-5, RAUP-8, RAUP-9, VKS/JKH-3/10, VKS/SCC-10/19, VKS/SCC-10/26, VKS/SCC-10/34, VKS/SCC-10/42, VKS/SCC-10/46, VKS/SCC-10/49, VKS/SCC-10/52, VKS/SCC-11/41, VKS/SCC-11/49, VKS/SCC-11/65, VKS/SCC-11/83A, VKS/SCC-9/83, VKS-12/12, VKS-12/13, VKS-12/2, VKS-12/45, VKS-12/25
Moderately susceptible	3	34	Bahar, IC-272038, IC-273154, IC-273158, IC-274730, IC-311466, ICP-10905, ICP-10913, ICP-10915, ICP-10918, ICP-10920, ICP-10921, ICP-1097, ICP-10977, ICP-11040, ICP-7119, ICP-7194, ICP-8117, ICP-8125, RAUP-15, RAUP-17, RAUP-18, RAUP-7, UPAS-120, VKS/SCC-10/1, VKS/SCC-10/25, VKS/SCC-10/38, VKS/SCC-10/41, VKS/SCC-10/54, VKS/SCC-10/57, VKS/SCC-10/59, VKS/SCC-10/6, VKS/SCC-11/71, VKS/SCC-12/53.
Susceptible	4	8	IC-273155, IC-273156, IC-273159, IC-273162, VKS/SCC-10/21, VKS/SCC-11/18, VKS/SCC-11/24, VKS-12/40
Highly susceptible	5	0	
Total number of entries		**109**	

reaction. Thirty-four entries showed moderately susceptible reaction (26-50% intensity) and eight entries were susceptible (51-75% intensity). None of the entries showed highly susceptible reaction (Table 1).

Entries in the second group (1-10% intensity) can be used as an effective source of resistance against *Alternaria* blight disease in genetic enhancement programme of pigeonpea for *rabi* cropping system.

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Plant Germplasm Registration Notice

The Germplasm Registration Committee of ICAR in its XII[th] meeting held on 31[st] May, 2004 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 79 germplasm lines out of the 133 proposals considered.

PD 27 (Khoda, CRRI Acc No. 36470) (INGR No. 04001; IC283020), Paddy (*Oryza sativa* L.) Landrace with Tolerance to Complete Submergence

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Khoda, a photosensitive rice (*Oryza sativa* L.) cultivar was collected from the farmer field in Brahmanigaon, Baranga, Cuttack, Orissa after the super cyclone of 1999. This was found standing in submerged waters and therefore, is a new source of submergence tolerance. Well known germplasm lines, namely FR 13A, FR 43B, identified earlier for submergence tolerance, could not be used in breeding programmes because of poor combining ability and other undesirable agronomic characters.

Khoda is an awn-less genotype and is better than FR 13A in seed quality and elongation ability (Table 1). Morphological characteristics of Khoda are-leaf length 43.4 cm, leaf width 0.9 cm, ligule length 1.9 cm, culm length 112.7 cm, culm number 7.2, panicle length 24.5 cm, 15 days seedling height 20.5 cm, panicle weight 3.54 gm, maturity duration 155 days, grain length 8.0 mm, grain breadth 3.0 mm, grain length width ratio 2.66, 1000 grain weight 26.4 g and grain shape medium.

Table 1. Effect of submergence on elongation and survival percentage

Name of the cultivars	Plant Height (cm)			Survival Rate
	BS	AS	Elongation	(%)
PD 27 (Khoda)	29	68	39	100
FR 13A (TC)	30	72	42	100
IR 42 (SC)	20	68	48	15

BS = before submergence; AS = after submergence; TC = tolerant check; SC = susceptible-check

RP-3135-97-1-11-5 (IET 15833) (INGR No. 04002; IC296643), Semi-dwarf *Basmati* Type Paddy (*Oryza sativa* L.)

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Directorate of Rice Research, Hyderabad-500030, Andhra Pradesh

The semi-dwarf RP 3135-97-1-11-5 was developed from a cross between PR 109 and Pak basmati using pedigree-breeding method at the Directorate of Rice Research, Hyderabad (DRR, 1999). Basmati varieties are tall, while this culture is semi-dwarf with all the desirable characters of basmati rice and high yield potential. It has long slender aromatic white translucent grains with high milling as well as head rice recovery, intermediate amylose content, intermediate alkali-spreading value, high kernel elongation on cooking with soft gel consistency, flaky texture and pleasant aroma.

It is 109 cm tall with moderate tillering, well-exerted intermediate panicle, awned spikelets and brown apiculus. It is a medium duration culture of 145 days from seed to seed. It was evaluated with promising results at Kaul, Karnal, R.S. Pura and with an overall mean yield of 3217 kg/ha, superior to Taroari Basmati with an increase of 23 per cent.

It is resistant to leaf blast. This culture is recommended for traditional basmati growing areas in Delhi, Haryana, Uttranchal, Punjab and Himachal Pradesh.

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DRR (1999) *The Directorate of Rice Research Annual Progress Report*, **Vol. 1:** Varietal Improvement; pp 1.291-1.308.

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PADDY GENETIC STOCK WITH RESISTANCE TO RICE GALL MIDGE DISEASE

Samridhi (INGR No. 04003; IC296614), paddy (*Oryza sativa* L.) Germplasm Line with *Gm1* Gene for Rice Gall Midge Resistance

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2. International Rice Research Institute, Manila, Philippines

Samridhi is a germplasm of paddy with the *Gm1* gene for resistance to rice gall midge disease caused by *Orseolina oryzae* Wood Mason, identified at the Indira Gandhi Krishi Vishwavidyalaya, Raipur. Over the last twenty years, the inheritance and allelic relationship of gene(s) for resistance present in more than two hundred donors obtained from different parts of India were studied. This has led to the identification of nine different genes for gall midge resistance. Chaudhary *et al.*, (1986) reported the identification of the first gall midge resistance *Gm1* gene in cultivar "Samridhi" (IR 22 x W1263). This genotype is derived the resistance from W 1263 (Eswarakora x MTU 15), which in turn derived its resistance from Eswarakora. Eswarakora, the source of the *Gm1* gene, is a local germplasm accession belonging to Andhra Pradesh. *Gm1* gene provides resistance against gall midge biotype 1 prevalent in Chhattisgarh and Andhra Pradesh; biotype 3 prevalent at Ranchi, Jharkhand; biotype 5 prevalent in Moncompu, Kerala and biotype 6 prevalent in Manipur. The genotype has a plant height of 89.2 cm, days to 50 percent flowering of 102 days; number of panicles/m^2 325 with grain yield of 3133 kg/ha.

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Chaudhary BP, PS Shrivastava, MN Shrivastava and GS Khush (1986) Inheritance of resistance to gall midge in some cultivars of rice. *Rice Genetics* 523-528.

Surekha (INGR No. 04004; IC296615), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm2* for Rice Gall Midge Resistance

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1. Indira Gandhi Krishi Vishwavidyalaya, Raipur 492006, Chhattisgarh
2. International Rice Research Institute, Manila, Philippines

Surekha, a paddy germplasm line with *Gm2* gene for resistance to rice gall midge caused by *Orseolia oryzae* Wood Mason was identified at the Indira Gandhi Krishi Vishwavidyalaya, Raipur. It was identified by Chaudhary *et al.*, (1986). The *Gm2* gene identified in cultivar "Surekha" (IR 8 x Siam 29) derived its resistance from "Siam 29", a local germplasm accession of Thailand. *Gm2* gene provides resistance against biotype 1 prevalent in Chhattisgarh and Andhra Pradesh; biotype 2 prevalent in Orissa and biotype 5 prevalent in Moncompu, Kerala. The genotype has plant height of 101.2 cm, days to 50 percent flowering of 102 days; number of panicles/m^2 290 and grain yield of 3111 kg/ha.

Reference

Chaudhary BP, PS Shrivastava, MN Shrivastava and GS Khush (1986) Inheritance of resistance to gall midge in some cultivars of rice. *Rice Genetics* 523-528.

PADDY GENETIC STOCK WITH RESISTANCE TO RICE GALL MIDGE DISEASE

Samridhi (INGR No. 04003; IC296614), paddy (*Oryza sativa* L.) Germplasm Line with *Gm1* Gene for Rice Gall Midge Resistance

BP Chaudhary[1], PS Shrivastava[1], MN Shrivastava[1] and GS Khush[2]
1. Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh
2. International Rice Research Institute, Manila, Philippines

Samridhi is a germplasm of paddy with the *Gm1* gene for resistance to rice gall midge disease caused by *Orseolina oryzae* Wood Mason, identified at the Indira Gandhi Krishi Vishwavidyalaya, Raipur. Over the last twenty years, the inheritance and allelic relationship of gene(s) for resistance present in more than two hundred donors obtained from different parts of India were studied. This has led to the identification of nine different genes for gall midge resistance. Chaudhary *et al.*, (1986) reported the identification of the first gall midge resistance *Gm1* gene in cultivar "Samridhi" (IR 22 x W1263). This genotype is derived the resistance from W 1263 (Eswarakora x MTU 15), which in turn derived its resistance from Eswarakora. Eswarakora, the source of the *Gm1* gene, is a local germplasm accession belonging to Andhra Pradesh. *Gm1* gene provides resistance against gall midge biotype 1 prevalent in Chhattisgarh and Andhra Pradesh; biotype 3 prevalent at Ranchi, Jharkhand; biotype 5 prevalent in Moncompu, Kerala and biotype 6 prevalent in Manipur. The genotype has a plant height of 89.2 cm, days to 50 percent flowering of 102 days; number of panicles/m^2 325 with grain yield of 3133 kg/ha.

Reference

Chaudhary BP, PS Shrivastava, MN Shrivastava and GS Khush (1986) Inheritance of resistance to gall midge in some cultivars of rice. *Rice Genetics* 523-528.

Surekha (INGR No. 04004; IC296615), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm2* for Rice Gall Midge Resistance

BP Chaudhary[1], PS Shrivastava[1], MN Shrivastava[1] and GS Khush[2]
1. Indira Gandhi Krishi Vishwavidyalaya, Raipur 492006, Chhattisgarh
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Reference

Chaudhary BP, PS Shrivastava, MN Shrivastava and GS Khush (1986) Inheritance of resistance to gall midge in some cultivars of rice. *Rice Genetics* 523-528.

RP2068-18-3-5 (INGR No. 04005; IC296616), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *gm3* for Rice Gall Midge Resistance

Arvind Kumar, MN Shrivastava and RK Sahu
Indira Gandhi Krishi Vishwavidyalaya, Raipur-492006, Chhattisgarh

RP2068-18-3-5, a paddy germplasm line with the *gm3* gene conferring resistance to rice gall midge caused by *Orseolia oryzae* Wood Mason was identified at the Indira Gandhi Krishi Vishwavidyalaya, Raipur. Kumar *et al.*, (1998) identified this gene. The allelic study revealed the non-allelic nature of the *gm3* gene from *Gm1, Gm2* and *Gm4* genes. The breeding line identified to possess the *gm3* recessive gene, derives its resistance from Velluthacheera (Swarnadhan x Velluthacheera), a local germplasm accession from Tamil Nadu. The *gm3* gene provides resistance against the gall midge biotype 1 prevalent in Raipur, Chhatisgarh; biotype 2 prevalent in Cuttack, Orissa and biotype 3 prevalent in Ranchi, Jharkhand. This genotype has plant height of 181.2 cm, days to 50 percent flowering of 124 days; number of panicles/ m^2 is 376 with grain yield of 4577 kg/ha.

Reference

Kumar, Arvind, MN Shrivastava and RK Sahu (1998) Genetic analysis of ARC5984 for gall midge resistance – a reconsideration. *Rice Genet. Newsl.* **15**: 142-143.

Abhaya (INGR No. 04006; IC296617), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm4*, for Rice Gall Midge Resistance

MN Shrivastava, Arvind Kumar, SK Shrivastava and RK Sahu
Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh

Abhaya, a paddy germplasm line with the gene *Gm4*, conferring resistance to rice gall midge was identified at the Indira Gandhi Krishi Vishwavidyalya, Raipur by Shrivastava *et al.*, (1993). The allelic study revealed the non-allelic nature of the *Gm4* genes from *Gm1, Gm2* and *Gm3* genes identified earlier. The resistant variety Abhaya (CR 157-392 x OR57-21) derived its resistance from CR 157-392 (Vijaya x Ptb 10), which in turn derived its resistance from Ptb 10, a local germplasm accession of Pattambi, Kerala, India. *Gm4* provides resistance against the gall midge biotype 1 prevalent in Raipur, Chhattisgarh; biotype 2 prevalent in Cuttack, Orissa and biotype 3 prevalent in Ranchi, Jharkhand and biotype 4 prevalent in Vijayanagram and Srikakulam districts of Andhra Pradesh. The genotype has a plant height of 91.3 cm, days to 50 percent flowering of 98 days; number of panicles/ m^2 is 361 with grain yield of 4067 kg/ha.

Reference

Shrivastava, MN, Arvind, Kumar, SK Shrivastava, and RK Sahu (1993) A new gene for resistance to gall midge in rice variety Abhaya. *Rice Genet, Newsl.* **10**: 79-80.

ARC 5984 (INGR No. 04007; IC296618), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm5* for Rice Gall Midge Resistance

Arvind Kumar, MN Shrivastava and RK Sahu
Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh

ARC 5984, a paddy germplasm line with the *Gm5* gene conferring resistance against rice gall midge was identified at the Indira Gandhi Krishi Vishwavidyalya, Raipur by Kumar *et al.*, (1998). The *Gm5* gene is non-allelic with respect to the genes, *Gm1, Gm2, Gm3* and *Gm4*. Assam Rice Collection accessions have been a rich source of resistance against gall midge. *Gm5* gene provides resistance against the gall midge biotype 1 prevalent in Raipur, Chhattisgarh; biotype 2 prevalent in Cuttack Orissa and biotype 5 prevalent in Moncompu

RP2068-18-3-5 (INGR No. 04005; IC296616), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *gm3* for Rice Gall Midge Resistance

Arvind Kumar, MN Shrivastava and RK Sahu
Indira Gandhi Krishi Vishwavidyalaya, Raipur-492006, Chhattisgarh

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Abhaya (INGR No. 04006; IC296617), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm4*, for Rice Gall Midge Resistance

MN Shrivastava, Arvind Kumar, SK Shrivastava and RK Sahu
Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh

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Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh

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Kerala. The genotype has a plant height of 166.7 cm, days to 50 percent flowering of 116 days; number of panicles/m^2 is 326 with grain yield of 3200 kg/ha.

Reference

Kumar Arvind, MN Shrivastava and RK Sahu (1998) Genetic analysis of ARC 5984 for gall midge resistance-a reconsideration. *Rice Genet, Newsl.* **15**: 142-143.

RP2333-156-8 (INGR No. 04008; IC296619), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm7* for Rice Gall Midge Resistance

Arvind Kumar, MN Shrivastava and BC Shukla
Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh

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Reference

Kumar Arvind, MN Shrivastava and BC Shukla (1999) A new gene for resistance to gall midge in rice cultivar RP2333-156-8. *Rice Genet, Newsl.* **16**: 85-87.

Jhitpiti (INGR No. 04009; IC296620), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm8* for Rice Gall Midge Resistance

Arvind Kumar, S Bhandarkara, DJ Pophlay and MN Shrivastava
Indira Gandhi Krishi Vishwavidyalaya, Raipur 492006, Chhattisgarh

Jhitpiti, rice with the *Gm8* gene conferring resistance against rice gall midge was identified at the Indira Gandhi Krishi Vishwavidyalaya, Raipur, from the accessions collected by Dr RH Richharia. One of the accessions of Chhattisgarh Rice Germplasm, "Jhitpiti" was found to possess the *Gm8* gene conferring resistance to gall midge resistance (Kumar *et al.*, 2000). Allelic study has proved the non-allelic nature of *Gm8* gene from the earlier identified genes, namely *Gm1*, *Gm2*, *Gm3*, *Gm4*, *Gm5* and *Gm7*. The *Gm8* gene provides resistance against biotype 1 prevalent in Raipur, and its reaction against other gall midge biotypes is to be tested. The genotype has a plant height of 122.1 cm, days to 50 percent flowering of 87 days; number of panicles/m^2 is 314 with grain yield of 2845 kg/ha.

Reference

Kumar Arvind, S Bhandarkar, DJ Pophlay and MN Shrivastava (2000) A new gene for gall midge resistance in rice cultivar Jhitpiti. *Rice Genet, Newsl.* **17**: 83-84.

Kerala. The genotype has a plant height of 166.7 cm, days to 50 percent flowering of 116 days; number of panicles/m^2 is 326 with grain yield of 3200 kg/ha.

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RP2333-156-8 (INGR No. 04008; IC296619), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm7* for Rice Gall Midge Resistance

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Reference

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Reference

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Reference

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Line 9 (INGR No. 04010; IC296621), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm9*, for Rice Gall Midge Resistance

MN Shrivastava, Arvind Kumar, S Bhandarkar, BC Shukla and KC Agrawal
Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh

Line 9 is a rice germplasm with the *Gm9* gene conferring resistance to rice gall midge was identified at the Indira Gandhi Krishi Vishwavidyalya, Raipur by Shrivastava *et al.*, (2003). The resistance against gall midge in Line 9 was presumed to might have arisen (i) by a spontaneous mutation or (ii) by one of the parent involved in the progenitor cross (Jaya x Dubraj) having a gene for resistance along with an inhibitory gene. The allelic study revealed non-allelic nature of *Gm9* gene from the earlier identified genes, *Gm1*, *Gm2*, *gm3*, *Gm4*, *Gm5*, *Gm7* and *Gm8*. The *Gm9* gene has been recorded to provide resistance against biotype 1 prevalent in Raipur, and its reaction against other gall midge biotypes prevalent in India needs to be tested. The genotype has a plant height of 122.1 cm, days to 50 percent flowering of 87 days; number of panicles/m^2 is 314 with grain yield of 2845 kg/ha.

Reference

Shrivastava MN, Arvind Kumar, S Bhandarkara, BC Shukla and KC Agrawal and (2003) A new gene for resistance in rice to Asian rice gall midge (*Orseolia oryzae* Wood Mason) Biotype I at Raipur, India. Euphytica **130**:143-145.

Mutant Cluster Rice (INGR No. 04064; IC396397), Paddy (*Oryza sativa* L.) Germplasm Line with Clustered Spikelets

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Mutant Cluster Rice is a novel mutant line of paddy (*Oryza sativa* L.) with clustered spiklelets, identified at AAI (DU). It has multiple caryopsis i.e. having 3-4 spikelets per node, 45-55 clusters per panicle. It was derived from Sonachur, an indigenous local variety through single plant selection. This mutant line has following morphological characteristics- plant height 105-109 cm, number of tillers 10-13, number of productive tillers 8-11, panicle length 17-19 cm, flag leaf length 27 cm, number of clusters/panicle 53.1, number of spikelets/clusters 3.1-3.8, total number of spikelets per panicle 189.5-192.0, kernel length 0.74 cm, kernel width 0.28 cm, test weight 23.0 g. The standard agronomic practices include transplanting of 25 days old seedlings into main field with 2-3 seedlings per hill at 20x15 cm spacing and fertilization with 60:40:40 NPK along with 20 kg $ZnSO_4$ both under transplanted wet land and direct seeded upland conditions. The crop matures in 120-125 days time.

Line 9 (INGR No. 04010; IC296621), Paddy (*Oryza sativa* L.) Germplasm Line with Gene *Gm9*, for Rice Gall Midge Resistance

MN Shrivastava, Arvind Kumar, S Bhandarkar, BC Shukla and KC Agrawal
Indira Gandhi Krishi Vishwavidyalya, Raipur-492006, Chhattisgarh

Line 9 is a rice germplasm with the *Gm9* gene conferring resistance to rice gall midge was identified at the Indira Gandhi Krishi Vishwavidyalya, Raipur by Shrivastava *et al.*, (2003). The resistance against gall midge in Line 9 was presumed to might have arisen (i) by a spontaneous mutation or (ii) by one of the parent involved in the progenitor cross (Jaya x Dubraj) having a gene for resistance along with an inhibitory gene. The allelic study revealed non-allelic nature of *Gm9* gene from the earlier identified genes, *Gm1*, *Gm2*, *gm3*, *Gm4*, *Gm5*, *Gm7* and *Gm8*. The *Gm9* gene has been recorded to provide resistance against biotype 1 prevalent in Raipur, and its reaction against other gall midge biotypes prevalent in India needs to be tested. The genotype has a plant height of 122.1 cm, days to 50 percent flowering of 87 days; number of panicles/m^2 is 314 with grain yield of 2845 kg/ha.

Reference

Shrivastava MN, Arvind Kumar, S Bhandarkara, BC Shukla and KC Agrawal and (2003) A new gene for resistance in rice to Asian rice gall midge (*Orseolia oryzae* Wood Mason) Biotype I at Raipur, India. Euphytica **130**:143-145.

Mutant Cluster Rice (INGR No. 04064; IC396397), Paddy (*Oryza sativa* L.) Germplasm Line with Clustered Spikelets

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Mutant Cluster Rice is a novel mutant line of paddy (*Oryza sativa* L.) with clustered spiklelets, identified at AAI (DU). It has multiple caryopsis i.e. having 3-4 spikelets per node, 45-55 clusters per panicle. It was derived from Sonachur, an indigenous local variety through single plant selection. This mutant line has following morphological characteristics- plant height 105-109 cm, number of tillers 10-13, number of productive tillers 8-11, panicle length 17-19 cm, flag leaf length 27 cm, number of clusters/panicle 53.1, number of spikelets/clusters 3.1-3.8, total number of spikelets per panicle 189.5-192.0, kernel length 0.74 cm, kernel width 0.28 cm, test weight 23.0 g. The standard agronomic practices include transplanting of 25 days old seedlings into main field with 2-3 seedlings per hill at 20x15 cm spacing and fertilization with 60:40:40 NPK along with 20 kg $ZnSO_4$ both under transplanted wet land and direct seeded upland conditions. The crop matures in 120-125 days time.

FLW 6 (INGR No. 04011; IC296606), Wheat (*Triticum aestivum* L.) Germplasm Line with Resistance to Brown and Black Rusts (*Lr9 + Lr 24 and Sr2 + Sr 24*)

Dibendu Datta[1], SK Nayar[1], M Prashar[1], SC Bhardwaj[1] and M Siwaswamy[2]
1. Directorate of Wheat Research (DWR), Regional Station, Shimla-171002, Himachal Pradesh
2. Indian Agricultural Research Institute, Regional Station Wellington-643231, Tamil Nadu

FLW 6 is a wheat germplasm line resistant to brown and black rust. It was derived through pedigree selection method from the cross, HP1633 x HP1776 at DWR, Regional Station, Flower dale. It possesses pyramided brown rust resistance genes *Lr9* and *Lr24* in addition to *Sr2* and *Sr24* unknown black rust resistance genes. The plants are 100 cm tall and mature in 120 days. It produces amber coloured grains with a test weight of 37.6 g and yield per meter row is at par with HP1776 the local check, but inferior than the best check PBW343. The disease reaction to various rusts is reflected in Table 1.

Table 1. Disease reaction of FLW 6 to various rusts

Genetic Stock	Field Data	Seedling Resistance Test			Genes Postulated
FLW 6	Brown rust	121R63-1	121R127	21R55	
	Resistant	;	; 12	;	Lr9, Lr24
	Black rust	62G29	62G29-1		
	10MR	2-	2+		Sr2, Sr24*

*Additional unknown resistance gene

FLW 8 (INGR No. 04012; IC296607), Wheat (*Triticum aestivum L.*), Germplasm Line with Resistance to Brown and Black Rust (*Lr19 and Sr25*)

Dibendu Datta[1], SK Nayar[1], M Prashar[1], SC Bhardwaj[1] and RN Brahma[2]
1. Directorate of Wheat Research, Regional Station, Shimla-171002, Himachal Pradesh
2. Indian Agricultural Research Institute, Regional Station Wellington-643231, Tamil Nadu

FLW 8, a wheat genotype, resistant to brown and black rusts derived through pedigree selection from the cross, HI1077 x Tc+*Lr19* at the Directorate of Wheat Research, Regional Station, Flower dale. It possesses unexploited rust resistance genes *Lr19* and *Lr25*. The plants of this genotype are 100 cm tall and mature in 118 days, producing non-amber coloured grains with 36.5 g test weight. Yield per meter row is at par with HI1077, but inferior than the best check PBW343. The disease reaction to various rusts are given in the Table 1 below.

Table 1. Disease reaction of FLW 8 to various rusts

Genetic Stock	Field Data	Seedling Resistance Test			Genes Postulated
FLW 8	Brown rust	121R63-1	121R127	21R55	
	Resistant	0;	0;	0;	Lr19
	Black rust	62G29	62G29-1		
	10MR	2-	2		Sr25

FLW 6 (INGR No. 04011; IC296606), Wheat (*Triticum aestivum* L.) Germplasm Line with Resistance to Brown and Black Rusts (*Lr9 + Lr 24 and Sr2 + Sr 24*)

Dibendu Datta[1], SK Nayar[1], M Prashar[1], SC Bhardwaj[1] and M Siwaswamy[2]
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FLW 6	Brown rust	121R63-1	121R127	21R55	
	Resistant	;	; 12	;	Lr9, Lr24
	Black rust	62G29	62G29-1		
	10MR	2-	2+		Sr2, Sr24*

*Additional unknown resistance gene

FLW 8 (INGR No. 04012; IC296607), Wheat (*Triticum aestivum L.*), Germplasm Line with Resistance to Brown and Black Rust (*Lr19 and Sr25*)

Dibendu Datta[1], SK Nayar[1], M Prashar[1], SC Bhardwaj[1] and RN Brahma[2]
1. Directorate of Wheat Research, Regional Station, Shimla-171002, Himachal Pradesh
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Table 1. Disease reaction of FLW 8 to various rusts

Genetic Stock	Field Data	Seedling Resistance Test			Genes Postulated
FLW 8	Brown rust	121R63-1	121R127	21R55	
	Resistant	0;	0;	0;	Lr19
	Black rust	62G29	62G29-1		
	10MR	2-	2		Sr25

02 seasons, i.e. of nine years and resistance to Karnal bunt pathogen under artificial screening.

WL-3526 (INGR No. 04020; IC296785)

WL-3526 is a wheat (*Triticum aestivum* L) germplasm line resistant to loose smut, Karnal bunt, stripe and leaf rust in a new genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, HD2009 x WG 377. The plants have intermediate growth habit with plant height of 99 cm and dark green foliage. Heading and maturity on an average take 95 and 128 days respectively. Ear is dense white coloured with tapering shape. Ear length is 10 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 36 g. Resistance to loose smut pathogen was tested 24 times since 1978, while to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons, i.e. for 9 years and resistance to Karnal bunt pathogen under artificial testing.

WL-5634 (INGR No. 04021; IC296603)

WL-5634 is a wheat (*Triticum aestivum* L.) germplasm line resistant to loose smut, Karnal bunt, stripe and leaf rust in a different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, kav kaz-Cno-Inia x WL 905. The plants have intermediate growth habit with height of 97 cm and dark green foliage. Heading and maturity on an average take 96 and 130 days respectively. Ear is dense, white coloured with tapering shape and white coloured awns. Ear length is 9 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 30 g. The resistance to loose smut pathogen was tested 23 times since 1980, while resistance to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons (9 years) and resistance to Karnal bunt pathogen under artificial testing

AKW 2862-1 (INGR No. 04022; IC296767), Wheat (*Triticum aestivum* L.) Germplasm Line with Heat Tolerance

DG Vitkare
Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444104, Maharashtra

AKW 2862-1 is a wheat germplasm line with tolerance to heat and early maturity. It was developed through pedigree selection method in germplasm VEE # 6 || DOVE "S"/BUC "S" CM 92225-66Y-OM at Wheat Research Unit, PDKV, Akola. It was screened in 15 Short Duration cum Heat Tolerance Screening Nurseries conducted at 17 locations with an aim to identify genotypes of early maturity and tolerance to high temperature during grain-filling period under late sowing conditions. The genotype AKW 2862-1 showed consistent performance for these important traits during three subsequent seasons (1999-2000, 2000-2001 and 2001-2002). Mean days to heading were 63 days (with range of 46 - 106) with maximum and minimum temperature of 37.26°C and 8.83°C, respectively, and 1000-grain weight of 49 g (with range of 30-56 g).

Harit-1 (M3) (INGR No. 04023; IC427810), Wheat (*Triticum aestivum* L.) Germplasm Line, a New Source of Leaf Blight Resistance

DP Singh, Jag Shoran and Pankaj Kumar
Directorate of Wheat Research, Karnal-132001, Haryana

Leaf blight is a major biotic factor causing yield losses up to 50 percent in susceptible wheat varieties under warmer and humid weather of Northeastern plains zone (NEPZ). The disease causing pathogen *Bipolaris sorokiniana* syn. *Helminthosporium sativum* is present in all the six agro-climatic zones of India, neighbouring south Asia, China, North and Latin America and Brazil. Genotype showing no or little halo around necrotic spot is considered highly resistant.

Harit-1 (M3) is a new wheat (*Triticum aestivum*)

KRL 35 (INGR No. 04013; IC408332), Wheat (*Triticum aestivum* L.) Germplasm Line with AmberColoured Grains and Agronomic Superiority over Parent Kharchia

KN Singh[1] and Ravish Chatrath[2]
1. *Central Soil Salinity Research Institute, Karnal-134201, Haryana*
2. *Directorate of Wheat Research, Karnal-134201, Haryana*

KRL 35 is a new wheat germplasm line with amber coloured grains and agronomic superiority over parent Kharchia, developed at the Central Soil Salinity Research Institute, Karnal. KRL 35 is tolerant to salinity and alkalinity/sodicity and was also found to be quite tolerant to water logging conditions in comparison to other wheat varieties. This genotype was tested in most of the northern states of the country coming under Northeastern plain I, and Northwestern plain zone. To improve salt tolerance and yield, a high yielding dwarf variety HD2160 was crossed with salt tolerant amber grained wheat variety KRL1-4, and KRL 35 was developed. It was first evaluated in the All India Coordinated Salinity/Alkalinity Tolerance Screening Nursery and was found promising, and promoted for salinity/alkalinity trial. Directorate of Wheat Research, Karnal regularly organises Salinity/ alkalinity nursery and trials under salinity/alkalinity conditions, at least at 10 different centres across the country in the states of Bihar, Uttar Pradesh, Haryana, Punjab, Gujarat, Maharashtra and Rajasthan. KRL35 was evaluated for three seasons from 2000-2001 to 2002-2003 under these trials and was found quite promising and yielded better than Kharchia 65 and high yielding check KRL 19 with overall average yield of 35.1 q/ha Singh and Chatrath (2003, 2002, 2001). However, it was found susceptible to leaf and strip rusts under artificially inoculated conditions.

KRL 35 is a two-gene dwarf wheat germplasm with an average plant height (recorded in salt affected soils and normal soil) of 98 cm with green leaf of intermediate width and waxy look. On an average it takes 90 days to heading and matures in about 145 to 150 days. It has medium awns and has parallel ears and intermediate ear density with average 1000-grain weight of 39 g.

Reference

Singh KN and R Chatrath (2003, 2002, 2001) *Reports presented in the All India Coordinated Wheat Research Workers Workshop* organized by Directorate of Wheat Research, Karnal.

WHEAT GENETIC STOCKS RESISTANT TO BROWN AND BLACK RUSTS

MK Menon[1], Bhojan[1], KA Nayeem[1], RN Brahma[1], M Sivasamy[1], AJ Prabakaran[1], R Asir[1], A Saikia[1], SMS Tomar[2], SK Nayar[2], M Prashar[2], SC Bhardwaj[2]and RK Gupta[4]
1. *Indian Agricultural Research Institute, Regional Station Wellington-643231, Tamil Nadu*
2. *Division of Genetics, Indian Agricultural Research Institute, New Delhi-110012*
3. *Directorate of Wheat Research, Regional Station, Shimla-171002, Himachal Pradesh*
4. *Directorate of Wheat Research, Karnal-134201, Haryana*

HW-2002 (INGR No. 04014; IC408333), Wheat (*Triticum aestivum* L.) Germplasm Line with Resistance to Brown and Black Rust (*Lr24* and *Sr24*)

HW-2002 is a wheat germplasm line carrying *Lr24* and *Sr24* linked genes, conferring resistance to brown rust and moderate resistance to black rusts. It was developed at the Indian Agricultural Research Institute, Regional Station, Wellington, through pedigree selection and backcrossing method involving Kalyansona*6/ TR 380-4*7/Ag#14. It has erect plant growth habit with 62 days to 50 percent heading and 114 days to maturity. It has white coloured elliptical grains with medium hard texture, 26.8 seeds/spike, and 1000-grain weight of 32 g. with 11.94 percent seed protein.

HW-2031 (INGR No. 04015; IC408334), Wheat (*Triticum aestivum* L.) Germplasm Line with Resistance to Brown Rust (*Lr28*)

HW-2031 is a wheat germplasm line carrying *Lr28* gene, conferring resistance to brown rust. It was

KRL 35 (INGR No. 04013; IC408332), Wheat (*Triticum aestivum* L.) Germplasm Line with AmberColoured Grains and Agronomic Superiority over Parent Kharchia

KN Singh[1] and Ravish Chatrath[2]
1. *Central Soil Salinity Research Institute, Karnal-134201, Haryana*
2. *Directorate of Wheat Research, Karnal-134201, Haryana*

KRL 35 is a new wheat germplasm line with amber coloured grains and agronomic superiority over parent Kharchia, developed at the Central Soil Salinity Research Institute, Karnal. KRL 35 is tolerant to salinity and alkalinity/sodicity and was also found to be quite tolerant to water logging conditions in comparison to other wheat varieties. This genotype was tested in most of the northern states of the country coming under Northeastern plain I, and Northwestern plain zone. To improve salt tolerance and yield, a high yielding dwarf variety HD2160 was crossed with salt tolerant amber grained wheat variety KRL1-4, and KRL 35 was developed. It was first evaluated in the All India Coordinated Salinity/Alkalinity Tolerance Screening Nursery and was found promising, and promoted for salinity/alkalinity trial. Directorate of Wheat Research, Karnal regularly organises Salinity/ alkalinity nursery and trials under salinity/alkalinity conditions, at least at 10 different centres across the country in the states of Bihar, Uttar Pradesh, Haryana, Punjab, Gujarat, Maharashtra and Rajasthan. KRL35 was evaluated for three seasons from 2000-2001 to 2002-2003 under these trials and was found quite promising and yielded better than Kharchia 65 and high yielding check KRL 19 with overall average yield of 35.1 q/ha Singh and Chatrath (2003, 2002, 2001). However, it was found susceptible to leaf and strip rusts under artificially inoculated conditions.

KRL 35 is a two-gene dwarf wheat germplasm with an average plant height (recorded in salt affected soils and normal soil) of 98 cm with green leaf of intermediate width and waxy look. On an average it takes 90 days to heading and matures in about 145 to 150 days. It has medium awns and has parallel ears and intermediate ear density with average 1000-grain weight of 39 g.

Reference

Singh KN and R Chatrath (2003, 2002, 2001) *Reports presented in the All India Coordinated Wheat Research Workers Workshop* organized by Directorate of Wheat Research, Karnal.

WHEAT GENETIC STOCKS RESISTANT TO BROWN AND BLACK RUSTS

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3. *Directorate of Wheat Research, Regional Station, Shimla-171002, Himachal Pradesh*
4. *Directorate of Wheat Research, Karnal-134201, Haryana*

HW-2002 (INGR No. 04014; IC408333), Wheat (*Triticum aestivum* L.) Germplasm Line with Resistance to Brown and Black Rust (*Lr24* and *Sr24*)

HW-2002 is a wheat germplasm line carrying *Lr24* and *Sr24* linked genes, conferring resistance to brown rust and moderate resistance to black rusts. It was developed at the Indian Agricultural Research Institute, Regional Station, Wellington, through pedigree selection and backcrossing method involving Kalyansona*6/ TR 380-4*7/Ag#14. It has erect plant growth habit with 62 days to 50 percent heading and 114 days to maturity. It has white coloured elliptical grains with medium hard texture, 26.8 seeds/spike, and 1000-grain weight of 32 g. with 11.94 percent seed protein.

HW-2031 (INGR No. 04015; IC408334), Wheat (*Triticum aestivum* L.) Germplasm Line with Resistance to Brown Rust (*Lr28*)

HW-2031 is a wheat germplasm line carrying *Lr28* gene, conferring resistance to brown rust. It was

developed at the Indian Agricultural Research Institute, Regional Station, Wellington, through pedigree selection and backcrossing method involving Sonalika*8/CS2A/2M#4/2. It has erect growth habit with early maturity. It takes 60 days to 50 percent heading and 110 days to matures; produces amber, elliptical semi-hard textured grains, 28.6 seeds/spike, and 1000-grain weight of 28.0 g with 12.9 percent seed protein.

HW-2049 (INGR No. 04016; IC408338), Wheat (*Triticum aestivum* L.) Germplasm Line, Best Recombinant with Resistance to Brown and Black Rust (*Lr19* and *Sr25*)

HW-2049 is a wheat germplasm line carrying *Lr19* and *Sr25* linked genes, conferring resistance to brown and black rusts. It was developed at the Indian Agricultural Research Institute, Regional Station, Wellington, Tamil Nadu, through pedigree selection and backcrossing method involving HD 2285/Sunstar*C/C80-1. It has an erect plant growth habit and takes 63 days to 50 percent heading and 113 days to maturity. The grains are amber coloured, oblong with hard texture with 22 seeds/spike, and 1000-grain weight of 29.4 g. with 12.2 percent seed protein.

WHEAT GENETIC STOCKS RESISTANT TO LOOSE SMUT, KARNAL BUNT, STRIPE AND LEAF RUSTS

Avtar Singh Grewal, GS Nanda and Karam Chand
Punjab Agricultural University, Ludhiana-141005, Punjab

ML-1194 (INGR No. 04017; IC296780)

ML-1194 is a wheat (*Triticum aestivum* L.) germplasm line with resistance to loose smut, Karnal bunt, stripe and leaf rust in new genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method from the cross between Bb-Nad and No66-Pi. The genotype has intermediate growth habit with a plant height of 98 cm and dark green foliage. Heading and maturity on an average takes 97 and 130 days respectively. Ears are dense, white coloured with tapering shape. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 32.0 g. Resistance to loose smut pathogen was tested 26 times since 1976, while resistance to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons, i.e. for nine years and resistance to Karnal bunt pathogen under artificial screening.

WL-3093 (INGR No. 04018; IC296781)

WL-3093 is a wheat (*Triticum aestivum* L.) germplasm line with resistance to loose smut, Karnal bunt, stripe and leaf rust in different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, USA251-WL223 x WG 377. The plants have semi-spreading growth habit with plant height of 116 cm and dark green foliage. Heading and maturity on an average take 105 and 130 days respectively. Ear is dense white coloured with tapering shape with a length of 9 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 37.0 g. Resistance to loose smut pathogen was tested 27 times since 1975, while that to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02, seasons i.e. for 9 years and resistance to Karnal bunt pathogen under artificial screening.

WL-3203 (INGR No. 04019; IC296784)

WL-3203 is a wheat (*Triticum aestivum* L) germplasm line with resistance to loose smut, Karnal bunt, stripe and leaf rust in different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, (USA255 x K816) x WL202. The plant has an intermediate growth habit with plant height of 97 cm and dark green foliage. Heading and maturity on an average take 101 and 130 days respectively. Ear is dense white coloured with tapering shape with a length of 11 cm. Grains are amber coloured, hard textured, elongated with an average 1000-grain weight of 35.0 g. The resistance to loose smut pathogen was tested 26 times since 1976, while to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-

developed at the Indian Agricultural Research Institute, Regional Station, Wellington, through pedigree selection and backcrossing method involving Sonalika*8/CS2A/2M#4/2. It has erect growth habit with early maturity. It takes 60 days to 50 percent heading and 110 days to matures; produces amber, elliptical semi-hard textured grains, 28.6 seeds/spike, and 1000-grain weight of 28.0 g with 12.9 percent seed protein.

HW-2049 (INGR No. 04016; IC408338), Wheat (*Triticum aestivum* L.) Germplasm Line, Best Recombinant with Resistance to Brown and Black Rust (*Lr19* and *Sr25*)

HW-2049 is a wheat germplasm line carrying *Lr19* and *Sr25* linked genes, conferring resistance to brown and black rusts. It was developed at the Indian Agricultural Research Institute, Regional Station, Wellington, Tamil Nadu, through pedigree selection and backcrossing method involving HD 2285/Sunstar*C/C80-1. It has an erect plant growth habit and takes 63 days to 50 percent heading and 113 days to maturity. The grains are amber coloured, oblong with hard texture with 22 seeds/spike, and 1000-grain weight of 29.4 g. with 12.2 percent seed protein.

WHEAT GENETIC STOCKS RESISTANT TO LOOSE SMUT, KARNAL BUNT, STRIPE AND LEAF RUSTS

Avtar Singh Grewal, GS Nanda and Karam Chand
Punjab Agricultural University, Ludhiana-141005, Punjab

ML-1194 (INGR No. 04017; IC296780)

ML-1194 is a wheat (*Triticum aestivum* L.) germplasm line with resistance to loose smut, Karnal bunt, stripe and leaf rust in new genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method from the cross between Bb-Nad and No66-Pi. The genotype has intermediate growth habit with a plant height of 98 cm and dark green foliage. Heading and maturity on an average takes 97 and 130 days respectively. Ears are dense, white coloured with tapering shape. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 32.0 g. Resistance to loose smut pathogen was tested 26 times since 1976, while resistance to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons, i.e. for nine years and resistance to Karnal bunt pathogen under artificial screening.

WL-3093 (INGR No. 04018; IC296781)

WL-3093 is a wheat (*Triticum aestivum* L.) germplasm line with resistance to loose smut, Karnal bunt, stripe and leaf rust in different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, USA251-WL223 x WG 377. The plants have semi-spreading growth habit with plant height of 116 cm and dark green foliage. Heading and maturity on an average take 105 and 130 days respectively. Ear is dense white coloured with tapering shape with a length of 9 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 37.0 g. Resistance to loose smut pathogen was tested 27 times since 1975, while that to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02, seasons i.e. for 9 years and resistance to Karnal bunt pathogen under artificial screening.

WL-3203 (INGR No. 04019; IC296784)

WL-3203 is a wheat (*Triticum aestivum* L) germplasm line with resistance to loose smut, Karnal bunt, stripe and leaf rust in different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, (USA255 x K816) x WL202. The plant has an intermediate growth habit with plant height of 97 cm and dark green foliage. Heading and maturity on an average take 101 and 130 days respectively. Ear is dense white coloured with tapering shape with a length of 11 cm. Grains are amber coloured, hard textured, elongated with an average 1000-grain weight of 35.0 g. The resistance to loose smut pathogen was tested 26 times since 1976, while to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-

02 seasons, i.e. of nine years and resistance to Karnal bunt pathogen under artificial screening.

WL-3526 (INGR No. 04020; IC296785)

WL-3526 is a wheat (*Triticum aestivum* L) germplasm line resistant to loose smut, Karnal bunt, stripe and leaf rust in a new genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, HD2009 x WG 377. The plants have intermediate growth habit with plant height of 99 cm and dark green foliage. Heading and maturity on an average take 95 and 128 days respectively. Ear is dense white coloured with tapering shape. Ear length is 10 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 36 g. Resistance to loose smut pathogen was tested 24 times since 1978, while to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons, i.e. for 9 years and resistance to Karnal bunt pathogen under artificial testing.

WL-5634 (INGR No. 04021; IC296603)

WL-5634 is a wheat (*Triticum aestivum* L.) germplasm line resistant to loose smut, Karnal bunt, stripe and leaf rust in a different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, kav kaz-Cno-Inia x WL 905. The plants have intermediate growth habit with height of 97 cm and dark green foliage. Heading and maturity on an average take 96 and 130 days respectively. Ear is dense, white coloured with tapering shape and white coloured awns. Ear length is 9 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 30 g. The resistance to loose smut pathogen was tested 23 times since 1980, while resistance to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons (9 years) and resistance to Karnal bunt pathogen under artificial testing

AKW 2862-1 (INGR No. 04022; IC296767), Wheat (*Triticum aestivum* L.) Germplasm Line with Heat Tolerance

DG Vitkare
Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444104, Maharashtra

AKW 2862-1 is a wheat germplasm line with tolerance to heat and early maturity. It was developed through pedigree selection method in germplasm VEE # 6 || DOVE "S"/BUC "S" CM 92225-66Y-OM at Wheat Research Unit, PDKV, Akola. It was screened in 15 Short Duration cum Heat Tolerance Screening Nurseries conducted at 17 locations with an aim to identify genotypes of early maturity and tolerance to high temperature during grain-filling period under late sowing conditions. The genotype AKW 2862-1 showed consistent performance for these important traits during three subsequent seasons (1999-2000, 2000-2001 and 2001-2002). Mean days to heading were 63 days (with range of 46 - 106) with maximum and minimum temperature of 37.26°C and 8.83°C, respectively, and 1000-grain weight of 49 g (with range of 30-56 g).

Harit-1 (M3) (INGR No. 04023; IC427810), Wheat (*Triticum aestivum* L.) Germplasm Line, a New Source of Leaf Blight Resistance

DP Singh, Jag Shoran and Pankaj Kumar
Directorate of Wheat Research, Karnal-132001, Haryana

Leaf blight is a major biotic factor causing yield losses up to 50 percent in susceptible wheat varieties under warmer and humid weather of Northeastern plains zone (NEPZ). The disease causing pathogen *Bipolaris sorokiniana* syn. *Helminthosporium sativum* is present in all the six agro-climatic zones of India, neighbouring south Asia, China, North and Latin America and Brazil. Genotype showing no or little halo around necrotic spot is considered highly resistant.

Harit-1 (M3) is a new wheat (*Triticum aestivum*)

02 seasons, i.e. of nine years and resistance to Karnal bunt pathogen under artificial screening.

WL-3526 (INGR No. 04020; IC296785)

WL-3526 is a wheat (*Triticum aestivum* L) germplasm line resistant to loose smut, Karnal bunt, stripe and leaf rust in a new genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, HD2009 x WG 377. The plants have intermediate growth habit with plant height of 99 cm and dark green foliage. Heading and maturity on an average take 95 and 128 days respectively. Ear is dense white coloured with tapering shape. Ear length is 10 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 36 g. Resistance to loose smut pathogen was tested 24 times since 1978, while to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons, i.e. for 9 years and resistance to Karnal bunt pathogen under artificial testing.

WL-5634 (INGR No. 04021; IC296603)

WL-5634 is a wheat (*Triticum aestivum* L.) germplasm line resistant to loose smut, Karnal bunt, stripe and leaf rust in a different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, kav kaz-Cno-Inia x WL 905. The plants have intermediate growth habit with height of 97 cm and dark green foliage. Heading and maturity on an average take 96 and 130 days respectively. Ear is dense, white coloured with tapering shape and white coloured awns. Ear length is 9 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 30 g. The resistance to loose smut pathogen was tested 23 times since 1980, while resistance to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons (9 years) and resistance to Karnal bunt pathogen under artificial testing

AKW 2862-1 (INGR No. 04022; IC296767), Wheat (*Triticum aestivum* L.) Germplasm Line with Heat Tolerance

DG Vitkare
Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444104, Maharashtra

AKW 2862-1 is a wheat germplasm line with tolerance to heat and early maturity. It was developed through pedigree selection method in germplasm VEE # 6 || DOVE "S"/BUC "S" CM 92225-66Y-OM at Wheat Research Unit, PDKV, Akola. It was screened in 15 Short Duration cum Heat Tolerance Screening Nurseries conducted at 17 locations with an aim to identify genotypes of early maturity and tolerance to high temperature during grain-filling period under late sowing conditions. The genotype AKW 2862-1 showed consistent performance for these important traits during three subsequent seasons (1999-2000, 2000-2001 and 2001-2002). Mean days to heading were 63 days (with range of 46 - 106) with maximum and minimum temperature of 37.26°C and 8.83°C, respectively, and 1000-grain weight of 49 g (with range of 30-56 g).

Harit-1 (M3) (INGR No. 04023; IC427810), Wheat (*Triticum aestivum* L.) Germplasm Line, a New Source of Leaf Blight Resistance

DP Singh, Jag Shoran and Pankaj Kumar
Directorate of Wheat Research, Karnal-132001, Haryana

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WL-5634 (INGR No. 04021; IC296603)

WL-5634 is a wheat (*Triticum aestivum* L.) germplasm line resistant to loose smut, Karnal bunt, stripe and leaf rust in a different genetic background. It was developed at the Punjab Agricultural University, Ludhiana through pedigree selection method in cross, kav kaz-Cno-Inia x WL 905. The plants have intermediate growth habit with height of 97 cm and dark green foliage. Heading and maturity on an average take 96 and 130 days respectively. Ear is dense, white coloured with tapering shape and white coloured awns. Ear length is 9 cm. Grains are amber coloured, hard textured, elongated with average 1000-grain weight of 30 g. The resistance to loose smut pathogen was tested 23 times since 1980, while resistance to stripe and leaf rust races prevalent in the region, since 1993-94 to 2001-02 seasons (9 years) and resistance to Karnal bunt pathogen under artificial testing

AKW 2862-1 (INGR No. 04022; IC296767), Wheat (*Triticum aestivum* L.) Germplasm Line with Heat Tolerance

DG Vitkare
Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444104, Maharashtra

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Harit-1 (M3) (INGR No. 04023; IC427810), Wheat (*Triticum aestivum* L.) Germplasm Line, a New Source of Leaf Blight Resistance

DP Singh, Jag Shoran and Pankaj Kumar
Directorate of Wheat Research, Karnal-132001, Haryana

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Harit-1 (M3) is a new wheat (*Triticum aestivum*)

germplasm resistant to leaf blight. It was bred at CIMMYT, Mexico by using multiple crosses in which *T. tauschii* is one of the parents. The pedigree of the genetic stock is Cando/R143//Mexi"S"/3/*T. tauschii* (CI18). Screening against leaf blight was done at the Directorate of Wheat Research, Karnal. The present genetic stock has been found resistant to both pathogen (Table 1) and its toxin, helminthosporol (Singh, 2003; Singh *et al.*, 2002).

Table 1. Reactions of Harit-1 against leaf blight in comparison with susceptible check

Test	Harit-1 (Resistant)		Sonalika (Susceptible)	
	2002-03	2003-04	2002-03	2003-04
Infection response (seedling and adult stage)	R	R	S	S.
Leaf blight score on Flag (F) and F-1 leaf (adult stage)	01	02	89	99

R-Resistant, S-Susceptible

Harit-1 (M3) has spreading growth habit with plant height 127 cm, pink coloured coleoptile, colourless auricle and hairy green foliage (boot stage), flag leaf angle erect, leaf length 38 cm, leaf width 2 cm; leaf sheath, leaf blade, peduncle and ear-non waxy, ear semi-drooper, brown, medium length; 18 spikelets/ spike, long brown awn, brown outer glume, densely pubescent, shoulder shape with elevated beak and short curvature; red grain, semi hard, oblong, medium; light brown phenol reaction and takes 98 days to heading. Reaction to brown rust 0, yellow rust total resistant (TR), leaf blight, Karnal bunt 0 (under natural conditions) and powdery mildew 2.

References

Singh DP (2003) Screening of wheat genotypes for leaf blight resistance at seedling stage based on infection response against *Bipolaris sorokiniana*- a rapid and effective technique. *Indian Wheat Newsletter* 9: 10-11.

Singh DP, H Maraite, E Duveiller, M Diego and E Renard (2003) Comparison of host resistance to *Bipolaris sorokiniana*, the casual agent of leaf botches and its toxin in wheat. In: JB Rasmussen, TL Friesen and S Ali (eds). *Proceedings of 4th International Wheat Tan Spot and Spot Blotch Workshop*, held at Bemidji, MN, USA, (21-24 July 2002). pp 74-78.

MAIZE INBRED LINES FOR DIFFERENT NOVEL TRAITS

Sai Kumar Ramanujam, E Satyanarayana, P Mary Rekha, S Ravindra Babu, P Shanthi and D Rajesham

Agricultural Research Station, Acharya NG Ranga Agricultural University, Amberpet, Hyderabad- 500013, Andhra Pradesh

BML-2 (INGR No. 04024; IC411279)

BML-2 is a maize inbred line with prolific rabbit ears, tolerance to banded leaf sheath blight (BLSB), sorghum downy mildew (SDM), post flowering stock rot (PFSR) and water logging, and general combining ability (GCA). This inbred line was derived through pedigree selection method from improved germplasm stock namely modified X_1Y pools (X_1Y 110-OP-b96k-) at Agricultural Research Station, Amberpet, Hyderabad by introgressing a series of elite materials and through the adaptation of restricted pollination coupled with pedigree selection.

This inbred has tall green sturdy plants with anthocyanin pigmentation on culm. Leaf is dark green, semi erect, broad and normal with green leaf sheath. It bears erect loose tassel with medium side branches, green silk with pink tinge, green tight husk. The white ears bear lemon yellow coloured semi-dented grains. It takes 74 days to 50 percent pollen shedding and 76 days of 50 percent silking. Ear length is 15 cm and girth is 13 cm. with 14 seed rows/ear, 26 seeds/ row, seed test weight of 34 g and shelling percentage of 87. It gave a mean yield of 4000 kg/ha.

BML-3 (INGR No. 04025; IC411280)

BML-3 is a maize (*Zea mays* L.) inbred line with long productive ears, resistant to post flowering stock rot (PFSR), maydis leaf blight (MLB) and banded leaf sheath blight (BLSB), and general combining ability (GCA). This inbred was derived through pedigree selection method from improved germplasm stock, namely, NMH 502-B97K at Agricultural Research Station, Amberpet, Hyderabad by introgressing series of elite materials and through adaptation of restricted pollination coupled with pedigree selection.

The inbred has short sturdy plants, green culm

germplasm resistant to leaf blight. It was bred at CIMMYT, Mexico by using multiple crosses in which *T. tauschii* is one of the parents. The pedigree of the genetic stock is Cando/R143//Mexi"S"/3/*T. tauschii* (CI18). Screening against leaf blight was done at the Directorate of Wheat Research, Karnal. The present genetic stock has been found resistant to both pathogen (Table 1) and its toxin, helminthosporol (Singh, 2003; Singh *et al.*, 2002).

Table 1. Reactions of Harit-1 against leaf blight in comparison with susceptible check

Test	Harit-1 (Resistant)		Sonalika (Susceptible)	
	2002-03	2003-04	2002-03	2003-04
Infection response (seedling and adult stage)	R	R	S	S.
Leaf blight score on Flag (F) and F-1 leaf (adult stage)	01	02	89	99

R-Resistant, S-Susceptible

Harit-1 (M3) has spreading growth habit with plant height 127 cm, pink coloured coleoptile, colourless auricle and hairy green foliage (boot stage), flag leaf angle erect, leaf length 38 cm, leaf width 2 cm; leaf sheath, leaf blade, peduncle and ear-non waxy, ear semi-drooper, brown, medium length; 18 spikelets/ spike, long brown awn, brown outer glume, densely pubescent, shoulder shape with elevated beak and short curvature; red grain, semi hard, oblong, medium; light brown phenol reaction and takes 98 days to heading. Reaction to brown rust 0, yellow rust total resistant (TR), leaf blight, Karnal bunt 0 (under natural conditions) and powdery mildew 2.

References

Singh DP (2003) Screening of wheat genotypes for leaf blight resistance at seedling stage based on infection response against *Bipolaris sorokiniana*- a rapid and effective technique. *Indian Wheat Newsletter* 9: 10-11.

Singh DP, H Maraite, E Duveiller, M Diego and E Renard (2003) Comparison of host resistance to *Bipolaris sorokiniana*, the casual agent of leaf botches and its toxin in wheat. In: JB Rasmussen, TL Friesen and S Ali (eds). *Proceedings of 4th International Wheat Tan Spot and Spot Blotch Workshop*, held at Bemidji, MN, USA, (21-24 July 2002). pp 74-78.

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BML-2 (INGR No. 04024; IC411279)

BML-2 is a maize inbred line with prolific rabbit ears, tolerance to banded leaf sheath blight (BLSB), sorghum downy mildew (SDM), post flowering stock rot (PFSR) and water logging, and general combining ability (GCA). This inbred line was derived through pedigree selection method from improved germplasm stock namely modified X_1Y pools (X_1Y 110-OP-b96k-) at Agricultural Research Station, Amberpet, Hyderabad by introgressing a series of elite materials and through the adaptation of restricted pollination coupled with pedigree selection.

This inbred has tall green sturdy plants with anthocyanin pigmentation on culm. Leaf is dark green, semi erect, broad and normal with green leaf sheath. It bears erect loose tassel with medium side branches, green silk with pink tinge, green tight husk. The white ears bear lemon yellow coloured semi-dented grains. It takes 74 days to 50 percent pollen shedding and 76 days of 50 percent silking. Ear length is 15 cm and girth is 13 cm. with 14 seed rows/ear, 26 seeds/ row, seed test weight of 34 g and shelling percentage of 87. It gave a mean yield of 4000 kg/ha.

BML-3 (INGR No. 04025; IC411280)

BML-3 is a maize (*Zea mays* L.) inbred line with long productive ears, resistant to post flowering stock rot (PFSR), maydis leaf blight (MLB) and banded leaf sheath blight (BLSB), and general combining ability (GCA). This inbred was derived through pedigree selection method from improved germplasm stock, namely, NMH 502-B97K at Agricultural Research Station, Amberpet, Hyderabad by introgressing series of elite materials and through adaptation of restricted pollination coupled with pedigree selection.

The inbred has short sturdy plants, green culm

and green brace root. Leaves are light green, semi erect, medium with green leaf sheath. It bears medium tassel that are loose, erect, medium side branches and green silk, while husk is green and tight. It has very long productive ears. The cobs are cylindrical and white with yellow semi-dented grains. It gave a mean yield of 4000 kg/ha with 80 days to 50 percent pollen shedding and 83 days to 50 percent silking. Ear length is 18 cm and girth is 13 cm with 14 seed rows/ear, 35 seeds/row, seed test weight of 35 g and shelling percentage 87. It is good as female parent.

BML-5 (INGR No. 04026; IC411281)

BML-5 is maize (*Zea mays* L.) inbred line with dwarf plants and tolerance to BLSB, MLB and Turcicum Leaf Blight (TLB), and high GCA. This inbred was derived through pedigree selection method in Nizamabad OP 7 at the Nizamabad, Andhra Pradesh, and improved at the Agricultural Research Station, Amberpet, Hyderabad by introgressing a series of elite materials and through the adaptation of restricted pollination coupled with pedigree selection.

The inbred has short internodal length, bending plant type, stem with green culm and green red brace roots. Leaves are green, drooping, broad and with green leaf sheath. It bears medium semi-compact tassel with semi-drooping side and purple silk. Husk is green and tight. It bears white cylindrical straight rowed, tip filled rigid cob with pink flinted grains. It gave a mean yield of 2666 kg/ha with 78 days to 50 percent pollen shedding, 78 days to 50 percent silking, ear length of 12 cm and girth 14 cm with 16 seed rows/ ear, 20 seeds/row, seed test weight of 26.0 g and shelling percentage 83.

BML-7 (INGR No. 04027; IC411283)

BML-7 is a maize (*Zea mays* L.) inbred line with orange colour seeds, tolerant to BLSB, MLB and SDM, and high GCA It was derived through pedigree selection method from F_1 progeny of X_2Y pool x CML-226 germplasm at the Nizamabad, Andhra Pradesh, and improved at the Agricultural Research Station, Amberpet, Hyderabad through adaptation of restricted pollination coupled with pedigree selection.

The inbred has tall plants with broad green leaves and orange coloured seeds. It is a good general and specific combiner. Leaves are broad normal green and drooping with green leaf sheath. The medium size loose tassels are erect with medium side branches. The glumes and anthers are purple pigmented and the silk is pink. Husk is green and tight. It bears white cylindrical straight rowed, tip filled rigid cob with pink flinted grains. It gave a mean yield of 3333 kg/ha with 74 days to 50 percent pollen shedding and 76 days of 50 percent silking. Ear length is 13 cm and girth is 12.5 cm. with 14 seed rows/ear and 20 seeds/row, seed test weight of 27.5 g. and shelling percentage of 83.

BML-8 (INGR No. 04028; IC411284)

BML-8 is a maize (*Zea mays* L.) inbred line with tall plants, conical shape ears and high GCA. This inbred line was derived through pedigree selection from stock rot resistant germplasm, SRRL 79 screened at pathology section of the station and it was modified and improved at the Agricultural Research Station, Amberpet, Hyderabad through adaptation of restricted pollination coupled with pedigree selection.

It has very tall plants, characteristic conical shaped ears with yellow dent grains with presence of aborted cluster of glumes, above the tip of the shank. Leaves are green and drooping with green leaf sheath. The medium size loose tassel are erect and with medium side branches. The glumes and silk are green and anthers are yellow. Husk is green and tight covering the tip. It bears white cylindrical straight rowed, tip filled rigid cob with yellow flint grains. It gave a mean yield of 3733 kg/ha and took 78 days to 50 percent pollen shedding and 82 days of 50 percent silking. Ear length is 16 cm and girth is 13 cm. 14 seed rows/ear and 30 seeds/row. Seed test weight was 27 g. and shelling percentage 85. It is good both as male and female parent.

BML-11 (INGR No. 04029; IC411285)

BML-11 is a maize inbred line with prolific ears, very peculiar tassel resembling sorghum panicle i.e. lateral branches arranged in a distinct manner and length. Anthers are very small. It was derived through pedigree selection from Suavan germplasm SUVAN3-B96 and improved for its adaptability and productivity at the Agricultural Research Station, Amberpet, Hyderabad through adaptation of restricted pollination coupled with pedigree selection.

It gave mean yield of 4000 kg/ha and took 73 days to 50 percent pollen shedding and 75 days to

50 percent silking. Ear length is 11 cm and girth is 14 cm with 14 seed rows/ear and 28 seeds/row. The seed test weight was 20.5 g and shelling percentage 83. It bears green culm with purple brace roots, light green semi-erect leaf and light green leaf sheath. The tassel is medium erect, with few side branches having purple tinge and green anther. The white cylindrical rigid cob bears orange yellow flint grains filled up to the tip in straight row.

BML-14 (INGR No. 04030; IC411286)

BML-14 is a maize inbred line with medium height plants, green tassel and extended pollen shedding period (7 days) and good combining ability. This maize inbred line was derived through pedigree selection from an improved germplasm stock, namely, modified XY_2 pools COIB 96K and improved at the Agricultural Research Station, Amberpet, Hyderabad, by introgressing a series of elite material and adopting restricted pollination coupled with pedigree selection.

It gives a mean yield of 3060 kg/ha and took 65 days to 50 percent pollen shedding and 68 days to 50-percent silking. Ear length is 11.0 cm and girth is 16 cm with 16 seed rows/ear and 25 seeds/row. The seed test weight was 25.0 g and shelling percentage 85. It bears green culm with green brace roots, light green broad drooping normal leaf and green leaf sheath. The tassel is loose and medium in size. The white cylindrical rigid cob with green tight husk bears orange flint grains. The central rachis of the tassel is U shaped at the tip.

BML-15 (INGR No. 04031; IC411287)

BML-15 is a maize inbred line used as tester and is endowed with water logging tolerance and resistant to maydis leaf blight, turcicum leaf blight, banded leaf sheath blight and Sorghum downy mildew, and have good general combining ability. This maize inbred line was derived through pedigree selection from F_1 progeny of X_2Y pools x CML-226, and improved at the Agricultural Research Station, Amberpet, Hyderabad for adaptability and productivity through adaptation of restricted pollination coupled with pedigree selection method.

BML-15 has tall plants, drooping light green long leaves and bold pointed seeds with light pigment at the base of the seed. The plants are sturdy bearing green culm. Leaves are normal dark green, broad, drooping with green leaf sheath and few purple spots. The big loose drooping tassels bare drooping large side branches. It has green glumes with purple tinge and pink silk. It has tight green husk covering the tip. It bears white cylindrical straight rowed, tip filled rigid cob with pink flint grains. It gave a mean yield of 2133 kg/ha and took 74 days to 50 percent pollen shedding and 78 days to 50 percent silking. Ear length is 15 cm and girth is 12.5 cm. with 12 seed rows/ ear and 25 seeds/row. The seed test weight is 27 g, while the shelling percentage is 87.

BML-20 (INGR No. 04032; IC411288)

BML-20 is a maize (*Zea mays* L.) inbred line with extra green stem, tolerant to lodging and good general combining ability. It has medium height dark green sturdy plant having angular bold orange seed with a small dot on the top. It was derived through pedigree selection from SUVAN-1 (D) and improved for its adaptability and productivity at the Agricultural Research Station, Amberpet, Hyderabad through adaptation of restricted pollination coupled with pedigree selection method.

Leaves are normal, dark green and broad, erect with green leaf sheath. The tassels are semi compact erect bearing large side branches. It bears green glumes with green anthers, green silk and tight green husk covering the tip. It cobs are white cylindrical straight rowed, tip filled rigid cob with orange flint grains. It gave a mean yield of 3333 kg/ha with 73 days to 50% pollen shedding and 75 days to 50% silking. Ear length is 13 cm and girth is 14 cm with 14 seed rows/ear and 25 seeds/row. The seed test weight is 29 g and 86 percent shelling.

BML-22 (INGR No. 04033; IC411289)

BML-22 is a maize (*Zea mays* L.) inbred line with big tassel, drooping large narrow leaves, without anthocyanin pigmentation on brace roots. This maize inbred line was derived through pedigree selection from improved germplasm stock, namely modified X_1Y pool improved at Agricultural Research Station, Amberpet, Hyderabad by introgressing series of elite materials and through the adaptation of restricted pollination coupled with pedigree selection.

It has medium tall plants with green culm and green brace roots. Leaves are normal, light green and with green leaf sheath. The medium tassel is semi-compact, erect bearing medium side branches. It bears green glumes, yellow anthers, and green silk and tight

green husk covering the tip. Cobs are white cylindrical straight rowed, tip filled rigid cob with orange yellow flinted grains. It gave a mean yield of 3066 kg/ha with 74 days to 50% pollen shedding and 76 days to 50% silking. Ear length is 14 cm and girth is 12 cm 12 seed rows/ear, 30 seeds/row. The seed test weight is 25.2 g and shelling percentage 85.

MAIZE INBRED LINES FOR DIFFERENT NOVEL TRAITS

Sain Dass and Kulbir Singh Dhanju

Chaudhary Charan Singh Haryana Agricultural University, Regional Research Station, Uchani, Karnal-132001, Haryana

HKI-139 (INGR No. 04065; IC405276)

HKI-139 is an early maize (*Zea mays* L.) inbred line, with an orange grain colour, cold tolerance, high general combining ability and resistance to maydis leaf blight (MLB) [(*Drechslera maydis* Nisik.) Subram. and Jain] (Table 1). It was developed at the Chaudhary Charan Singh Haryana Agricultural University (CCSHAU), Regional Research Station, Uchani, Karnal (Annual Report, 1999-2001). The line was developed by utilizing exotic germplasm, Pozarica 80 MBRS from CIMMYT Mexico. Inbreeding was initiated in this population and ear to row selection was practiced. After six generations of selfing the line was evaluated for different characters along with combining ability. It has long cob (9.0-11.5 in different seasons) with attractive grain colour, medium maturity (95-110 cm in *kharif* and 75-85 cm in *rabi*), dark green, semi-drooping leaf; green stem, dense tassel, medium secondary branches, green anther, green glume, green silk, husk cover green and tight, cylindrical ear, purple heart, grain up to tip, straight kernel rows, flint grain orange, round, medium bold in size. It takes 50-54 days and 134-137 days to 50 per cent tasselling and 53-57 days and 136-141 days to silking in *kharif* and *rabi*, respectively. This line could survive during the month of January at around 4°C, suggesting; it possessed fair tolerance to cold (Table 1). The productivity of this line in winter is high as compared to *kharif* season.

Table 1. Disease reaction of hki-139 under artificial inoculation conditions and cold tolerance under natural field conditions

Year	MLB		Common Rust		Cold Tolerance (1-5)
	HKI 139	CM-600*	HKI 139	CM-202*	139
2001	2.5	4.5	2.0	4.5	1.5
2002	2.0	5.0	2.5	5.0	1.5
2003	2.0	5.0	2.5	4.5	1.5
Mean	2.2	4.8	2.3	4.6	1.5

* Susceptible check

Reference

Annual Report (1999-2001) Evaluation of selected/new inbred lines of maize against excess soil moisture. Directorate of Maize Research, Cummings Laboratory, Pusa Campus, New Delhi, pp102-104.

HKI-323-8 (INGR No. 04066; IC405278)

HKI-323-8 is a medium maturing MLB (*Drechslera maydis* Nisik.) Subram. and Jain] resistant inbred line with orange grain colour and high GCA, developed from subtropical Pool-28 population from CIMMYT. It was developed at the CCS HAU, Regional Research Station, Uchani, Karnal (Annual Report, 1999-2001). This line was derived through continuous selfing till the line became uniform for morpho-physiological traits.

It has medium maturity, medium height (100-115 cm), medium broad and dark green drooping leaf, green stem, lax, semi-drooping, medium, without secondary branches tassel, pink anther, purple glume, purple silk and attractive, green with purple patches, tight husk cover, cylindrical long (10.5-13.0 cm) ear, white heart, grain up to tip and straight kernel rows. It has shining flint grain with white thin gully, orange colour, round with medium bold size. It takes 52-54 and 134 days to 50 percent tasselling and 54-56 and 136 days to silking in *kharif* and *rabi*, respectively. The yield potential of the line varies from 20.0-24.4 q/ha in different seasons. This line was evaluated for MLB under artificial disease condition to confirm the level of resistance to disease (Table 1). High yielding hybrids with dark orange grain colour were produced, when HKI-1105, 288, 295, 488, 1040-7 were crossed with 323-8.

Table 1. Disease reaction of HKI 323-8 against Maydis Leaf Blight under artificial inoculation conditions.

Kharif	HKI-323-8	CM-600*
2001	2.0	4.5
2002	2.5	5.0
2003	2.0	5.0
Mean	2.2	4.6

*Susceptible check

Table 1. Cold tolerance and disease reaction of HKI 586

Year	Cold Tolerance	Common Rust	
	HKI 586	HKI 586	CM-202*
2001	1.5	1.0	4.5
2002	1.0	1.5	5.0
2003	1.5	1.5	5.0
Mean	1.3	1.3	4.8

* Susceptible Check

Reference

Annual Report (1999-2001) Description of HAU maize inbred lines, Directorate of Maize Research, Cummings Laboratory, Pusa Campus, New Delhi, pp 102-104.

HKI-1344 (INGR No. 04075; IC408330)

HKI-1344 is a maize inbred line with white, flint, bold grain, maydis leaf blight [(*Drechslera maydis* Nisik.) Subram. and Jain] and rust resistance (Table 1), productive and good general combiner. It was derived from subtropical heterotic Group-B, CIMMYT, Mexican population through continuous inbreeding, following ear to row selection procedure at the CCSHAU, Regional Research Station, Uchani, Karnal (Annual Report,1999-2001). It belongs to medium to full season maturity group and takes 57-58 days to flower in *kharif* and 90-95 days to maturity. It takes 60 days in *kharif* and 137-139 days in *rabi* to 50 percent silking. Leaves are broad, erect and dark green, white glume, green silk, green and tight husk cover, cylindrical, medium long (10.5-12.0 in different seasons) ear, white heart, bold, flat, flint/semi-flint grain with a yield of 24-28.0 q/ha.

Table 1. Disease reaction of HKI-1344 against maydis leaf blight and common rust under artificial inoculation conditions

Year	MLB		Rust	
	1344	CM-600*	1352-58-9	CM-202*
2001	1.0	4.5	1.0	4.5
2002	1.0	5.0	1.0	5.0
2003	1.0	5.0	1.5	4.5
Mean	1.0	4.8	1.2	4.6

Reference

Annual Report (1999-2001) Description of HAU maize inbred lines, Directorate of Maize Research, Cummings Laboratory, Pusa Campus, New Delhi, pp 102-104.

JCR/TRS-489 (INGR No. 04034; IC258233), an Easy De-hulling Type Buckwheat (*Fagopyrum tataricum* Gaertn.)

JC Rana[1], TR Sharma[2], VD Verma[1], SK Yadav[1] and K Pradheep[1]

1. National Bureau of Plant Genetic Resources, Regional Station Shimla-171004, Himachal Pradesh

2. Centre of Hill Bioresources and Biotechnology, Himachal Pradesh Agricultural University, Palampur-176 062, Himachal Pradesh

JCR/TRS-489 is an easy de-hulling type buckwheat, (*Fagopyrum tataricum* Gaertn.), identified from a local germplasm at NBPGR, Regional Station Shimla. Buckwheat in general is bitter and difficult to de-hull, thus produces black flour, which is not liked for bread making. Easily de-hulled type germplasm are very rare. Germplasm accession IC258233 collected from Kullu district of Himachal Pradesh has non-adhering hull and can be de-hulled just by rubbing with hands. Easily de-hulled varieties give white flour, which has great potential in the noodle/by product industry of buckwheat. Generally, sweet buckwheat is used in the noodle industry because of its easy de-hulling characteristic, although bitter buckwheat has more nutritional and medicinal value, but due to difficulty in de-hulling it has limited use in the industry. This type of buckwheat is popularly known as 'rice buckwheat' due to its white kernels. The material can be directly brought into cultivation or after selection of high yielding materials. This accession has also been found high yielding and included in the All India Coordinated Research Network on Under-utilised Crops in the year 2004. The data showed that it has average seed weight, plant height and fall in medium flowering and maturity group. The grain yield is above average. The details of other morphological characters are given in Table 1.

Table 1. Characteristic feature of the germplasm accessions JCR/TRS-489

Characters	Mean Value	Characters	Mean Value
Plant height (cm)	53.65	No. of seed/cyme	10.00
Leaf length (cm)	7.45	1000 seed wt. (g)	15.40
Leaf width (cm)	9.00	Seed yield/plant (g)	28.96
No. of leaves	12.50	Leaf colour	Green
No. of internodes	11.50	Leaf margin colour	Pink
Petiole length (cm)	5.80	Leaf blade shape	Hastate
No. of primary branches	4.50	Early plant vigour	Very good
No. of cymes/plant	14.50	Plant growth habit	Erect
Length of cyme (cm)	2.55	Seed shattering	Moderate
Days to 50% flowering	39.00	Seed shape	Ovate
Days to 80% maturity	107.00	Seed colour	Black

Table 1. Cold tolerance and disease reaction of HKI 586

Year	Cold Tolerance	Common Rust	
	HKI 586	HKI 586	CM-202*
2001	1.5	1.0	4.5
2002	1.0	1.5	5.0
2003	1.5	1.5	5.0
Mean	1.3	1.3	4.8

* Susceptible Check

Reference

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Length of cyme (cm)	2.55	Seed shattering	Moderate
Days to 50% flowering	39.00	Seed shape	Ovate
Days to 80% maturity	107.00	Seed colour	Black

CMS 67A & B, (INGR No. 04036; IC296622 & IC296623), Pigeonpea (*Cajanus cajan* L.) Germplasm Line with Cytoplasmic Male Sterility Conferred by a New Cytoplasm (*Cajanus sericeus*)

PP Zaveri[1] and BB Singh[2]
1. *Gujarat State Fertilizer and Chemical Ltd., Vadodara, Gujarat*
2. *Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh*

CMS 67A is a cytoplasmic male sterile (CMS) line carrying cytoplasm of wild *Cajanus sericeus* (Benth. Ex Bak.) van der Maesen. The material was developed by wide hybridisation followed by mutagenesis and backcross [*Cajanus sericeus* x ICPL85010 x Mutant of QMS 1 (M_7)] (Singh *et al.*, 2004). This line was evaluated. purified and is being maintained at the Indian Institute of Pulses Research, Kanpur. CMS 67A is an early maturing, determinate type, but is susceptible to wilt (60% mortality), moderately resistant to sterility mosaic and *Phytophthora* stem blight diseases. The plants are 100 percent male sterile with white translucent anthers, which are devoid of pollen grains.

The plants are 102-106 cm tall with an average of 6.6 branches per plant, flowering in about 80-85 days, bearing yellow coloured flowers. The average number of pods per plant is 182.33. The pods are 4-6 cm long and their colour is green with black strips. Average number of seeds per pod is 3.66. The test weight of seed is 8.02. Seeds are dark red in colour. The seed yield was optimum at proportion of 6 female: 1 male row and 60 cm row spacing.

Reference

Singh BB, IP Singh, Sudha Asthana, G Singh and ND Majumdar (2004) Diversification and evaluation of CMS lines in pigeonpea. *Indian J. Pulses Research* (In Press).

CMS ICPL 84023 A & B (INGR No. 04035; IC296624 & IC296625), Pigeonpea (*Cajanus cajan* L.) Germplasm Line with Cytoplasmic Male Sterility in Early and Multiple Disease Resistance Background

BB Singh, IP Singh, Sudha Asthana, G Singh and ND Majumdar
Indian Institute of Pulses Research, Kanpur-208 002, Uttar Pradesh

ICPL 84023 A is a converted cytoplasmic genetic male sterile line obtained at BC_7 stage by crossing CMS 67A with ICPL 84023 maintained in the gene bank of IIPR Kanpur (Singh *et al.*, 2004). It was produced through recurrent selection, individual plants in CMS as well as in recurrent parents were tagged. Crosses were made on plant-to-plant basis. The individual plants of ICPL 84023 used in crossing programme were selfed to get pure seed for next season. The hybrid seed were grown along with selfed seed of recurrent parent (ICPL 84023). The individual F_1 plants were tested for pollen sterility. The sterile plants were crossed with the recurrent parent till BC_5F_1 generation. For the seed production of CMS 84023 A, proportion of 6 female : 1 male row is found to be better with 60 cm spacing between rows.

ICPL 84023 A has creamy white anthers devoid of pollen grains and was found to be 100% male sterile during *kharif* 2002-2003 and 2003-2004. It is high yielding, resistant to wilt and sterility mosaic virus, and tolerant to *Phytophthora* stem blight. The plants are 188-190 cm tall having 6-8 branches per plant and flower in about 88 days. Flowers are yellow in colour. There are about 155-168 pods per plant, which are light green in colour. The average pod length is about 4.4 cm. Each pod has 3.3 (average) seeds, which are reddish in colour. The test weight of seeds is 8.12 g.

Reference

Singh BB, IP Singh, Sudha Asthana, G Singh and ND Majumdar (2004) Diversification and evaluation of CMS lines in pigeonpea. *Indian J. Pulses Research* (In Press).

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GDM–1, Guar Determinate Mutant (INGR No. 04037; IC296671), Cluster Bean (*Cyamopsis tetragonoloba* (L). Taub.)

A Henry
Central Arid Zone Research Institute, Jodhpur-342003, Rajasthan

GDM–1 is a cluster bean (*Cyamopsis tetragonoloba* (L). Taub.) mutant with determinate plant type. It was developed at the Department of Plant Sciences and Biotechnology, Central Arid Zone Research Institute, Jodhpur through mutation breeding by treating the seeds of variety FS-277 with Ethyl Methane sulphonate (0.25%) (Henry, 2001). This mutant has determinate growth habit in comparison to indeterminate habit of its parent. It has relatively less plant height (average 70.6 cm) over the parent with slight reduced maturity (average 70.6 days), with more number of pods per plant and higher grain yield potential.

Reference

Henry A (2001) Performance of determinate plant type mutant vis-à-vis indeterminate varieties of clusterbean. In: *Plant physiology for sustainable forestry agri-horticulture and industry, stress and environmental plant physiology* KK Bora, Karan Singh and Arvind Kumar (eds.), Pointer Publishers, Jaipur, Chapter 15.

CAZC-B (INGR No. 04038; IC296672), Cowpea (*Vigna unguiculata* (L.) Walp.) Germplasm Line with Black Seed Coat Colour

A Henry
Central Arid Zone Research Institute, Jodhpur-342 003, Rajasthan

CAZC-B 38 is a cowpea mutant with black seed coat colour. It was developed at the Department of Plant Sciences and Biotechnology, Central Arid Zone Research Institute, Jodhpur through mutation breeding by treating variety Charodi-1 with gamma irradiation (Henry, 2001). It is suitable for cowpea growing areas particularly arid regions. This mutant has marginally excelled the parent variety with increased plant height (IVT mean of 70.0 cm; Jodhpur it was 58.2 cm), pods/plant (28.3), days to maturity (IVT mean of 73.2 days; in Jodhpur mean is 70.0 cm) and 100-seed weight (IVT mean of 8.2 g; in Jodhpur it was 8.0 g). The performance is superior to most of the check varieties including Pusa Phalguni in All India Coordinated Research Project on arid legumes. The disease incidence in arid regions it was low.

Reference

Henry A (2001) Performance of induced black seed cost mutant in cowpea. A short communication. *Indian J. Genet.* **61:** 381-382.

TG-18AM (INGR No. 04039; IC296610), Groundnut (*Arachis hypogaea* L.) Germplasm Line with Leaf Disease Like Mimic Lesion

Chandra Mouli, DM Kale, AM Badigannavar and GSS Murty
Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai-400085, Maharashtra

In groundnut (*Arachis hypogaea* L.) a leaf mutant with mimic disease lesion, designated as TG-18AM, was isolated in M3 generation of TG 18A produced by irradiating seeds with 300 Gy g rays at the Bhabha Atomic Research Centre, Mumbai (Chandramouli and Kale, 1982). It is characterized by the basal four to five leaves remaining green and subsequent newly opened leaves showing light green colour with yellow specks, which start from the leaflet tip and progress towards the base of leaflet. Coalescence of specks result in yellow blotches, which gradually spread to make the whole leaflet yellow. Simultaneously, brown

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specks start appearing and cover the entire leaflet, resembling rust disease symptom. With the advancement of age, the lower leaves gradually turn green. Unopened leaves on the main axis have a few yellow specks. The 10^{th} – 12^{th} leaf below the shoot apex has green colour with or without brown specks. Leaves on branches exhibit a similar pattern. Chlorophyll a, chlorophyll b, and total chlorophyll in the upper leaves of mutants were much lower than parent. Two suppressive genes govern the mutant traits, which are also found allelic to disease lesion mimic leaf of somaclonal variant derived from cv. TAG-24 (Badigannavar *et. al.*, 2002). Mutant is inferior to its parent TG-18A with respect to pod yield. It has papery thin shell resulting in very high kernel out turn of 84% (Chandramouli, *et. al.*, 1989).

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TGE-1 (INGR No. 04040; IC296612), Groundnut (*Arachis hypogaea* L.) Germplasm Line with Foliaceous Stipule

Chandra Mouli and DM Kale

Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai-400085, Maharashtra

In groundnut (*Arachis hypogaea* L.), early maturity facilitates the crop to fit into diverse cropping systems. Trombay Groundnut Early (TGE-1) with an early maturity and foliaceous stipules was obtained in F_3 generation from a cross between TG-9 and tall mutant during *kharif* 1974 at the Bhabha Atomic Research Centre, Mumbai (Chandramouli and Kale, 1982). In TGE-1, the basal two leaves on main stem and branches were modified from the usual sickle shaped stipules to oval shaped leafy stipules. Presence of modified stipules gave the false appearance of a pinnate leaf with three-paired leaflets. In a comparative study involving TGE-1, TG-3 and Chico, TGE-1 was found taller than Chico and shorter than TG-3. It had more number of primary and secondary branches, dark green leaves, pods with shallow constriction, smooth reticulation and more three seeded pods. TGE-1 matured in 95 days, which was 10 days earlier than TG-3. Besides, it had comparatively high kernel out turn (80%) and oil content (51%).

TGE-1 was identified for earliness (less than 90 days) among Spanish bunch types in All India Coordinated Research Project on Oilseeds (Anonymous, 1988). By using TGE-1, new varieties, such as, TAG-24 (Patil *et al.*, 1995) and JCC-88 were bred (Bandyopadhyay and Manivel, 2001).

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specks start appearing and cover the entire leaflet, resembling rust disease symptom. With the advancement of age, the lower leaves gradually turn green. Unopened leaves on the main axis have a few yellow specks. The 10^{th} – 12^{th} leaf below the shoot apex has green colour with or without brown specks. Leaves on branches exhibit a similar pattern. Chlorophyll a, chlorophyll b, and total chlorophyll in the upper leaves of mutants were much lower than parent. Two suppressive genes govern the mutant traits, which are also found allelic to disease lesion mimic leaf of somaclonal variant derived from cv. TAG-24 (Badigannavar *et. al.*, 2002). Mutant is inferior to its parent TG-18A with respect to pod yield. It has papery thin shell resulting in very high kernel out turn of 84% (Chandramouli, *et. al.*, 1989).

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TGE-1 (INGR No. 04040; IC296612), Groundnut (*Arachis hypogaea* L.) Germplasm Line with Foliaceous Stipule

Chandra Mouli and DM Kale

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In groundnut (*Arachis hypogaea* L.), early maturity facilitates the crop to fit into diverse cropping systems. Trombay Groundnut Early (TGE-1) with an early maturity and foliaceous stipules was obtained in F_3 generation from a cross between TG-9 and tall mutant during *kharif* 1974 at the Bhabha Atomic Research Centre, Mumbai (Chandramouli and Kale, 1982). In TGE-1, the basal two leaves on main stem and branches were modified from the usual sickle shaped stipules to oval shaped leafy stipules. Presence of modified stipules gave the false appearance of a pinnate leaf with three-paired leaflets. In a comparative study involving TGE-1, TG-3 and Chico, TGE-1 was found taller than Chico and shorter than TG-3. It had more number of primary and secondary branches, dark green leaves, pods with shallow constriction, smooth reticulation and more three seeded pods. TGE-1 matured in 95 days, which was 10 days earlier than TG-3. Besides, it had comparatively high kernel out turn (80%) and oil content (51%).

TGE-1 was identified for earliness (less than 90 days) among Spanish bunch types in All India Coordinated Research Project on Oilseeds (Anonymous, 1988). By using TGE-1, new varieties, such as, TAG-24 (Patil *et al.*, 1995) and JCC-88 were bred (Bandyopadhyay and Manivel, 2001).

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Small Leaf Mutant (INGR No. 04041; IC296613), Groundnut (*Arachis hypogaea* L.) Germplasm Line

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Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai-400085, Maharashtra

A small leaf mutant with light yellow flower colour was isolated in groundnut (*Arachis hypogaea* L.) in M4 generation during 1968 at the Bhabha Atomic Research Centre, Mumbai (Patil and Mouli, 1984), following g-ray treatment to the seeds of Spanish Improved variety. It is characterized by reduced plant height (20-25%) and reduced leaflet size (>50%) compared to its parent variety. Its leaves were light green with approximately 10% imparipinnate and 20% accessory leaflets. The flowering axils were absent on the main stem resembling the ssp. *hypogaea* var. *hypogaea*, with an irregular flowering pattern on the branches. The mutant has greater number of thin branches. The flower colour was light yellow unlike orange in the parent. Pod size was smaller leading to 50% reduced kernel weight. The mutant matured two weeks earlier. It is inferior in yield, however it can be used as a marker. Inheritance study by involving small leaf mutant and its parents indicate a deviation from monohybrid segregation due to reduced frequency of mutant types, presumably due to "preferential" segregation favouring normal leaf size (Patil and Mouli, 1984).

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MH 34 (INGR No. 04076; IC401583), Groundnut (*Arachis hypogea* L.) Germplasm Line with High Oil Content (54%)

JS Malik[1], TP Yadava[1], DC Nijhawan[1], RK Sheoran[1], Parkash Kumar[2] and SK Gupta[1]
1. *Chaudhary Charan Singh Haryana Agricultural University, Hisar-125004, Haryana*
2. *National Oilseed and Vegetable Oil Development Board, 86, Sector-18, Gurgaon, Haryana*

MH 34 is a selection from the germplasm maintained at the CCSHAU, Hisar and was tested in large-scale trials of groundnut with 14 strains/genotypes for six continuous years. On the basis of average of six years, MH 34 was found giving 22.6% higher pod yield and 9.35% higher oil content as compared to check, MH4 (Annual Report 1997-98 to 2002-03). Under Coordinated Initial Varietal Trial of groundnut during *kharif* 2001-02, it gave 54% oil content on average of three locations (Range 52 to 56%) [Annual Progress Report of AICRPO (Groundnut) 2001]. Several other workers have also observed high oil contents in this line (Singh, 2003; Singh and Malik, 2003; Malik and Gupta, 2004).

MH 34 is an erect, tall line with dark green foliage, pods peak absent and pods reticulation very prominent. Kernels are bold (100 kernel wt. above 40 gm) with reddish brown colour and oil content up to 56%. The genotype is tolerant/resistant to diseases like leaf spots compared to existing varieties.

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Singh Paramjeet (2003) *Studies on character association and path analysis in groundnut* (*Arachis hypogaea* L.), M.Sc. Thesis submitted to Department of Plant Breeding, CCS HAU, Hisar.

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Small Leaf Mutant (INGR No. 04041; IC296613), Groundnut (*Arachis hypogaea* L.) Germplasm Line

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TERI-UTTAM, TERI (00) R9903 (INGR No. 04077; IC405232), Mustard (*Brassica napus* L.) Germplasm Line with Canola Quality and Early Maturity

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For development of varieties meeting the nutritionally desired international canola quality standards (<2% erucic acid in the seed oil and <30mm glucosinolate/ g oil free meal), work to introgress agronomic and quality traits through intergeneric/interspecific hybridisation was undertaken at the Tata Energy and Resources Institute (TERI). Transgressive segregants with low erucic acid, early maturity and shattering tolerance were selected from the advanced generation backcross progeny of hybrids (*B. napus* ISN-706 x *Raphanobrassica*) x *B. napus* obtained through embryo rescue (Agnihotri *et al.*, 1990, 1995). The selected strains were crossed with exotic canola quality *B. napus* cultivar 'Cyclone' for introgression of the low glucosinolate trait. The seeds were analysed for fatty acids and glucosinolate content by GLC and HPLC (Kaushik and Agnihotri, 1997, 1999). The selected plants were grown in single plant progenies and advanced through pedigree method, selections were made in each generation for the desired agronomic and quality traits (days to maturity, shattering tolerance, fatty acids, oil content and glucosinolate content) to develop double low *B. napus* (Agnihotri and Kaushik, 2003).

TERI-UTTAM, TERI (00) R9903 with low erucic acid (0 to 2%) and glucosinolate content (10 to 25 mm/g), also have high oil content (42 to 44%) and high oleic acid (60 to 64%) content desired for better shelf life, resistant/tolerant to pod shattering and white rust. It yielded 20 percent higher than the *B. napus* national check var. GSL-1 under AICRP R&M, giving 25 percent higher oil yield/ha than GSL-1 and 5 percent higher oil yield than most popularly grown *B. juncea* var. Varuna (Anonymous, 2000-2002). Morphologically, it has erect compact plant with height of 125 to 130 cm, 5 to 6 primary branches and 6 to 7 secondary branches, 40-46 silique on main branch, silique length 6 to 6.8 cm, 20 to 25 seeds per silique, 1000 seed weight 3.2 to 3.5 g, very high self-compatibility, brown medium size seed, days to 50 percent flowering 45 to 47 and days to maturity 130 to 135.

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TERI-GZ-05 (INGR No. 04078; IC405233), Mustard (*Brassica juncea* L.) Germplasm Line with High Oleic and Linoleic Acid, Double Low and Yellow Seed

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The 'triple low' i.e. yellow seed coat colour, low erucic acid in the seed oil and low glucosinolate in the oil free meal are the most sought for quality traits for genetic enhancement of oilseed brassica. In order to achieve this, a unique three way cross; *B. juncea* (var. Varuna x Zem-1) x BJ-1058 was carried out at the Tata Energy and Resources Institute (TERI) for transfer of double low traits, i.e. low erucic acid in the seed

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oil and low glucosinolate in the oil free meal. The fatty acids and glucosinolates were analysed through improved methods of GC and HPLC respectively (Kaushik and Agnihotri, 1997, 1999). The progenies of selected plants were advanced through pedigree and recurrent selection method to derive yellow seeded double low strain of *B. juncea* having low erucic acid, high oleic and linoleic acid in the seed oil, and low glucosinolate 10-27mm/g in the oil free meal (Agnihotri and Kaushik, 1999, 2000).

TERI-GZ-05 has high oleic (42 to 47%) and high linoleic acid (37 to 43%), low erucic acid (0 to 2%), low glucosinolate in the oil free meal (10 to 28 mm/g), and yellow seed coat colour. The low glucosinolate and yellow seed coat imparts improved meal quality with low fibre content, while high oleic acid gives better oxidative stability, increasing the shelf life of the oil. Morpho-agronomically, it is erect with plant height of 200 to 220 cm, 6 to 7 primary branches, 10 to 12 secondary branches, 30 to 40 silique on main branch, silique length 2.5 to 3.0 cm, number of seeds per silique 10 to 15, 1000 seed weight 1.5 to 2.0 g, high self-compatibility, days to 50 percent flowering 90 and days to maturity 145 to 150.

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DCH-7 (INGR No. 04042; IC296674), Castor (*Ricinus communis* L.) Germplasm Line with Short Duration and Multiple Resistance

DS Jatasra[1], RS Sangwan[2] and Ashwani Kumar[1]

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2. *Department of Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125004, Haryana*

DCH-7 is a castor (*Ricinus communis* L.) short duration multiple resistance line developed at the Dryland Research Farm CCSHAU, Hisar using mass selection (Kumar et al., 2003). The plant of DCH-7 has early plant vigour, green petiole, leaf lamina and stem with about four secondary and four tertiary branches. Its capsule is spiny with spotted brown collared seeds. It is early in flowering (38 days) with very bold seeds (32g/100 seeds). It is a very good yielder with 28q/ha seed yield. It is drought tolerant and disease resistant genotype. Hairy caterpillar and semi-looper attack is also very low. Comparative performance of the DCH-7 (Table 1) was significantly better than the national check (Aruna) and local check (CH 1) with 54 and 34 per cent more seed yield than these checks, respectively (Reddy *et al.*, 1999). Seeds are much bolder than the checks. It was 5 and 25 days early than the checks and can escape terminal drought.

References

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Table 1. Seed yield and its attributes of DCH-7 with respect to National and Local Check

Genotype	Days to 50% of flowering		Days to maturity		Height (cm)		Average spikes per plant	Capsules per raceme	Seeds per raceme	100-Seed. weight(g)	Oil content(%)	Seed yield per plant (g)	Increase over checks (%)
DCH-7	38	118	45	621	34	85	32	50	122	-			
Aruna (NC)	60	145	85	409	26	64	24	50	79	54			
CH 1 (LC)	45	120	38	406	27	76	26	49	91	34			

*DCH-7 yielded 54 per cent more than the Aruna and 34 per cent more than the CH 1
**NC = National check; LC = Local check

oil and low glucosinolate in the oil free meal. The fatty acids and glucosinolates were analysed through improved methods of GC and HPLC respectively (Kaushik and Agnihotri, 1997, 1999). The progenies of selected plants were advanced through pedigree and recurrent selection method to derive yellow seeded double low strain of *B. juncea* having low erucic acid, high oleic and linoleic acid in the seed oil, and low glucosinolate 10-27mm/g in the oil free meal (Agnihotri and Kaushik, 1999, 2000).

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Chawghat Green Dwarf (IND 029) (INGR No. 04043; IC296656), Coconut (*Cocos nucifera* L.) Germplasm Line with Dwarfness, Early Flowering and Tolerance to Root Wilt Disease

MM Krishna Marar, MC Nambiar, K Sathybalan, KUK Nampoothiri, RV Pillai and CK Sukumaran
Central Plantation Crops Research Institute, Kasargod-671124, Kerala

Chowghat Green Dwarf is a coconut cultivar with trees attaining a height of 4.5 m. The stem is thin without a 'bole'. The leaves are shorter (about 4 m long) with 196 leaflets. The leaf scars are closer with about 56 in one metre of stem. It starts flowering 3-4 years after planting. The inflorescence is short with a length of 87 cm. The palms are self-pollinating, as there is an overlapping of male an female phases within as well as between the inflorescence. The nuts are green in colour and oblong in shape with characteristic beak when the nuts are fully matured. The kernel shells are thin.

The palm yields from 10th year onwards and produces about 9 branches per annum. At Kasargod, the number of nuts per palm per year is 75 with a range of 30 to 100 nuts. At Veppankulam Tamil Nadu, the palm produces 35 nuts with 2 kg of copra per palm per year (Anon., 1999). The fruits are small weighing about 0.45 kg. The weight of the husked nut is about 190 g. The husk portion is high with 58.4 percent of the whole fruit weight. The copra content is low with a mean of 75 g per nut (38-100 g). Oil content of copra is 66 percent (Ratnambal *et al.*, 1995). Detailed characterisation has been done at CPCRI, Kasargod (Ratnambal *et al.*, 1995).

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Ratnambal MJ, MK Nair, K Muralidharan, PM Kumaran, EVV Bhaskara Rao, RV Pillai (1995) *Coconut Descriptors Part – I*, CPCRI, Kasargod, 197p.

Andaman Giant Tall (AGT) (IND 006) (INGR No. 04044; IC296657), Coconut (*Cocos nucifera* L.) Germplasm Line with Large Fruits and High Copra Yield

JS Patel, CM John and MC Nambiar
Central Plantation Crops Research Institute, Kasaragod-671124, Kerala

Andaman Giant Tall (AGT) (IND 006) is a cultigen collected and identified from Andamans and Nicobar Islands and evaluated at the Central Plantation Crops Research Institute, Kasargod. This cultivar is also called 'gigantea'. The palm is very strong and robust exhibiting gigantic morphological features. The height of the palm reaches up to 12 m. with about 34 leaves on the crown. The leaves are long (5.1 m) with strong petiole of about one-thrid of the length of the leaf. The leaf has 235 leaflets, which are 121 cm long and 6.4 cm wide. The trunk is thick with about 95 cm girth, with a distinct bole. It takes 95-98 months to flowering. It produces 8-13 inflorescence per annum. The setting percentage is 36.5 percent (Ratnambal *et al.*, 1995). The palms are highly heterozygous due to the cross-pollinating nature. The fruit is very large, oval in shape and green in colour.

It yields from 12th year onwards and is a regular bearer. The fruits are bigger weighing around 1200 g with 692.7 g nut weight. The copra content is 193.6 g. per nut with 65.5 percent oil. The nut yield varies from 58 to 110 nuts under rain-fed conditions with an average of 80 nuts per palm. The average copra yield per hectare is 1.8 t (Ratnambal *et al.*, 1995). At Ratnagiri, Maharashtra, this cultivar gives 61 nuts/ palm. At Veppangulam, the mean yield of nuts per palm is 72 with 7.5 Kg of copra (Anonymous, 1999). Due to the high copra content, this variety can be popularised among farmers and used for the production of T x T hybrids.

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Chawghat Green Dwarf (IND 029) (INGR No. 04043; IC296656), Coconut (*Cocos nucifera* L.) Germplasm Line with Dwarfness, Early Flowering and Tolerance to Root Wilt Disease

MM Krishna Marar, MC Nambiar, K Sathybalan, KUK Nampoothiri, RV Pillai and CK Sukumaran
Central Plantation Crops Research Institute, Kasargod-671124, Kerala

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The palm yields from 10th year onwards and produces about 9 branches per annum. At Kasargod, the number of nuts per palm per year is 75 with a range of 30 to 100 nuts. At Veppankulam Tamil Nadu, the palm produces 35 nuts with 2 kg of copra per palm per year (Anon., 1999). The fruits are small weighing about 0.45 kg. The weight of the husked nut is about 190 g. The husk portion is high with 58.4 percent of the whole fruit weight. The copra content is low with a mean of 75 g per nut (38-100 g). Oil content of copra is 66 percent (Ratnambal *et al.*, 1995). Detailed characterisation has been done at CPCRI, Kasargod (Ratnambal *et al.*, 1995).

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Kenthali Orange Dwarf (KDOT) (IND 074) (INGR No. 04045; IC296658), Coconut (*Cocos nucifera* L.) Germplasm with Dwarfness, Orange Fruits and Tender Nut

MC Nambiar, KUK Nampoothiri, RV Pillai, CK Sukumaran and G Vijayakumar
Central Plantation Crops Research Institute, Kasargod-671124, Kerala

Kenthali Orange Dwarf (KDOT) (IND 074) is a coconut cultivar collected from Karnataka. This palm grows up to 4-5 m in height. The stem is rather thin without 'bole' and with compressed internodes. The girth of the stem at one m, height is 64 cm and the number of nodes of one m length is 52.7. It comes to bearing in about 6-7 years. The inflorescence is of 98 cm. with overlapping of male and female phases. The setting percentage of fruit is about 30 percent. The colour of the fruit is deep orange with oval shape. The husked nut is more flat at the bottom. The husk, kernel and shell are thinner.

The fruiting starts at about 9 years. The water in 7 month-old nut is sweet with 6.0 g. of total sugar content in 100 ml of water, but the quantity of tender nut water is somewhat less i.e. 198-250 ml per nuts. The average number of fruits per annum per tree is 52 with range of 45 to 58 nuts. At Aliyarnagar the palm gives 36 nuts/palm while at Konark (Orissa) the palm produces 43 nuts (Anon., 1999). The fruits are small and weigh 456 g. The husk constitutes 30 percent of the whole fruit weight and meat contributes 59 percent to the husked nut. Copra content per nut is 116.5 g. with 64 percent oil. The copra and oil yield in one hectare are 1.1 tonnes and 0.7 tonne, respectively, at Kasargod (Ratnambal *et al.*, 1995). At Konark (Orissa), the copra content per nut is 134 g. (Anon., 1999). This genotype is fairly tolerant to burrowing nematode-*Radopholus similis*. This cultivar can be used for tender nut water. This can be used as pollen and pistil parent in breeding work.

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CYTOPLASMIC MALE STERILE LINE IN COTTON

CAK–84635 A (Rajat) & AK-84635 B (INGR No. 04046; IC296639 & IC296640), Cotton (*Gossypium hirsutum* L.) Cytoplasmic Male Sterility Line with *G. aridum* Cytoplasm

LD Meshram, BR Patil and MB Wadodkar
Dr. Punjabrao Deshmukh Krishi Vidyapeeth, Akola-444104, Maharashtra

CAK-84635 A (Rajat) is a cytoplasmic male sterile (CMS) line based on *Gossypium aridum* cytoplasm. Earlier, CMS lines have been developed at USA using *Gossypium harknessii* Brandgee by Mayer (1975). To obtain a diverse CMS lines, efforts were made at the Cotton Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, resulting in production CMS using *G. aridum* (Meshram *et. al.*, 1997). The genotype, which is used for conversion in CMS background, is a popular variety of Maharashtra. PKV Rajat or AKH – 84635 is a selection made from a cross between (AC-938 x SRT-1) x derivative of (*G. anomalum* x *G. thurberii*). It was selected for conversion, because of being suitable for rain-fed conditions and high yielding with semi-naked seeds. The cytoplasmic male sterility (*G. aridum* based) has been transferred into AKH-84635 by backcross breeding method.

It has leaves with two broad lobes and slightly hairy, flower yellow with cream anthers, boll round pointed at tip with four locules of medium size. Semi-naked seeds would provide better oil recovery. It posses high ginning out turn and better survival under saline soils. Other characters are- days to 50 percent flowering 65-70, to 1st boll bursting 110-115 and to maturity 170-180, boll weight 3.0-3.5 g, seed index 7-8 g, lint index 4.5-5.0, ginning percentage 38-39 percent, 2.5

Kenthali Orange Dwarf (KDOT) (IND 074) (INGR No. 04045; IC296658), Coconut (*Cocos nucifera* L.) Germplasm with Dwarfness, Orange Fruits and Tender Nut

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percent span length 24-25 mm, bundle strength 17.7 g/tex, uniformity ratio 49, fibre fineness 4.5.

The maintainer of this line is AKH-84635 (PKV Rajat), has given higher seed cotton yield and lint yield than DHY-286, SRT-1 and LRA-5166 in all trials conducted at different locations in different regions during last ten years. The fibre qualities are more or less comparable with DHY-286, SRT-1 and LRA-5166. This is moderately resistant to major pests and diseases. The percentage infestation of bollworms in green bolls is more or less similar to LRA-5166, but less than DHY-286, but in loculi damage this has shown superiority over LRA-5166, DHY-286 and SRT-1.This is suitable for cotton growing tract of Maharashtra. This genotype is non-lodging, suitable for rain-fed conditions and can be grown at 60 x 60 cm or more spacing for crossing, with a fertilizer dose of 50:25:0 kg NPK/ha.

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RCMS 3A & 3B (INGR No. 04047; IC296644 & IC296645), a Cotton (*Gossypium hirsutum* L.) Line, Incorporating Cytoplasmic Male Sterility in a Variety with Resistance to Cotton Leaf Curl Virus

CJ Kapoor, BS Meena and P Pundhir

Agricultural Research Station, (Rajasthan Agricultural University) Karni Marg, Sriganganagar-335001, Rajasthan

In cotton (*G. hirsutum* L.) both genetic and cytoplasmic genetic male sterility has been used in hybrid breeding. In hirsutum cotton partial to complete male sterility have been identified (Meyer, 1969; Bowmen *et al.*, 1978). Cotton leaf curl virus (CLCuV) caused by *Gemini* virus of genus *Begomovirus* and transmitted by cotton whitefly (*Bemisia tabaci*) has posed threat to cotton cultivation with yield losses up to 50 to 70 percent in North India. Considering the economic importance of the disease, a leaf curl virus resistant and well adapted variety RS-2013 derived from a cross (F-520 X (LH-511 X Bombasa) and developed at Agricultural Research Station (Rajasthan Agricultural University), Sriganganagar was selected for diversification of male sterility. The cytoplasmic genetic male sterile line (RCMS-3) has been developed through backcross breeding, using JCMSK2 as the male sterility source. It has robust plant habit with plant height of 130-135 cm, light green leaves, yellow petal and pollen grains completely sterile. The line is resistant to CLCuV. Beside CLCuV, it has tolerance for whitefly and jassids too. The RCMS-3 B line, the counterpart is also having multiple resistances. Morphologically it has yellow flower, light green leaves, GOT 34 percent, boll weight 2.95 g, lint index 4.01 g, micronaire value 4.6, 2.5 percent, span length 24.6 mm, uniform ratio 47 percent and strength 22.4 g/tex.

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RGMS-3 (INGR No. 04048; IC296646), a Cotton (*Gossypium arboreum* L.) Line Incorporating Genetic Male Sterility in an Adopted Variety

CJ Kapoor, P Pundhir and Bhim Singh Meena

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In desi cotton (*G. arboreum* L.) genetic male sterility have been used in the development of hybrids. Nuclear genes cause the genetic male sterility. Some workers from India have reported male sterility in *arboreum* cotton (Singh and Kumar, 1993 and Meshram *et. al.*, 1994). In diploid cotton (*G. arboreum* L.) two loci have been identified for male sterility, which are governed by single recessive gene (ams_1, arms). In

percent span length 24-25 mm, bundle strength 17.7 g/tex, uniformity ratio 49, fibre fineness 4.5.

The maintainer of this line is AKH-84635 (PKV Rajat), has given higher seed cotton yield and lint yield than DHY-286, SRT-1 and LRA-5166 in all trials conducted at different locations in different regions during last ten years. The fibre qualities are more or less comparable with DHY-286, SRT-1 and LRA-5166. This is moderately resistant to major pests and diseases. The percentage infestation of bollworms in green bolls is more or less similar to LRA-5166, but less than DHY-286, but in loculi damage this has shown superiority over LRA-5166, DHY-286 and SRT-1.This is suitable for cotton growing tract of Maharashtra. This genotype is non-lodging, suitable for rain-fed conditions and can be grown at 60 x 60 cm or more spacing for crossing, with a fertilizer dose of 50:25:0 kg NPK/ha.

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RGMS-3 (INGR No. 04048; IC296646), a Cotton (*Gossypium arboreum* L.) Line Incorporating Genetic Male Sterility in an Adopted Variety

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order to generate variability for male sterility, a germplasm line AC-6 has been selected to convert into genetic male sterility using GMS-1 as a source in backcross breeding. The newly developed RGMS-3 line has robust plant habit; narrow lobed green leaves, wider adaptability and tolerance to root rot disease. RGMS-3 line has shown 50:50 sterile: fertile segregation ratios at Sriganganagar and Central Institute for Cotton Research, Nagpur. The line is being utilized for the development of GMS based arboreum hybrids.

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HGMS-1 (INGR No. 04049; IC296648), Cotton (*Gossypium hirsutum* L) Germplasm Line Incorporating Genetic Male Sterility in an Adopted Variety

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HGMS-1 is a new genetic male sterile line of American cotton (*Gossypium hirsutum* L). It was developed at the CCSHAU, Hisar through hybridisation between B-59, an old GMS line and H 777, a commercial variety of Haryana state (Chhabra *et al.*, 2003), followed by backcross breeding. It has a lanky tall plant of 170-180 cm height, with normal cup shaped medium broad green and hairy leaves. The monopods are 4-6 with normal flower bracts. Petals are cream coloured with no pollen formation in sterile homozygous plants. Balls are round and medium with pointed tips and with 11.0 g of seed index. Ginning percent is 35 with white lint colour, micronair value 4.2 and strength of 22.7 g/tex and fibre quality index (FQI) value is 352 spins at 40's. It is tolerant to Cotton Leaf Curl Virus. This GMS line is maintained by crossing the sterile recessive homozygous plants with the fertile dominant heterozygote plants within the population.

Reference

Chhabra BS, RS Sangwan, BPS Lather, SS Siwach and SS Nehra (2003) A new genetic male sterile line in American cotton; HGMS-1. *J Cotton Res. Dev.* **17**: 242

CINA-316 (INGR No. 04079; IC296596), Cotton (*Gossypium arboreum* L) Germplasm Line with High Locule Retention and Low Short Fibre Content

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CINA 316 is a genotype of desi cotton with high locule retention and low short fibre content (*Gossypium arboreum*). It was developed at the Central Institute for Cotton Research, Nagpur, through a cross between AKA 8401 (*G arboreum* race *bengalense*) x Bisnoor (*G. arboreum* race indicum), followed by pedigree selection. Under All India Coordinated trial and technology mission on cotton it recorded good performance for locule retention and short fibre content.

Gossypium arboreum Linn. is a native of India, which covers about 25 percent of the total cotton area of India, contributing about 18 percent to the total production. Shedding or scattering of locules from fully opened mature bolls is a serious problem. Keeping this in view research programme was initiated. In CINA 316 double vascular supply was observed from placental region to locular compartment. With the gradual increase in age of capsule, these double vascular supplies convert into thread like structure and make unbroken attachment between basal portion of placenta and seed cotton loaded locules. It has five narrow lobed leaf and short stalk, reticulate and palmate divergent venation. Flowers are yellow with long pedicle, and petal blotch red, anthers yellow with short filaments. It has three small bracteoles with serrated margins at acute apex and 3-4 teeth present at anterior portion. Capsules are big with 3-4 locules, oval shaped, tapering apex with average volume of 10.8 cc. Capsules surface is sparsely pitted. Boll weight is 3.29 g and locule retention capacity is 17 to 23

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