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Collection and Characterization of Indian Sorghum Landraces

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Landraces are the varieties nurtured and cultivated by the farmers through traditional method of selection over the decades. The "landrace" is a primitive cultivar grown by farmers and their successors since ancient times. We explored seven states and collected 674 accessions. Out of which, 138 are popular landraces. These collections have specific traits and traditional utilities. Moli jowar from MP fetches higher prices due to attractive grains. The irungu cholam from Tamil Nadu yields best quality porridge and mathappu cholam is for preparing a jelly like food called khali. The beed maldandi and bidri from Maharashtra produce best quality jowar roti or unleavened bread. Karnataka's kodumurugu jola and allin jola are used to make laddus and papads, respectively. The allur jola from Karnataka is for pops (allu). The pachcha jonna from Andhra Pradesh, barmuda local, deshi chari and gudli local from Rajasthan and bendri dagdi and khondya from Maharashtra are excellent fodder types. Valsangh maldandi local, Vadgaon dagdi maldandi, tongraligaon maldandi, tongraligaon dagdi, sultanpur local dagdi, sultanpur maldandi, harni jogdi (dagdi), harni jogdi, chungi maldandi, musti local (Maldandi), chungi kuch-kachi, baddi jowar, chakur maldandi from Maharashtra, and sai jonna from Andhra Pradesh are considered by the farmers as drought tolerant landraces. These landraces were characterized both for qualitative and quantitative traits. The correlation coefficients of the quantitative traits revealed highly positive correlations among many characters. These trait linkages can serve as best source information on these materials to breed high yielding sorghums targeting food traits and industrial utility.

Key Words: Characterization, Evaluation, Germplasm, Sorghum, Landraces

Introduction

Plant genetic resources represent the inter- and intra-specific reservoir of potentially useful genetic material. Landraces or farmer varieties constitute the basic material for developing any variety or hybrid. Landraces are the varieties nurtured and cultivated by the farmers through traditional method of selection over the decades. An autochthonous landrace is a variety with a high capacity to tolerate biotic and abiotic stress, resulting in high yield stability and an intermediate yield level under a low input agricultural system (Zeven, 1998). The Biodiversity Act (2002) describes "*landrace*" as primitive cultivar that was grown by ancient farmers and their successors.

Early domestication of sorghum occurred from Ethiopian borders extending west through Sudan and up to Lake Chad (Harlan, 1975). There is great prevalence of diversity in this area as apart from the presence of the primitive race *bicolor* (Harlan and de Wet, 1972). It is likely that this race arose from the domestication of *Aethiopicum verticilliflorum* complex some 3,000 to 5,000 years ago. The finding at Nabta Playa may cause some rethinking of dates; however, it is not clear if these 8,000 year old seeds were from plants that did not shatter grains, although altered chemical composition would indicate some selection. *Bicolor* sorghum has spread across much of the old sorghum growing world including India. It is the likely progenitor of the *kaoliongs* of China. The race *guinea* arose from *bicolor* with possible interaction with the wild race *arundinaceum* in the high rainfall areas of West Africa. The *guinea* is now the dominant sorghum of West Africa but has spread also around Tanzania and Malawi. The *guinea* race arose more than 2,000 years ago. The race *caudatum* also possibly evolved from *bicolor*. Today, the *caudatums* are most abundant from East Nigeria to eastern Sudan and southward into Uganda. The race *durra* was selected from early *bicolor* that had moved into India some 3,000 years ago. With Arab migration the *durra* moved into Ethiopia around 615 A.D., and is today the dominant race in India, Ethiopia, the Nile Valley of Sudan and Egypt. Race *kafir* was probably derived from *bicolor* but there is also evidence of association with the wild race *verticilliflorum*. The *kafir* is found primarily in eastern and southern Africa. Later sorghum found its way into the Americas after 1850.

Sorghum is of African origin (Kimber 2003) and Africa has largest diversity of cultivated and wild sorghum (Doggett 1988; deWet, 1977), in the Indian Subcontinent there is evidence for early cereal cultivation discovered at an archaeological site in western parts of Rojdi (Saurashtra) which dating back to about 4,500 before present (Damania, 2002) and India is considered to be secondary center of origin of sorghum (Vavilov, 1992).

The process of genetic resource management's greatest contribution for sorghum improvement has been the establishment of a world sorghum collection. This collection is an outgrowth of an effort which began in

1959 to collect the sorghums and also several of the millets in India, funded by the Rockefeller Foundation. The collection was assembled because of request from different sorghum growing countries. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) along with NARS partners was responsible for this collection, and the programme continues to till date. The collection has grown from about 10,000 accessions in 1972 to 36,774 accessions till date. The total collections encompass landraces (83%), breeding lines (16%) and wild races (1%). During 1999 – 2005, National Research Centre for Sorghum (NRCS) has collected 674 accessions from seven sorghum growing states. This paper discusses about the sorghum landraces collection and characterization at NRCS, under the Indian Council of Agricultural Research (ICAR).

Materials and Methods

National Research Centre for Sorghum under the Indian Council of Agricultural Research is one of the National Active Germplasm Sites (NAGS) with the mandate to collect, conserve, document and utilize the sorghum genetic resources and act as a "National Repository" for sorghum germplasm. In the last decade, we have explored seven states, undertook 15 collection missions and collected 674 accessions, out of which 138 are popular landraces traditionally cultivated by the farmers.

The preliminary characterization of 138 accessions of sorghum landraces was carried out at NRCS, Rajendranagar, Hyderabad during 2002-05. The centre is located at $17^0$19' N latitude and $78^0$24' E longitude and at an altitude of 538 m above MSL with temperature varying from 10^0C to a maximum of 30^0C during the cropping season. The accessions were raised in an augmented design in the sandy soil with check varieties (M35-1, Swati and CSV-15) in each block. The accessions were grown in 4 m rows with row spacing of 60 cm with plant to plant distance of 10 cm. Standard agronomic and plant protection practices were followed during the cropping season. The data on qualitative and quantitative descriptors were recorded using minimal descriptor developed by NBPGR (Mahajan *et al.,* 2000) and NRCS (Elangovan, *et al*., 2004). Five representative plants in each accession were tagged for recording the qualitative and quantitative characters. Brix percentage of each accession was estimated by refractometer. The quantitative data was analysed statistically.

Results and Discussion

There is great variability in sorghum, making selection possible for most traits of economic importance. Germplasm, in the form of breeding stock, collected accessions, and converted tropical cultivars, now moves readily world wide and has contributed significantly to the crop's improvement in terms of yield, resistances and utilization/quality traits (House, 1985). Seven states were explored under the NATP (MM – BD) and 674 accessions were colleted. In which, 138 accessions are popular landraces traditionally cultivated by the farmers. The state-wise list of sorghum landraces is presented in Table 1.

Table 1. State-wise sorghum landrace collections

State	No. of landraces
Andhra Pradesh	18
Karnataka	19
Madhya Pradesh	42
Maharashtra	44
Rajasthan	5
Tamil Nadu	6
Uttar Pradesh	4
Total	138

In these collections, the sorghum landraces are mostly named with the village name prefixed to the landrace (ex. *Tongraligaon maldandi*, *Sultanpur maldandi* etc), landraces are also named based on the grain colour (ex. *tella jonna, bili jola* etc.) and size (ex. *moti rabi jowar*), ear head compactness (ex. *mudda jola*), use of the stem or grain (ex. *dagdi, gundu, allur* etc.) for varieties utilities. A similar observation was made by Teshome *et al.,* (1997) because the midrib color, grain color, grain size, glume color, glume hairiness, and grain shape were the leading morphological characters used by the farmers naming the sorghum landraces. The list of 138 sorghum landraces collected is given in Table 2.

The landraces are being grown by farmers over the years for many reasons. The *moli jowar* grains are attractive and fetch higher price in the market compared to other released varieties in Madhya Pradesh. Some are used for specific food preparations. The *irungu cholam* flour is boiled with water to prepare food. The *mathappu cholam* is used to prepare a jelly like food known as *khali* in Tamil Nadu. The *beed maldandi* and *bidri* from Maharashtra are used to make quality jowar roti. Karnataka's *kodumurugu jola* and *allina jola* are used to make laddu's and pappads,

Table 2. List of sorghum landraces collections

S.No.	Collector number	Indigenous Collection number	Vernacular name	District	State
1	EP – 123	IC420938	Jowri	Nashik	Maharashtra
2	EP – 124	IC420939	Khondya	Ahmednagar	Maharashtra
3	EP – 127	IC420942	Mutka	Pune	Maharashtra
4	EP – 128	IC420943	Bidri	Pune	Maharashtra
5	EP – 132	IC420947	Dagdi maldandi	Pune	Maharashtra
6	EP – 138	IC420953	Bendri dagdi	Satara	Maharashtra
7	E – 101	IC415792	Sabet deshi	Kanpur Dehat	Uttar Pradesh
8	E – 106	IC415797	Jonnari	Unnao	Uttar Pradesh
9	E – 109	IC415800	Jonndi	Rae Bareli	Uttar Pradesh
10	E – 143	IC415834	Bani	Lucknow	Uttar Pradesh
11	E – 89	IC369120	Tella jonna	Mahaboobnagar	Andhra Pradesh
12	PEC – 2	IC392125	Jungala local	Lathur	Maharashtra
13	PEC – 5	IC392128	Baddi jowar	Lathur	Maharashtra
14	PEC – 7	IC392130	Chakur maldandi	Lathur	Maharashtra
15	PEC – 15	IC392138	Maldandi	Bidar	Karnataka
16	PEC – 22	IC392145	Sai Jonna	Medak	Andhra Pradesh
17	PEC – 26	IC392149	Tandur local	Ranga Reddy	Andhra Pradesh
18	EC – 1	IC345703	Tella jonna	Mahaboobnagar	Andhra Pradesh
19	EC – 11	IC345713	Mudda jonna	Kurnool	Andhra Pradesh
20	EC – 12	IC345714	Raichur jonna	Kurnool	Andhra Pradesh
21	EC – 20	IC345722	Oola jonna	Cuddapah	Andhra Pradesh
22	EC – 21	IC345723	Eduakula jonna	Cuddapah	Andhra Pradesh
23	EC – 33	IC345735	Palar jonna	Prakasam	Andhra Pradesh
24	EC – 34	IC345736	Mudda jonna	Prakasam	Andhra Pradesh
25	SEVS – 2	IC347568	Pachcha jonna	Khammam	Andhra Pradesh
26	SEVS – 3	IC347569	Nattu jonna	Khammam	Andhra Pradesh
27	SEVS – 7	IC347573	Tella jonna	Khammam	Andhra Pradesh
28	SEVS – 8	IC347574	Konda jonna	Khammam	Andhra Pradesh
29	SEVS – 17	IC347583	Konda	Khammam	Andhra Pradesh
30	SEVS – 18	IC347584	Kade jonna	Khammam	Andhra Pradesh
31	SEVS – 20	IC347586	Gompu jonna	Khammam	Andhra Pradesh
32	SEVS – 26	IC347592	Koda muddu jonna	Khammam	Andhra Pradesh
33	EP – 54	IC343553	Gorani maldandi	Osmanabad	Maharashtra
34	EP – 55	IC343554	R - 8	Osmanabad	Maharashtra
35	EP – 57	IC343556	Beedari	Beed	Maharashtra
36	EP – 59	IC343558	Beed maldandi	Beed	Maharashtra
37	EP – 64	IC343563	Sedam maldandi gurang	Aurangabad	Maharashtra
38	EP – 65	IC343564	Gurang maldandi	Aurangabad	Maharashtra
39	EP – 68	IC343567	Dadar	Dhule	Maharashtra
40	EP – 78	IC343577	Gurang	Ahmednagar	Maharashtra
41	EP – 79	IC343578	Bandri	Ahmednagar	Maharashtra
42	EP – 80	IC343579	Gurang sabet	Solapur	Maharashtra
43	EP – 81	IC343580	Gurang dagdi	Solapur	Maharashtra
44	EP – 82	IC343581	Sabet ganga gopargaon	Solapur	Maharashtra
45	EP – 84	IC343583	Valsangh maldandi local	Solapur	Maharashtra
46	EP – 86	IC343585	Vadgaon maldandi	Solapur	Maharashtra
47	EP – 87	IC343586	Vadgaon dagdi maldandi	Solapur	Maharashtra
48	EP – 88	IC343587	Tongraligaon maldandi	Solapur	Maharashtra
49	EP – 89	IC343588	Tongraligaon dagdi	Solapur	Maharashtra
50	EP – 90	IC343589	Sultanpur local dagdi	Solapur	Maharashtra
51	EP – 91	IC343590	Sultanpur maldandi	Solapur	Maharashtra
52	EP – 92	IC343591	Harni jogdi (dagdi)	Solapur	Maharashtra
53	EP – 93	IC343592	Harni jogdi	Solapur	Maharashtra
54	EP – 94	IC343593	Chungi maldandi	Solapur	Maharashtra
55	EP – 95	IC343594	Musti local (maldandi)	Solapur	Maharashtra
56	EP – 96	IC343595	Chungi kuch-kachi	Solapur	Maharashtra
57	EP – 97	IC345186	Bile maldandi	Raichur	Karnataka
58	EP – 102	IC345191	Bili jola	Raichur	Karnataka
59	EP – 103	IC345192	Kodumurugu jola	Raichur	Karnataka
60	EP – 104	IC345193	Kanaggu jola	Raichur	Karnataka
61	EP – 105	IC345194	Allin jola	Raichur	Karnataka
62	EP – 106	IC345195	Bili jola	Raichur	Karnataka
63	EP – 107	IC345196	Kanaggu jola	Raichur	Karnataka
64	EP – 112	IC345201	Kadapu jola	Raichur	Karnataka

S.No.	Collector number	Indigenous collection number	Vernacular name	District	State
65	EP – 114	IC345203	Maldandi bili	Raichur	Karnataka
66	EP – 115	IC345204	Allur jola	Raichur	Karnataka
67	EP – 117	IC345206	Bili maldandi	Kappal	Karnataka
68	EP – 120	IC345209	Farm maldandi	Bellary	Karnataka
69	EA – 1	IC345243	Irungu cholam	Dindigul	Tamil Nadu
70	EA – 2	IC345244	Vella cholam	Dindigul	Tamil Nadu
71	EA – 4	IC345246	Karum cholam	Dindigul	Tamil Nadu
72	EA – 6	IC345248	Matthappu cholam	Dindigul	Tamil Nadu
73	EA – 10	IC345252	Irungu cholam	Dindigul	Tamil Nadu
74	EA – 11	IC345253	Sevappu cholam	Madurai	Tamil Nadu
75	GGUB - 19	IC319862	Moli jowar	Jhabua	Madhya Pradesh
76	GGUB - 20	IC319863	Chikni jowar	Jhabua	Madhya Pradesh
77	GGUB - 21	IC319864	Pili local	Jhabua	Madhya Pradesh
78	GGUB - 22	IC319865	Dhavali jowar	Jhabua	Madhya Pradesh
79	GGUB - 23	IC319866	Dadar rabi jowar	Jhabua	Madhya Pradesh
80	GGUB - 25	IC319868	Syalu rabi	Jhabua	Madhya Pradesh
81	GGUB - 27	IC319870	Katrae	Jhabua	Madhya Pradesh
82	GGUB - 29	IC319872	Local jowar	Jhabua	Madhya Pradesh
83	GGUB - 30	IC319873	Lahi jowar	Jhabua	Madhya Pradesh
84	GGUB - 31	IC319874	Barsati jowar	Jhabua	Madhya Pradesh
85	GGUB - 32	IC319875	Badi jowar	Jhabua	Madhya Pradesh
86	GGUB - 34	IC319877	Meethi jowar	Jhabua	Madhya Pradesh
87	GGUB - 35	IC319878	Local kajri jowar	Jhabua	Madhya Pradesh
88	GGUB - 36	IC319879	Syalu rabi jowar	Jhabua	Madhya Pradesh
89	GGUB - 37	IC319880	Chikni pilia	Jhabua	Madhya Pradesh
90	GGUB - 38	IC319881	Kale tonsa ki jowar	Jhabua	Madhya Pradesh
91	GGUB - 39	IC319882	Bajri jowar	Jhabua	Madhya Pradesh
92	GGUB - 40	IC319883	Moti rabi jowar	Jhabua	Madhya Pradesh
93	GGUB - 43	IC319886	Chikni jowar	Jhabua	Madhya Pradesh
94	GGUB - 44	IC319887	Lahi jowar	Betul	Madhya Pradesh
95	GGUB - 46	IC319889	Somji jowar	Betul	Madhya Pradesh
96	GGUB - 47	IC319890	Local sehra	Betul	Madhya Pradesh
97	GGUB - 48	IC319891	Ramtak local	Betul	Madhya Pradesh
98	GGUB - 50	IC319892	Charsi local	Betul	Madhya Pradesh
99	GGUB - 51	IC319893	Aathner mohali	Betul	Madhya Pradesh
100	GGUB - 52	IC319894	Badi sahera jowar	Betul	Madhya Pradesh
101	GGUB - 54	IC319895	Satpari	Khargaom	Madhya Pradesh
102	GGUB - 55	IC319896	Kantolli	Khargaom	Madhya Pradesh
103	GGUB - 56	IC319897	Safeda	Dewas	Madhya Pradesh
104	GGUB - 57	IC319898	Gudagi	Vidisha	Madhya Pradesh
105	GGUB - 58	IC319899	Pili safed	Vidisha	Madhya Pradesh
106	GGUB - 59	IC319900	Safed tinopal	Vidisha	Madhya Pradesh
107	GGUB - 60	IC319901	Somkatch safeda	Vidisha	Madhya Pradesh
108	GGUB - 61	IC319902	Mehara jowar	Vidisha	Madhya Pradesh
109	GGUB - 62	IC319903	Pilimotia	Vidisha	Madhya Pradesh
110	GGUB - 63	IC319904	Murga jowar	Vidisha	Madhya Pradesh
111	GGUB - 64	IC319905	Somkath safea	Guna	Madhya Pradesh
112	GGUB - 65	IC319906	Arom safed	Guna	Madhya Pradesh
113	GGUB - 67	IC319907	Safed jowar	Vidisha	Madhya Pradesh
114	GGUB - 68	IC319908	Mehara jowar	Vidisha	Madhya Pradesh
115	E – 1	IC338968	Jowari local	Udaipur	Rajasthan
116	E – 3	IC338970	Barmada local	Udaipur	Rajasthan
117	E – 4	IC338971	Gudli local	Udaipur	Rajasthan
118	EJ – 3	IC338983	Commedi	Pali	Rajasthan
119	EJ – 42	IC339022	Deshi-chari	Tonk	Rajasthan
120	EB – 1	IC332460	Deshi sabet	Indore	Madhya Pradesh
121	EB – 2	IC332461	Deshi dhawli	Indore	Madhya Pradesh
122	EP – 1	IC305882	Tamalwadi dhagdi	Osmanabad	Maharashtra
123	EP – 9	IC305890	Yermala joot	Osmanabad	Maharashtra
124	EP – 11	IC305892	Yemala lakdi	Osmanabad	Maharashtra
125	EP – 12	IC305893	Yermala dukri	Osmanabad	Maharashtra
126	EP – 13	IC305894	Shirala dagdi	Osmanabad	Maharashtra
127	EP – 14	IC305895	Shirala gota	Osmanabad	Maharashtra
128	EP – 16	IC305897	Jamgaon dagdi	Solapur	Maharashtra
129	EP – 17	IC305898	Jamgaon joot	Solapur	Maharashtra

S.No.	Collector number	Indigenous collection number	Vernacular name	District	State
130	EP – 22	IC305903	Dagdi maldandi	Solapur	Maharashtra
131	EP – 23	IC305904	Dagdi local	Solapur	Maharashtra
132	EP – 24	IC305905	Local maldandi	Solapur	Maharashtra
133	EP – 37	IC305918	Dharunyak danda local	Gulberga	Karnataka
134	EP – 41	IC305922	Hurdajola	Gulberga	Karnataka
135	EP – 42	IC305923	Jevari local	Gulberga	Karnataka
136	EP – 45	IC305926	Gundu jola	Gulberga	Karnataka
137	EP – 46	IC305927	Bagadahali local	Gulberga	Karnataka
138	EP – 52	IC305933	Hale jola	Bijapur	Karnataka

respectively. The *allur jola* from Karnataka is used to prepare allu dish during the nagapanchami (festival of snake God). The *pachcha jonna* from Andhra Pradesh, *barmuda local*, *deshi chari* and *gudli local* from Rajasthan and *bendri dagdi* and *khondya* from Maharashtra are very good fodder types.

Valsangh maldandi local, Vadgaon dagdi maldandi, tongraligaon maldandi, tongraligaon dagdi, sultanpur local dagdi, sultanpur maldandi, harni jogdi (dagdi), harni jogdi, chungi maldandi, musti local (Maldandi), chungi kuch-kachi, baddi jowar, chakur maldandi from Maharashtra, and *sai jonna* from Andhra Pradesh are considered by the farmers as drought tolerant landraces.

The accessions studied exhibited good variability in both qualitative and quantitative traits. In quantitative traits, the time to 50% flowering (56 – 121), plant height (110 – 411 cm), earhead length (8 – 36.2 cm), stem fresh weight (110 – 955 g/plant), stem dry weight (30 – 557 g/plant) and grain yield (3.6 – 92 g/plant) showed good variability. The preliminary characterization of sorghum landraces revealed that stem fresh weight, stem dry weight, plant height, and grain yield are the most variable characters. The descriptive statistics on the quantitative characters of sorghum landraces are presented in Table 3.

The qualitative characters have also shown variability. The higher seedling vigour (59 acc.), tan leaf pigmentation (128 acc.), dark green leaf colour (118 acc.), drooping leaf orientation (80 acc.), white midrib colour (55 acc.), elliptical earhead shape (80 acc.), semi compact earhead (91 acc.), straw glume colour (52 acc.), 50% glume coverage (44 acc.), presence of awns (105 acc.), bold seed size (71 acc.), pearly white seed colour (81 acc.), non-senescence (stay green) plant type (133 acc.), durra race (78 acc.), and non-lustrus seed (52 acc.) recorded maximum frequency in qualitative characters. The frequency of qualitative characters is given in Table 4.

The correlation coefficients of the quantitative traits revealed highly positive correlations for in time to 50% flowering and time to maturity; number of leaves with leaf length, leaf width, plant height, stem thickness, stem fresh weight, and stem dry weight; leaf length with leaf width, plant height, stem thickness, stem fresh weight and stem dry weight; leaf width with stem fresh weight and stem dry weight; plant height with stem fresh weight and stem dry weight; stem thickness with stem fresh weight and stem dry weight; stem fresh weight with stem dry weight; and grain yield with 100-seed weight (Table 5). Highly negative correlations were observed for grain yield with number of leaves, leaf length, plant height and earhead

Table 3. Statistical analysis of quantitative characters

Characters	Min.	Max.	Range	Mean	SE	SD	Variance
Time to 50% flowering (days)	56.0	121.0	65.0	79.0	0.8	9.1	82.9
Number of leaves	6.0	19.0	13.0	12.0	0.2	2.8	7.7
Leaf length (cm)	50.9	101.6	50.7	71.2	1.1	12.8	163.9
Leaf width (cm)	4.8	10.8	6.0	7.5	0.1	1.3	1.6
Plant height (cm)	110.0	411.0	302.0	218.0	6.0	70.0	4902.9
Ear head length (cm)	8.0	36.2	28.2	17.9	0.5	5.3	28.5
Ear head width (cm)	3.3	10.9	7.5	6.4	0.1	1.4	1.9
Stem thickness (cm)	1.0	2.9	1.9	1.6	0.0	0.3	0.1
Stem fresh weight (g)	110.0	955.0	845.0	343.2	13.2	153.2	23482.8
Stem dry weight (g)	30.0	557.0	527.0	172.5	7.6	87.9	7730.3
Brix (%)	3.0	23.0	20.0	15.0	0.3	4.0	16.0
Grain yield (g)	3.6	92.0	88.4	41.7	1.7	19.6	383.0
100-seed weight (g)	0.9	4.6	3.7	2.9	0.1	0.8	0.6

Table 4. Frequency of qualitative characters

Character	Frequency
Seedling vigour	Good-47
	Poor-30
	Very good-59
	Unclassified-2
Leaf pigmentation	Non-tan-8
	Tan-128
	Unclassified-2
Leaf colour	Dark green-118
	Light green-17
	Pale green-1
	Unclassified-2
Leaf orientation	Drooping-80
	Erect-56
	Unclassified-2
Midrib colour	Colourless-16
	Dark green-1
	Dull green-51
	Green-1
	Pale green-7
	Purple-5
	White-55
	Unclassified-2
Ear head shape	Broom corn-1
	Elliptical-80
	Loose-1
Ear head shape	Oblong-24
	Ovate-23
	Round-2
	Unclassified-7
Ear head compactness	Compact-34
	Loose-2
	Semi compact-91
	Semi loose
	Unclassified-7
Glume colour	Black-10
	Brown-20
	Dark red-2
	Light red-3
	Orange-3
	Pink-1
	Purple-8
	Red-30
	Straw-52
	Unclassified-9
Glume covering	25% -12
	50% -44
	75% -26
	100% - 25
	Unclassified -31
Awn	Absent-26
	Present-105
	Unclassified-7
Seed size	Bold-71
	Medium-21
	Small-9
	Very bold-25
	Unclassified-12
Seed colour	Brown-1
	Chalky white-7
	Light brown-1
	Light orange-2
	Light yellow-1
	Orange-3
	Pearly white-81
	White-27
	Yellow-2
	Unclassified-13
Stay green	Non-senescence-133
	Senescence-1
	Unclassified-4
Race	Bicolor-5
	Durra-78
	Durra bicolor-2
	Durra caudatum-13
	Guinea-6
	Guinea caudatum-6
	Unclassified-28
Lustre	Lustrus-24
	Non lustrus-52
	Unclassified-62
Remarks	Broad leaves-7
	Good-10
	Late flowering-4
	Red pigmented seed-2
	Twin seed-2
	Very good-15
	Very good, blunt end of panicle-1

length; the 100-seed weight with leaf length, plant height, and earhead length; and the time to maturity with leaf width.

The variation in sorghum landraces for morphological characters has been reported by many workers in different countries. The evaluation of 152 accessions collected from Rwanda showed that the sorghum from Rwanda grows very tall (up to 500 cm), and takes more days to flower during long days (rainy season) and less no. of days during short days indicating strong photoperiod sensitivity. Enormous variation was observed for panicle and grain characters (Appa Rao *et al.,* 1999).

Thirty four sorghum landraces collected from five agroecological sites (ecosites) in North Shewa and South Welo regions of Ethiopia have exhibited morphological variation for the 14 qualitative characters that showed two or more phenotypic classes. Panicle compactness and shape contributed relatively more to altitudinal and ecological

differentiation. This differential distribution of landraces with panicle types with respect to compactness and shape revealed the adaptive significance of panicle compactness and shape that reflected the patterns of distribution of different races in North Shewa and South Welo (Abdi *et al*., 2002). The present study also observed the variation in panicle compactness.

The study to assess the phenotypic diversity and pattern of distribution among Sudanese sorghum landraces collected from different geographical regions revealed high phenotypic diversity among landraces with large range of variation for mean quantitative traits. Collections from Kassala showed a higher frequency of landraces with kernels that were more difficult to thresh. Landraces from Blue Nile tended to have greater agronomic eliteness with higher proportion of landraces with white kernels, poorly covered and were easy to thresh. Sorghums from the Upper Nile tended to have loose panicles with poorly covered kernels that may have resulted from the adaptation to high rainfall area in southern region (Grenier *et al.,* 2004).

Field survey data of sorghum landrace populations grown by traditional farmers in four adjacent communities in the Ethiopian highlands were used to analyze and project the local risk of loss of individual landraces under three scenarios: wild population, traditional farming and agricultural modernization. The risk of loss in the wild population scenario is based on landscape ecology theory which evaluates total population size, spatial distribution and patch occupancy, with high values for each factor and the sum of the factors decreasing the risk. In the traditional farming scenario, the deliberate actions of farmers must be taken into account like farmers favour for various traits of the sorghum for specific reasons – yield, taste, storability etc., which will balance plant numbers according to quantity and quality requirements. In the agricultural modernization scenario, introduction of high-yielding varieties tendency toward monocultures, use of agricultural chemical force the traits of the landraces that are most likely to be displaced and also bring in nature of the landraces that are likely to be retained on the basis of cultural or other factors (Tunstall *et al.,* 2001). Hence, the collection and protection of Indian sorghum landraces is very important.

Landraces are the sources of diversity for further use in crop improvement programmes. Unless landraces are collected, and conserved and protected, we can not

Table 5. Correlation coefficient of quantitative characters

Characters	DFL	NOL	LL	LW	PH	EHL	EHW	ST	SFW	SDW	BX	GY	SW	DM
Time to 50% flowering (days)	1.00													
Number of leaves	0.012	1.00												
Leaf length (cm)	-0.078	0.838**	1.00											
Leaf width (cm)	-0.138	0.672**	0.681**	1.00										
Plant height (cm)	-0.068	0.852**	0.791**	0.463**	1.00									
Ear head length (cm)	-0.243**	0.338**	0.407**	0.118	0.389**	1.00								
Ear head width (cm)	0.278**	-0.020	-0.173*	-0.052	-0.058	0.091	1.00							
Stem thickness (cm)	0.268**	0.612**	0.542**	0.437**	0.424**	0.191*	0.172*	1.00						
Stem fresh weight (g)	0.106	0.688**	0.622**	0.504**	0.672**	0.081	0.021	0.636**	1.00					
Stem dry weight (g)	0.101	0.665**	0.607**	0.491**	0.672**	-0.001	-0.029	0.550**	0.902**	1.00				
Brix (%)	-0.063	0.426**	0.473**	0.305**	0.361**	0.167	-0.115	0.250**	0.272**	0.324**	1.00			
Grain yield (g)	0.309**	-0.494**	-0.580**	-0.206*	-0.590**	-0.435**	0.256**	-0.204*	-0.351**	-0.335**	-0.272**	1.00		
100-seed weight (g)	0.338**	-0.341**	-0.433**	-0.128	-0.471**	-0.452**	0.299**	-0.113	-0.229*	-0.133	-0.144	0.651**	1.00	
Time to maturity (days)	0.690**	-0.250**	-0.277**	-0.442**	-0.301**	-0.176*	0.240**	0.072	-0.210*	-0.172*	-0.058	0.380**	0.411**	1.00

** Significant at 1% level; * Significant at 5% level

• DFL=Days to 50% flowering (days), NOL=Number of leaves, LFL=Leaf length (cm), LFW=Leaf width (cm), PHT=Plant height (cm), EHL=Ear head length (cm), EHW=Ear head width (cm), STS=Stem thickness (cm), SFW=Stem fresh weight (g), SDW=Stem dry weight (g), BRX=Brix (%), GRY=Grain yield (g), SWT=100-seed weight (g), DYM=Days to maturity (days)

have legal right on these diverse lines. Hence, they need to be registered first with NBPGR and then protect them under Plant Variety Protection Act 2001 in India, so that bio-piracy and extinction of these valuable resources, is prevented. It is the responsibility of all engaged in sorghum research to collect, conserve and protect them in a scheduled timeframe on mission mode basis.

Sorghum in India is grown in two seasons, namely, rainy (*kharif*) and post-rainy (*rabi*) season in India. The requirements of varieties are different for two seasons. The emphasis is that the rainy season adapted varieties should be photosensitive, dwarf stature, and short duration to escape with infection by grain mold. On the other hand, varieties for the post-rainy season adaptation should be tall, high yielding with reasonable levels of terminal drought tolerance to sustain receding residual moisture. During the past four decades, remarkable progress has been made by diversifying the parental lines for yield (both grain and fodder), maturity, height, disease and insect resistance and quality improvement by utilization of indigenous and exotic germplasm.

Notable varieties developed during the early period through the landraces and still under cultivation are the Co-series in Tamil Nadu; the PJ kharif and rabi selections, Saoner, Ramkel, Aispuri, the Maldandi, Guntur and Anakapalle series of Andhra Pradesh; the bilichigan, fulgar white, fulgar yellow, kauvi, Nandyal, hagari, yanigar varieties of the erstwhile Mysore state. Indian germplasm line *karad local* was crossed with American material IS 3922 to develop the MS line 296A, which was the best combiner. By utilizing local variety Vidisha 60-1 at Indore centre, the ms line of CSH 18 (ms IMS 9A) was developed. The local variety, Vidisha 60-1 not only contributes for high stover yield but also for improved grain quality. The grain yield levels of rainy season hybrids have reached the plateau and there is a need to exploit unused germplasm and land races to diversify the genetic base (Elangovan *et al*., 2005).

Post-rainy season varieties were developed by crossing Indian locals, M 35-1 and IS 2644 with American germplasm lines. Marginal improvement was achieved for grain yield over the most popular local variety M 35-1. Recently released variety, CSV 216R (CSV 16) is a landrace selection from *rabi* germplasm from Maharashtra. Another variety which became very popular, SPV 462, (from Coimbatore) was developed from multiple cross involving IS 2947 and IS 3687 from USA and IS 1151 and BP 53, locals of Maharashtra and Gujarat in India, respectively.

The need for further critical evaluation of germplasm and its utilization in grain and forage sorghum improvements is keenly felt. Sorghum collection missions may be further arranged on the specific targeted germplasm availability areas based on the usage like sweet sorghum, pop sorghum, dual-purpose sorghum and sorghums resistant to pests and diseases etc. Landraces are known to possess local adaptation and stability and may offer opportunities for direct utilization. On the other hand, improved varieties with diverse genetic base are likely to show wider adaptation and enhanced performance. Judicious combination of both in recombination breeding programmes can further lead to upgradation of yield potential. So far *caudatum* and *durra* types have been exploited. Inclusion of *guinea* germplasm may bring further increase in yield potential, tolerance to grain mold and lodging resistance.

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Effect of Wheat Parent and Embryo Age on Haploid Formation in Wheat x Maize Crosses

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Key Words: ***Triticum aestivum, Zea mays,*** **Chromosome elimination, Embryo stimulation, Wide hybridization**

Introduction

The aim of wheat breeding is to improve the quality, sustainability and productivity of wheat. The improvement of wheat can be achieved through wide hybridization. Wide hybridization is considered to be a useful tool in plant breeding for creating new species, gene transfer or induction of haploids. Techniques to produce haploids that have been used in wheat include anther culture, microspore culture and intergeneric crosses (Laurie and Bennett, 1986; Mujeeb-Kazi *et al.,* 2006). Doubled haploid production by means of hybridization between hexaploid wheat and maize is potentially of great value to wheat breeding programme because it may reduce the time required to achieve homozygosity in breeding lines. The relative insensitivity of maize to the action of Kr_1 and Kr_2 alleles of wheat suggests that wheat × maize crosses could be a valuable alternative to other techniques for the production of wheat haploids (Daniel *et al.,* 2005; Guzy-Wrobelska *et al*., 2007). In wheat x maize crosses, the embryo soon aborts; however, exogenous treatment with synthetic auxin 2, 4-D promotes seed and embryo development until the embryo can be excised and plated onto a synthetic medium for continued growth and plant regeneration.

Haploid production efficiency is also influenced by genotype of the wheat parent and the proportion of haploid embryos which germinate and develop into plantlets. One factor which is likely to influence the germination success of haploid embryos is the time of embryo rescue. In most recent reports, haploid embryos have been rescued from 2 to 3 weeks after pollination. Therefore, the present investigation was undertaken to study the effect of wheat genotypes on embryo formation, embryo germination and haploid plantlet production as well as to investigate the effect of age of embryo rescue on embryo germination.

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Materials and Methods

The experimental material consisted of four wheat F_1s UP2113 × UP2338 (W1), PBW396 × UP2338 (W2), PBW396 × UP2425 (W3) and UP2113 × UP2425 (W4). For making inter-generic crosses between wheat and maize, maize variety 'Surya' with good pollen shedding ability was chosen. The following crosses were made: W1 × Surya; W2 × Surya; W3 × Surya; W4 × Surya. Emasculation of wheat spikes was done by cut glume method; while spikes were still half inside the flag leaf sheath. The emasculated spikes were covered with cellophane bags and tagged. Two days later, when the stigma was feathery and receptive, the pistils were hand-pollinated by dusting with pollen from the dehiscing anthers of the male parents and spikes were covered with glassine paper bag to avoid any pollination by undesired foreign pollen. After one day of pollination, the spikes were sprayed with 100 ppm 2, 4-D solution, one shot along each side. This was done for three consecutive days and the spikes were left as such for about 15-18 days. For embryo culture, after 15-18 days of pollination spikes were collected and seeds (or enlarged ovaries) were taken out with the help of the forcep. Number of seeds were counted and recorded for each of the wheat genotype. A total of 122 embryos were excised from the enlarged ovaries with the help of sterilized scalpel and cultured on the surface of the modified MS media (MS + 0.5 mg/l BAP). After this, culture tubes were closed and transferred to a refrigerator at 4°C in the dark after recording the number of embryos cultured. After 5-6 days, cultures were transferred to incubator at 25°C temperature and 16/8 light and darkness cycle. The germination and growth of the embryos were then observed. Confirmation of haploidy was done by counting the chromosomes of the root tip at metaphase stage.

Experiment 1*: Influence of wheat genotype on embryo formation, embryo germination and haploid production in wheat × maize crosses.*

To reveal the effect of wheat genotype on embryo formation, embryo germination and haploid production, all the four hybrids (W_1-W_4) were compared. The pollinated ears were collected after 15-18 days of pollination and the number of pollinated florets, the number of seed like structures formed, embryos obtained and embryos germinated were recorded using the following formulae:

$$\text{Seed set (\%)} = \frac{\text{Number o f seeds obtained}}{\text{Number o f florets pollinated}} \times 100$$

$$\text{Embryo formation (\%)} = \frac{\text{Number o f embryo containing seeds}}{\text{Number o f seeds obtained}} \times 100$$

$$\text{Embryo germination (\%)} = \frac{\text{Number o f embryos germinated}}{\text{Number o f embryos obtained}} \times 100$$

$$\text{Haploid formation (\%)} = \frac{\text{Number o f haploids obtained}}{\text{Number o f embryos obtained}} \times 100$$

Experiment 2*: Influence of age of embryo on haploid plantlet production in wheat × maize crosses*

In order to investigate the effect of age of embryo to be rescued on embryo germination, the immature embryos from young wheat spikeletes were collected after 11-20 days of pollination and cultured on modified MS (Murashige and Skoog, 1962) media (MS+ 0.5 mg/l BAP). The cultures were maintained at 4°C in the dark. After 5-6 days, cultures were transferred to 25°C and 16/8 light/dark cycle.

Results and Discussion

Experiment 1: The mean comparison for per cent embryo formation among the four F_1s showed that, W_3 showed highest per cent of embryo formation (9.62%). Mean values for the trait have been shown using Table 1. The grand average of per cent embryo formation over all the four wheat F_1 and replications was 6.83 per cent. Analysis of variance showed a highly significant F value for the differences among wheat hybrids suggesting that the response of these four hybrids for per cent embryo formation in crossing with maize was different (Table 2). Several other workers have also reported the genotypic effect of hexaploid wheat parent on percentage of embryo formation. (Suenaga *et al.,* 1989; Ahmed *et al.,* 2005; Mujeeb-Kazi *et al.,* 2006).

Analysis of variance showed no significant difference among the four hybrids for per cent embryo germination and per cent haploid formation, which means that the genotypes of wheat did not affect germination of haploid embryos and haploid formation (Table 2). Since, the F value for this trait was not significant, there was no necessity of mean comparison but for the demonstration of individual performance of the genotype, mean have been presented in Table 3. In case of euploid or normal wheat, once a seed is formed properly, the germination of that seed is not affected by the genotype of maternal parent. In case of haploid embryos, it can be expected that a complete or bipolar embryo on the nutritional media should be able to germinate and produce a plantlet, but if not, it can be due to its developmental stage and other conditions (media composition, seasonal variations etc.) rather than the genotype of wheat parent. Campbell *et al.* (2000) reported the effect of media composition, seasonal variations, etc. on recovery of haploid plants. Daniel *et al.* (2005) reported the effect of wheat varieties and colchicines treatment on the regeneration of wheat embryos to plants.

Experiment 2: Influence of embryo age on haploid plantlet production in wheat × maize crosses

The stage of development of the hybrid embryos at the time of culture was found to be very important as their growth was strongly influenced by their age. Once the abortion process began (in the absence of endosperm), they were difficult to grow. The best age of the embryo was found to be 15-17 days after pollination in which plantlets were healthy and showing growth. The younger embryos i.e. 12-14 days had a tendency to stop growing after an initial increase in size and they were difficult to

Table 1. Influence of wheat F_1s for seed set and embryo formation

Wheat genotype (%)	No. of florets pollinated	No. of seed set (%)	No. of embryo formed(%)
W_1	492	430 (87.39)	31 (7.20)
W_2	478	402 (84.10)	14 (3.48)
W_3	536	478 (89.17)	46 (9.62)
W_4	518	476 (91.89)	31 (6.51)
Total	2024	1786 (88.24)	122 (6.83)

Table 2. Analysis of variance for embryo formation, embryo germination and haploid formation

Source of Variation	Degree of Freedom	Embryo Formation (%)*		Embryo Germination (%)#		Haploid Formation (%)##	
		SS	F value	SS	F value	SS	F value
Genotype	3	3.78	8.45**	157.99	0.910 ns	45.07	0.11 ns
Error	16	2.39		925.11		2108.26	
Total	19	6.18		1083.11		2153.34	

* CV= 14.73 † CV=16.97 †† CV=43.72

Table 3. Effect of wheat genotypes on percent embryo germination and per cent haploid formation

Wheat Genotype	Embryos Obtained and Cultured	No. of Embryo Germinated (Per cent)	No. of Haploid Formed (Per cent)
W_1	31	16 (51.61)	6 (19.35)
W_2	14	5 (35.71)	1 (7.14)
W_3	46	26 (56.52)	10 (21.73)
W_4	31	15 (48.33)	6 (19.35)
Total	122 (6.83)	62 (50.81)	23 (18.85)

isolate and culture. The older embryos 18-20 days started shriveling and showed signs of degeneration as the process of abortion had already set in by that age. Such embryos either aborted on the spikelet itself or often dried in the culture medium.

The two basic stages of embryo growth exist with regard to nutritional independence. The heterotrophic stage of growth is the period during which the embryo depends on the endosperm for its nutrition; it extends from the fertilization to approximately the heart stage. The autotrophic phase starts from the late heart stage. This stage is significant for the *in vitro* culture as the embryo becomes sufficiently independent of the endosperm for the subsequent growth. As the embryo matures, its growth requirements for the artificial culture become less complex. Older, healthy embryos are, therefore, easier to culture than the younger ones. The culture of young embryos is also more difficult due to their size, damage during desiccation and sensitivity to osmotic shock.

Suenaga and Nakajima (1989) found that larger embryos tended to show better germination. Embryo size not only depends on their age but also on the fitness of the donor plant, amount of auxin applied and other factors. Chen *et al.* (1996) cultured 10-14 days old embryos and found that most of the embryos larger than 400 µm germinated and produced normal plantlets because the smaller ones failed to germinate. Kammholtz *et al.* (1996) reported that embryos rescued 12-15 days after pollination were large and easily rescued and also had a significantly higher germination (51-80%) than embryos rescued 9, 17, 19 or 21 days after pollination (6.4-31%). Wedzony and Lammeren (1996) observed that when excised at 14 days after pollination, haploid embryos were rescued by *in vitro* culture from 14% of the pollinated florets. Campbell *et al.* (2000) reported that 16-day old embryos resulted in improved frequency of haploid plant formation in wheat x maize system. Ahmad *et al.* (2005) reported low embryo viability in tetraploid wheat compared to hexaploid wheat because of the size of embryos.

Thus, from the present investigation and the reports given by various workers, it can be inferred that the right age for transferring the hybrid embryos to the culture medium varies from genotype to genotype and needs to be standardized in each case separately. In the present case, the optimum time of rescue was when the embryos were 15-17 days old.

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Trypsin and Chymotrypsin Proteinase Inhibitors from Cereal Seed Extracts

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Proteinase inhibitory activity was assayed from the seeds of 57 accessions of five species of cereal germplasms. Barley and maize had both trypsin inhibitory (TI) and chymotrypsin inhibitory (CI) activity. Chymotrypsin inhibitory activity is not found in the accessions of rice, wheat and oats studied. TI and CI activities in barley and maize are higher than those of the other cereals tested. Oat accessions contained the lowest trypsin inhibitory activity. TI protein was highest in barley accession IC82680 followed by maize CIMMYT line 51705 and lowest in rice cultivar, Pusa Sugandha. Protein and CIU content were positively correlated in barley ($r=0.877^{**}$). TI and CI activity are positively correlated in barley seed extracts.

Key Words: Cereals, Trypsin, Chymotrypsin inhibitory activity, Correlation

Introduction

Proteinase inhibitors (PIs) are present in multiple forms in numerous tissues of animals and plants as well as microorganisms. The defensive capacities of plant PIs rely on inhibition of proteases present in insect guts or secreted by microorganisms, causing a reduction in the availability of amino acids necessary for their growth and development (De Leo *et al*., 2002). Proteinase inhibitors comprise one of the most abundant classes of proteins in plants. Most storage organs such as seeds from families Leguminosae and Graminae and tubers from family Solanaceae contain only 1 to 10% of their total proteins as proteinase inhibitors, which inhibit different classes of enzymes (Ryan, 1990). These inhibitors are also widely distributed among different botanical families.

Soybean trypsin inhibitor was the first PI isolated and characterized. The presence of high levels of protease inhibitors on a continual basis can lead to chronic hypersecretion by the pancreas, loss of proteolytic activity in the gut, loss of appetite, starvation and eventual death. The decline of PI content during germination correlated with increased activation of these proteases in the mobilization of storage proteins (Richardson, 1977).

Members of the serine and cysteine proteinase inhibitor families have been more relevant to the area of plant defense than metallo and aspartyl proteinase inhibitors (Laskowski *et al*., 1988). Serine Proteinase Inhibitors are universal throughout the plant kingdom and have been described in many plant species. The limited studies made so far indicate a wide variability of proteinase inhibitors in cereals in India. Keeping this in view, the present study was undertaken to find out the presence of proteinase inhibitors (Trypsin and chymotrypsin) in various germplasm collections of cereals.

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Materials and Methods

The present investigation was conducted in the Division of Entomology, Indian Agricultural Research Institute, New Delhi during 2004-2007.

Seed Materials and Chemicals

Seeds of different cereal germplasms were procured from Regional Stations of National Bureau of Plant Genetic Resources, Division of Genetics (IARI), Directorate of Maize Research and Directorate of Rice Research (DRR). Bovine trypsin (EC 3.4.21.4) and chymotrypsin (EC 3.4.21.1) were purchased from SRL (India). Standard substrates, *viz*., Benzoyl-DL-Arginine para-Nitroanilide (BA*p*NA) and Benzoyl-DL-Tyrosine-para-Nitroanilide (BT*p*NA) were procured from Sigma, Chemical CO. (St. Louis, Mo, U.S.A.). All other chemicals and reagents used were of analytical grade.

Extraction of Proteinase Inhibitors from Legumes and Cereals

Crude extract was obtained according to Hajela *et al.* (1999) with some modifications. The defatted flour was extracted with 0.01M Na-phosphate buffer (1:10 w/v) pH 7.0 containing 0.15M NaCl. It was homogenized for 10-15 minutes by using homogenizer and then stirred for 2 h at room temperature; the homogenate was centrifugate at 8,000 to 10,000 rpm for 30 minutes. The supernatant (crude extract) was diluted with distilled water. The supernatant (crude extract) was precipitated with ammonium sulfate at concentrations of 0-30, 30-60 and 60-90%. The fraction obtained at 30-60% ammonium sulfate saturation showed high inhibitory activity against bovine trypsin. This fraction was used for the estimation of protein content as well as for the presence of PI activity.

Measurement of Inhibitor Activity

Different volumes of ammonium sulfate precipitated at 30-60% fractions (25 to 100 µl) were added to 20 µg of

trypsin in 200 µl of 0.01M Tris-HCl (pH 8.0) containing 0.02M $CaCl_2$ and incubated at 37^{0}C in a water bath for 5-10 minutes. Residual trypsin activity was measured by adding 1 ml of 1mM BApNA (in 10% of DMSO) and incubated at 37^{0}C for 10 minutes (Erlanger *et al*., 1961). Reactions were stopped by adding 200 µl of 30% glacial acetic acid. After centrifugation, the liberated *p*-nitroaniline in the clear solutions was measured at 410 nm using UV/VIS-double beam Perkin Elmer λ3B spectrophotometer. Only 20 µg of trypsin in 200 µl of buffer without ammonium precipitated fractions was considered as control. Inhibitor activity was calculated by the amount of ammonium precipitated fractions required to inhibit 50% of trypsin activity, which is considered as one unit of trypsin inhibitor and expressed as trypsin inhibitor units per mg seed protein (Ignacimuthu, 1999). Protein content in all extracts was determined according to the method of Lowry *et al*. (1951) using bovine serum albumin, fraction V (M.wt. 66kDa, Sigma) as the standard.

The chymotrypsin inhibitor activity was also measured in a similar way except that the substrate used was BT*p*NA. One millimolar BT*p*NA was prepared in 0.01M Tris-HCl (pH 8.0) containing 40% ethanol (Hajela *et al.,* 1999).

Statistical Analysis

Data were subjected to analysis of variance (ANOVA) and compared by using LSD. Tests were carried out at the 1% and 5% level of significance.

Results and Discussion

The inhibitory activities in cereals against trypsin and chymotrypsin are presented in Table 1 (a, b) and Fig. 1. Most of the investigated accessions/cultivars of cereals have trypsin inhibitory activity (TI) while only barley and maize contained chymotrypsin inhibitory activity (Table 1b). In this experiment, results revealed that the TI and CI activities in barley and maize are generally higher than in wheat, rice and oats. Protein content in all the accessions/cultivars was below the expected level because in the present study, the fractions obtained from ammonium precipitated at 30-60% were used for the assay of protein and PI activity in all the cereals tested. The other fractions precipitated at 0-30 and 60-90% was not included in the assay. Only part of the protein was used for the testing the PI activity.

Rice, wheat and oat accessions recorded the lowest TI values (7.4-170.50 TIU/g seed). These accessions also failed to show chymotrypsin inhibitory activity. In the present study, the concentration of the ammonium sulfate precipitated fractions from rice, wheat and oat was increased to a maximum of 200 µl for testing the presence of chymotrypsin activity but assay failed to show the presence of CI activity. Barley and maize have both TI and CI activity (Hejgaard and Boisen, 1980). Similar results are given in the review paper of Boisen (1983). He mentioned that both TI and CI activity in barley, TI and weak CI activity in wheat, TI and no CI activity in rice and low TI and CI activity in oat. Lekes *et al*. (1989) also reported the presence of chymotrypsin inhibitory activity in different barley accessions.

Of the twenty-three rice accessions evaluated, the highest trypsin inhibitory activity was found in Vikas which was significantly different from all other accessions of rice. Of the wild species of *Oryza* tested, *officinalis* contained the highest TIU of 57.1/g seed. Among the wheat accessions evaluated, significantly higher activity was recorded in the cultivar, Pusa T-1336 and *T. abysinicum*. Oat accessions had the lowest TIU/g seed. Accession IC82680 of barley had the highest activity of 785.0 TIU/g seed. Maize CIMMYT line 51705 had the highest TIU value of 483.40/g seed, which was significantly different from all the other CIMMYT lines and cultivars.

The specific activity of the trypsin inhibitory protein was the highest in barley accession IC82680 whereas in rice cultivar, Pusa Sugandh it was very low. All the five accessions of barley had higher TIU per mg protein when compared to all other cultivars/accessions of cereals tested. Accessions of oat recorded low TIU per mg protein. Barley accession IC82680 had CI activity of 301.0 units/g seed, which was higher than that of all the other 4 accessions. Among CIMMYT lines of maize, 51705 had the highest CIU/ g seed compared to all other CIMMYT lines and cultivars.

Very few literature on the studies on the assay of proteinase inhibitors in cereals are available.

Table 2 presents the results of correlation studies in cereals. Rice, wheat, oats and maize had significant positive correlation between protein and TI activity. No significant correlation was observed in barley. Protein and CI activity was positively correlated in barley and maize though the correlation is statistically not significant. Correlation between TI and CI activity was positively significant at 1% in barley (r= 0.877**). Wheat also had positive correlation between TI and CI activities but not significant (Table 2).

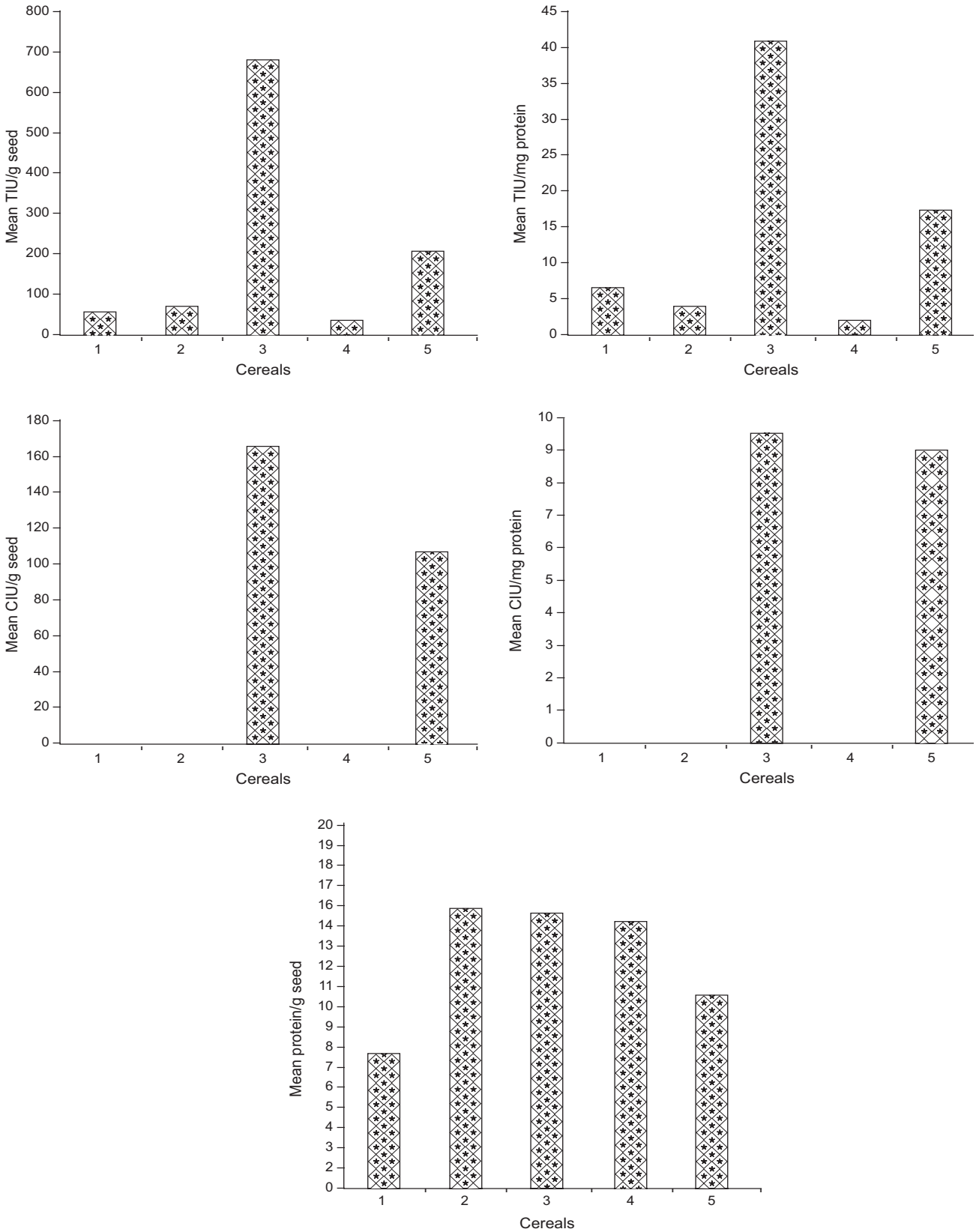

Fig. 1: Species mean values of TIU/g seed, TIU/mg protein, CIU/g seed, CIU/mg protein and protein content of various cereals
1. *Oryza sativa,* 2. *Triticum aestivum*, 3. *Hordeum vulgare*, 4. *Avena sativa*, 5. *Zea mays*

Table 1a. Trypsin inhibitory activity and protein content of germplasm accessions of rice, wheat and oats

S.No.	Accession no/cultivars	Protein mg/g seed	TIU/g seed	TIU/mg protein
Rice (*Oryza sativa*)				
1	Pusa Sugandh	8.7	7.4	0.8
2	IR-64	8.0	53.3	6.8
3	P-44	9.3	62.1	6.6
4	Jaya	8.8	46.4	5.2
5	P-1121	8.8	52.6	5.9
6	Phalguna	8.5	57.3	6.7
7	TKM-6	10.6	65.1	6.1
8	Suraksha	7.1	51.5	7.2
9	Kavya	9.1	20.8	2.2
10	9313 (Javanica)	11.0	112.5	10.2
11	Taroari Basmati	7.4	51.9	6.9
12	Mugad sugandha	8.6	91.0	10.5
13	MTU-1001	8.5	59.3	6.9
14	Abhaya	8.8	54.8	6.1
15	Taipei-309	7.7	75.1	9.7
16	IET-14590	9.8	48.7	4.9
17	Vikas	11.6	67.0	5.7
18	W-1263	6.9	70.6	10.2
19	FR-13A	5.6	44.5	7.9
20	TN-1	8.0	73.0	9.1
21	Ajaya	8.2	73.9	8.9
22	BSI-115	9.3	36.6	3.9
23	Chaitanya	8.0	70.7	8.8
	Wild Species			
24	*O. nivara*	4.7	26.3	5.5
25	*O. officinalis*	8.7	57.1	6.5
26	*O. rufipogon*	4.4	20.9	4.7
	Mean	8.31	55.78	6.68
Wheat (*Triticum aestivum* L.)				
1	IC138900	11.80	15.20	1.28
2	IC138895	14.50	40.51	2.79
3	IC138896	13.23	38.90	2.93
4	IC118796	11.10	21.18	1.90
5	IC118774	16.5	51.10	3.11
6	Pusa T-1336	20.16	107.87	5.34
7	WR-544	16.20	96.46	5.97
	Wild Species			
8	*T. amplissifolium*	19.36	89.20	4.60
9	*T. compactum*	15.86	52.06	3.28
10	*T. sphaerococum*	21.06	138.60	6.59
11	HD	19.33	61.03	3.16
12	*T. durum*	12.83	41.76	3.25
13	*T. dicocoides*	23.03	64.96	2.82
14	*T. dicocum*	23.30	55.53	2.39
15	*T. abysinicum*	16.0	170.50	10.66
16	Synthetic wheat	22.56	99.56	4.41
	Mean	17.30	71.52	4.03
Oat (*Avena sativa*)				
1	EC159067	13.0	29.3	2.2
2	EC96553	20.0	35.1	1.7
	Mean	16.5	32.2	1.95
	L.s.d. (P<0.05)	0.76	19.16	1.77

Table 1 b. Trypsin inhibitory activity and chymotrypsin inhibitory activity and protein content of germplasm accessions of barley and maize

S.No.	Accession no /cultivars	Protein mg/g seed	TIU/g seed	TIU/mg protein	CIU/g seed	CIU/ mg protein
Barley (*Hordeum vulgare* L.)						
1	IC82680	17.8	785.0	43.9	301.0	16.91
2	IC82512	15.0	644.7	43.0	137.9	9.19
3	IC82506	17.2	659.5	38.2	91.3	5.30
4	IC79590	17.7	704.6	39.8	156.7	8.85
5	IC60712	17.5	622.6	35.4	126.1	7.20
	Mean	17.04	683.28	40.06	162.60	9.49
5. Maize (*Zea mays*)						
1	51701	10.87	146.13	13.44	126.70	11.65
2	51702	9.20	112.26	12.54	131.10	14.50
3	51703	11.53	147.90	12.82	115.30	10.00
3	51704	14.20	147.2	10.49	109.70	7.74
4	51705	15.66	483.40	30.88	134.50	8.59
5	Surya	12.33	148.73	12.06	68.30	5.53
6	Pro-311	11.63	237.36	20.40	71.56	6.15
7	PMZ-150	10.03	225.66	22.50	80.80	8.07
	Mean	11.93	206.08	16.89	104.71	9.02
	L.s.d. (P<0.05)	0.76	19.16	1.77	12.27	1.37

Note: Specific information on IC or EC of wild species of rice, wheat and maize (lines) was not given at the time of collection from DRR, Division of Genetics (IARI) and DMR.

Table 2. Correlation coefficient between protein content, trypsin and chymotrypsin inhibitory activities of different cereals

Crops	Parameters	TIU	CIU	Significant at 1% or 5%
Rice	Protein	R=0.371**	–	1 %
	TIU	–	–	–
Wheat	Protein	R=0. 472**	–	1 %
	TIU	–	–	–
Barley	Protein	r=0. 445	r=0.206	–
	TIU	–	r=0.877**	1%
Oat	Protein.05	r=0.837*	–	5 %
	TIU	–	–	–
Maize	Protein	R=0.607**	r=0.157	1 %
	TIU	–	r=0.193	

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Screening of Soil for Lead-Tolerant Fungi

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Soil samples were screened for fungi tolerant to lead (lead nitrate) using poisoned food technique. Control media as well as media supplemented with 40 ppm, 200 ppm and 400 ppm concentrations of lead (in the form of lead nitrate) were used to isolate fungi by serial dilution plate method. In total, 19 species of fungi were isolated. Out of these, six species, *i.e. Aspergillus niger* var. *niger* Tiegh, an unidentified sterile species, *Sepedonium chrysospermum* (Bull) Fr., *Trichoderma lignorum* var. *lignorum* (Tode) Harz, *Penicillium implicatum* var. *implicatum* Biourge and *Aspergillus candidus* var. *candidus* Link could tolerate the highest concentration (*i.e.,* 400 ppm) of lead. In addition to the above six fungal strains, *Aspergillus ustus* var. *ustus* (Bainier) Thom and Church could tolerate and grew well on the media with moderate concentrations (200 ppm) of lead nitrate. *Cladosporium herbarum* var. *herbarum* (Pers.) Link, *Curvularia* sp. Boedijn, *Scopulariopsis brevicaulis* var. *brevicaulis* (Sacc.) Bainier and *Scopulariopsis communis* var. *communis* Svilv. are moderately resistant as these could grow and flourish at 40 ppm concentration only. *Fusarium* sp. (isolate-III) Link cannot tolerate even low doses of lead nitrate. Out of these 19 species, 5 fungal species, *i.e., Aspergillus candidus, Aspergillus niger, Penicillium implicatum, Sepedonium chrysospermum* and *Trichoderma lignorum* were selected for studying the effect of different concentrations of lead nitrate on the *in vitro* growth of individual species. Thus, these species can be further tried for their utilization as biosorbents for remediation of lead in the effluents.

Key Words: Lead tolerance, *Aspergillus*, Serial dilution plate method

Introduction

Significant amount of heavy metals including lead are introduced into the aquatic systems as a result of sludge disposal, ore-refining, metal-smelting, welding, refining, agricultural sources and manufacturing of pesticides (Singh, 2001). Even if these metals are present in undetectable quantities, their recalcitrance and consequent persistence in water bodies might ultimately, through biomagnification, increase their concentrations to such an extent that these begin exhibiting toxic characteristics. Heavy metals, once released into the soil matrix, also find their way into the food web through ground water aquifers (Walton, 1995). Hence, it is necessary to remove these metals before these enter the complex ecosystem. Physio-chemical treatments developed to deal with very diluted metal-containing effluents (precipitation, flocculation, coagulation and ion-exchange etc.) are very expensive (Lacina, 2003). The ability of fungi to serve as biotraps for heavy metals and biosorb them has attracted the attention of a number of workers for purification of such water (Bellion *et al*., 2006; Duruibe *et al*., 2007). The purification of the metal-containing water using fungal biomass is not only cheaper but also presents several advantages such as: (i) fast removal, (ii) production of residual small volume, (iii) easy installation of the process, (iv) possibility of valorization of fungal waste biomasses from industrial fermentations. Since soil constitutes reservoir of immense variety of the fungi, it would be pertinent to exploit the possibilities of getting suitable fungal strains from soil which are capable of removing metals from the wastewater effectively. The present communication deals with an attempt to discern the soil fungal species capable of surviving lead nitrate *in vitro*.

Materials and Methods

Serial dilution plate method (Waksman, 1927) was followed to isolate fungi from the soil samples. 20 g of the sample collected from C.C.S. University Campus, Meerut were placed in 200 ml of sterile water and stirred for fifteen minutes using a magnetic stirrer to get a stock solution (1:10 dilution). 10 ml of this solution are immediately transferred to a conical flask containing 90 ml of sterile distilled water to get a suspension of 1:100 dilution. This suspension was used for the preparation of further serial dilutions (1:1000 and 1:10,000). The suspension of 1:10 dilution was discarded. From the suspension of each of the remaining three dilutions (1:100, 1:1000, 1:10,000), 1 ml aliquots were transferred to each of a set of three Petri dishes followed by the addition of approximately 20 ml of sterilised and cooled (45°C) Czapek Dox Agar medium (Raper and Thom, 1949) with 30 ppm of rose bengal and 30 mg of streptomycin. In addition to the normal medium, media amended with different concentrations (40 ppm, 200 ppm and 400 ppm) of Pb (as lead nitrate) were also prepared. Thus, 36 Petri dishes were used, *i.e.*, three dilutions × four types of media (control amended with 40 ppm, 200 ppm and 400 ppm) × three replicates. These

Petri dishes containing the media and the inocula were incubated at 25 ± 1°C for 6 to 8 days. The total number of colonies of individual fungal species growing in each Petri dish were recorded. The fungal strains obtained were identified using standard keys (Gilman, 1957; Nagamani *et al.*, 2006).

Mycelial discs (8 mm diameter) cut from the margins of actively growing cultures of the given fungal species were centrally inoculated onto separate Petri plates containing media of normal, 40 ppm, 200 ppm and 400 ppm concentrations of lead nitrate with the help of corkborer aseptically on agar plate. Thus, for each fungal species and for a given metal, 12 Petri dishes were used, *i.e.*, 4 (normal medium + 3 media with varying heavy metal concentrations) × 3 replicates. The inoculated agar plates were incubated at 25 ± 1°C for 4 to 5 days (2-3 days in case of some fast-growing fungi). The diameters of fungal colonies were measured to observe the differences between the growth of test fungal species at different heavy metal levels.

Results and Discussion

A total of 19 species of fungi could be isolated from the soil using Czapek's Dox Agar normal medium and that amended with different concentration of lead nitrate (Table 1).

Nine species of fungi colonized agar plates containing normal medium. *Aspergillus niger,* an unidentified sterile species and *Fusarium* sp. (isolate-III) dominated the plates accounting for 42%, 27% and 15.3%, respectively of the isolates. These were followed by *A. fumigatus* var. *fumigatus* Fresen*, A. candidus, Fusarium* sp. (isolate-IV) Link and *Penicillium citrinum* Link each of which accounted for 3.2% of the isolates. *P. implicatum* and *Sepedonium chrysospermum* were megerly represented by only one isolate each.

Colonies belonging to twelve fungal species developed on the agar plates containing low concentrations (40 ppm) of lead nitrate. Six species, *i.e., A. sulphureus, Scopulariopsis communis, S. brevicaulis, Curvlaria* sp., *Cladosporium herbarum* and *Trichoderma lignorum* which failed to appear on the normal plates, did appear on these agar plates with low concentrations of lead nitrate. On the other hand, *Fusarium* sp. (isolate-III) failed to appear on plates with the low concentration as well as higher concentration for lead nitrate. The plates were dominated by unidentified sterile species, *A. niger* and *Sepedonium chrysospermum* which accounted for 30%, 23% and 16.7% of the isolates, respectively.

A. fumigatus, Fusarium sp. (isolate-IV), *Scopulariopsis communis, Curvularia* sp., *Scoplariopsis brevicaulis, Cladosporium herbarum, Trichoderma lignorum,*

A. candidus and *A. sulphureus* var. *sulphureus* (Fresen.) Thom and Church were represented by 1 to 3 isolates only.

Ten fungal species were isolated on agar plates with 200 ppm lead nitrate. *A. niger,* an unidentified sterile species and *Penicillium implicatum* dominated the plates comprising 39%, 30% and 10% plates of the isolates, respectively. These were followed by *A. ustus, Sepedonium chrysospermum* and *Trichoderma lignorum* which accounted for 4.2%, 6% and 6% respectively of the isolates. *A. candidus, A. flavus* var. *flavus* Link*, Alternaria alternate* (Fr.) Keissl. and *Torula* sp. Persoon appeared on the plates, though these were represented by one isolate each only.

Seven fungal species could survive on the agar plates containing 400 ppm lead nitrate. *A. niger* and the unidentified sterile species heavily dominated the plates comprising 33.3% and 27.5%, respectively of the isolates.

A. candidus, *P. implicatum*, *S. chrysospermum* and *Trichoderma lignorum* lagged far behind with only 7%, 13%, 9% and 9% of the isolates, respectively. *P. citrinum* was megerly represented by one isolate only. The number of species was greater in the plates containing 40 ppm and 200 ppm lead nitrate as compared to the control plates. However, there was a decrease in the number as the concentration of the metal increased. The number of isolates did not vary much with the change in metal concentration though it was much lesser in amended plates as compared to the control plates. It can be concluded that:

a) *A. niger*, an unidentified sterile species, *S. chrysospermum, T. lignorum, P. implicatum* and *A. candidus* are resistant to very high concentration (400 ppm) of lead nitrate.

b) *A. ustus* could tolerate and grow with moderate concentrations (200 ppm) of lead nitrate.

c) *Cladosporium herbarum, Curvularia* sp., *Scopulariopsis brevicaulis* and *S. communis* are moderately resistant as these could grow and flourish at 40 ppm concentration only.

d) *Fusarium* sp. (isolate-III) cannot tolerate even low doses of lead nitrate.

Table 1. Frequency and number of isolates of fungal species colonising agar plates containing unamended medium (Normal) as well as that amended with different concentrations of lead nitrate

S. No.	Fungal species	Normal medium			Medium amended with lead nitrate									Total isolates
					40 ppm			200 ppm			400 ppm			
		%F	FC	Isolates	%F	FC	Isolates	%F	FC	Isolates	%F	FC	Isolates	
1.	*Alternaria alternata*							11.1	I	1				1
2.	*Aspergillus candidus*	22.2	II	3	11.1	I	1	11.1	I	1	11.1	I	5	10
3.	*Aspergillus flavus*							11.1	I	1				1
4.	*Aspergillus fumigatus*	33.3	II	3	33.3	II	3							6
5.	*Aspergillus niger*	77.7	IV	38	66.6	IV	15	66.6	IV	27	66.6	IV	23	103
6.	*Aspergillus sulphureus*				11.1	I	1							1
7.	*Aspergillus ustus*							11.1	I	3				3
8.	*Cladosporium herbarum*				22.2	II	2							2
9.	*Curvalaria* sp.				11.1	I	3							3
10.	*Fusarium* sp. (isolate-III)	11.1	I	14										14
11.	*Fusarium* sp. (isolate-IV)	22.2	II	3	33.3	II	3							6
12.	*Penicillium citrinum*	11.1	I	3							22.2	II	1	4
13.	*Peniillium implicatum*	11.1	I	1				33.3	II	7	11.1	I	6	14
14.	*Scopulariopsis brevicaulis*				11.1	I	2							2
15.	*Scopulariopsis communis*				11.1	I	3							3
16.	*Sepedonium chrysospermum*	11.1	I	1	33.3	II	11	22.2	II	4	44.4	III	9	25
17.	*Torula* sp.							11.1	I	1				1
18.	*Trichoderma lignorum*				11.1	I	2	22.2	II	4	22.2	II	6	12
19.	Sterile species	77.7	IV	25	66.6	IV	20	77.7	IV	21	66.6	IV	19	85
		9		91	12		66	10		70	7		69	296

%F = Percentage frequency; FC = Frequency class

Five fungal species, *i.e., A. candidus, A. niger, P. implicatum, S. chrysospermum* and *T. lignorum* were selected for the study. The results are presented in the Table 2.

When grown individually in the medium containing different concentrations of lead nitrate, *S. chrysospermum* did not seem to be much affected either positively or negatively; while 40 ppm concentration had a positive effect on the growth of all the five fungal species *i.e.*, *A. candidus*, *A. niger*, *P. implicatum*, *S. chrysosperum* and *T. lignorum* tested at least in the early period of two days. Slightly longer exposure upto four days had either

Table 2. Radial growth (in mm) of the selected fungal species in control medium as well as media containing different concentrations of lead nitrate after 2 days and 4 days of incubation

S. No.	Fungal species	Days of incubation	Control media	Media amended with lead nitrate		
				40 ppm	200 ppm	400 ppm
1.	*Aspergillus candidus*	2	14.33	19.00 (+32.58)	17.00 (+18.63)	16.33 (+13.95)
		4	18.00	22.00 (+22.22)	17.00 (–5.55)	13.66 (–24.11)
2.	*Aspergillus niger*	2	16.33	17.00 (+4.10)	18.00 (+10.23)	17.33 (+6.12)
		4	28.00	24.33 (–13.10)	24.33 (–13.10)	32.00 (+14.28)
3.	*Penicillium implicatum*	2	10.00	12.66 (+26.60)	11.33 (+13.30)	11.66 (+16.60)
		4	16.33	18.33 (+12.24)	18.33 (+12.24)	17.33 (+6.12)
4.	*Sepedonium chrysospermum*	2	87.33	87.66 (+0.37)	87 (–0.37)	87.33 (=0)
		4	87.66	87.66 (=0)	87.66 (=0)	87.66 (=0)
5.	*Trichoderma lignorum*	2	62.33	64.00 (+2.67)	68.00 (+9.09)	72.66 (+16.57)
		4	81.66	82.00 (+0.41)	82.66 (+25.89)	86.33 (+31.48)

slightly inhibitory effect or the positive effect was diminished.

The growth of *T. lignorum* exhibited an increase with the increase in metal concentration, thus, corroborating the results obtained on isolation plates where also the frequency and isolates of *T. lignorum* were found to increase with an increase in the metal concentration. Low concentrations of metal stimulated the *in vitro* growth of *A. candidus* but as the concentration increased, either the growth was inhibited or the stimulatory effect was decreased. More or less similar trend was observed with *P. implicatum*. Of course, these results do not tally with those obtained on isolation plates.

Rai *et al*. (1995) observed 37.74% inhibition of *A. niger* and 21.1% inhibition of *T. harzianum* after seven days of incubation in the medium containing 200 ppm of lead. However, in the present investigation both the species exhibited more growth than that in the control in the first two days. Later, by the fourth day, the growth of *A. niger* was inhibited by 13.10% while that of *T. lignorum* was further stimulated (+25.89%).

The lead is the metal which is absorbed in very high amounts by the fungal biomass. This raises the possibility of reduced uptake as one of the factor responsible for the apparent metal tolerance of *A. niger*, *S. shrysospemum*, *T. lignorum* and other species. In the present investigation, rich nutrient medium amended with heavy metals has been used. Babich and Stotzky (1982) believed that this may provide overestimation of tolerant populations as a result of complexing and detoxification of the heavy metals by inorganic and organic constituents of the medium. Further studies therefore, must be carried out before branding these strains as lead-resistant.

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Variability and Cluster Analysis of Morphological, Fodder and Seed Yield Attributes of Cowpea *Vigna unguiculata* (L.) Walp; Germplasm for Identification of Donor Sources

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Cowpea is a multipurpose crop grown for fodder, grain and improving soil fertility. For improving cowpea, a set of 168 exotic and indigenous genotypes of cowpea *Vigna unguiculata* including three cultigroups, *i.e. unguiculata, catjang, sesquipedalis,* with three checks and one local control were evaluated at Experimental farm, Crop Improvement Division, Indian Grassland and Fodder Research Institute, Jhansi, during 2004-05 and 2005-06 in augmented block design. Pooling of the data, Non Heirarchical Euclidean Cluster analysis using SPAR-1, formed 12 clusters for 20 trait variables. Genetic variability, and frequency distribution of forage and grain yield, yield attributing characters were also performed for selection. On the basis of clustering in the present study identification of donor sources in respect of forage and grain yield was done, *i.e.,* for higher biomass/plant, IL-1177, IL-3171 and IL-966-B; higher fresh leaf/stem ratios, HY6P52-3, IL893 and IL-99-171; dry matter yield/plant, IL-1177; IL-3171 and IL-449; the maximum pod bearing lines were IL-90, EC240809, IL3117.

Key Words: Cowpea, Variability, Frequency distribution, Cluster analysis

Introduction

Among legumes, cowpea is being grown in almost all parts of India, except high hills. It is a unique pulse crop with manifold uses such as pulse, green vegetable, green fodder and as a cover crop for stopping soil erosion. But due to low yield it is not easy to exploit the crop efficiently. For any crop improvement programme, variability is the first requirement (Anku *et al*., 2001). For proper utilization of variability in breeding programme an efficient screening, evaluation and documentation of germplasm lines for useful traits is essential so that the potential value of particular germplasm line may be assessed. Therefore, a set of exotic and indigenous germplasm was evaluated and cluster analysis was performed for identification of donor sources of various morphological attributes showing high effect for improving fodder and grain yield.

Materials and Methods

A set of 29 exotic and 139 indigenous genotypes of cowpea *Vigna unguiculata* including three cultigroups, i.e., *unguiculata, catjang, sesquipedalis,* with three checks, Bundel lobia-1, Bundel lobia-2, UPC-5286 and one local control IGFRI-95-1 were evaluated at Experimental farm of Crop Improvement Division of Indian Grassland and Fodder Research Institute, Jhansi, during the years 2004-05 and 2005-06 in augmented block design. The layout consisted of 7 blocks with 24 germplasm lines, 3 checks and 1 control in each block. The observations were recorded according to minimal descriptor for Agri-horti crops. (Srivastava *et al.,* 2001). The recorded 29 traits were, early plant vigour, plant growth habit, plant height, length of main shoot per branch, number of nodes, number of primary branches, number of secondary branches, number of leaves per plant, leaf length, leaf width, leaf weight per plant, stem weight per plant, biomass per plant, fresh leaf/stem ratio, dry leaf weight, dry stem weight, dry weight per plant and dry leaf per stem ratio, days to flowering initiation, days to 50 per cent flowering, days to maturity initiation and days to total maturity, number of pod clusters/plant, number of pods per plant, pod length, seeds per pod, 100 seed weight, seed weight per plant and number of seeds per plant. Clustering pattern of the germplasm as a whole was analyzed based on average data of two years. Pooling of the data was done by taking out the average value of the trait recorded for the year 2004-05 and 2005-06. Non Heirarchical Euclidean Cluster analysis, performed on the pooled data, formed 12 clusters for 20 trait variables. Table 1 shows morphological character's mean and standard deviation for different clusters of the data pooled for the years 2004-05 and 2005-06. The morphological data of twenty nine forage and yield traits for years 2004-05, 2005-06 and pooled average of both years was analyzed, using statistical package software, SPAR -1. Clustering of 172 germplasm lines was done based on morphological attributes. A study of genetic variability, and frequency distribution of forage and grain yield, yield attributing characters were also performed for selection.

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Table 1. Morphological character's mean and standard deviation for different clusters of pooled data for the years 2004-05 and 2005-06

Cluster No.	Days to 50 per cent flower	Days to total flower	Plant height	No. of nodes	No. of primary branch	No. of secondary branch	Stem girth	Leaves/ plant	Leaf length	Leaf width	Leaf weight/ plant	Stem weight/ plant	Dry stem weight/ plant	Dry weight/ plant	Days to total maturity	No. of pod cluster/ plant	No. of pods/ plant	Pod length	No. of seeds/ pod	No. of seeds/ plant
I	49.62	66.78±	163.78±	20.29±	5.24±	3.82±	1.14±	67.15±	12.86±	**8.67±**	325.11±	149.51±	15.65±	79.42±	136.07±	5.74±	14.99±	12.47±	11.57±	175.46±
	±6.53	6.30	20.06	3.11	0.87	1.29	0.14	11.72	0.99	**1.30**	59.27	28.88	3.57	10.01	4.32	2.47	6.10	1.82	2.15	74.97
II	59.98	76.10±	158.92±	22.28±	6.62±	7.87±	1.32±	93.89±	11.54±	7.48±	446.90±	221.25±	16.15±	86.90±	131.14±	4.76±	12.35±	12.99±	11.71±	139.72±
	±9.96	10.48	30.51	2.76	1.28	3.02	0.16	23.25	1.82	1.06	104.28	57.85	4.18	9.83	7.91	2.52	7.19	2.19	2.69	77.79
III	46.78±	63.22±	151.45±	19.28±	5.96±	4.00±	1.24±	69.20±	11.81±	7.32±	365.64±	175.11±	15.19±	76.22±	133.28±	6.85±	19.35±	15.45±	16.11±	07.83±
	4.71	7.56	25.34	1.81	1.17	1.57	0.14	19.41	1.69	1.23	71.19	43.10	1.79	8.55	5.60	3.03	8.10	1.96	1.48	120.83
IV	47.00±	84.00±	**205.72±**	**27.98±**	**8.58±**	2.32±	**1.36±**	**185.29±**	**14.25±**	8.00±	503.33±	277.28±	16.72±	**116.00±**	135.00±	12.22±	28.31±	**18.98±**	**20.82±**	90.98±
	0.00	0.00	**0.00**	**0.00**	**0.00**	0.00	**0.00**	**0.00**	**0.00**	0.00	0.00	0.00	0.00	**0.00**	0.00	0.00	0.00	**0.00**	**0.00**	0.00
V	52.10±	69.76±	150.42±	19.45±	4.98±	3.63±	1.05±	61.29±	9.36±	5.82±	286.83±	130.10±	12.12±	81.35±	136.62±	5.26±	14.06±	12.76±	12.32±	173.23±
	7.42	8.33	21.32	2.78	0.99	1.69	0.14	14.80	0.77	0.70	44.46	19.21	3.54	12.15	6.40	1.75	6.10	1.85	2.31	81.91
VI	68.84±	**93.29±**	149.70±	21.25±	5.60±	4.88±	1.26±	91.46±	9.61±	5.97±	386.53±	211.45±	14.65±	109.58±	**138.87±**	5.25±	11.85±	14.03±	13.52±	159.97±
	10.47	**6.08**	24.33	2.48	0.80	1.92	0.16	29.88	2.19	1.38	85.17	52.65	2.22	11.94	**6.22**	2.62	5.72	1.70	2.20	82.28
VII	56.19±	71.75±	188.60±	17.72±	4.23±	2.93±	0.89±	39.87±	9.77±	6.19±	206.35±	104.44±	**17.51±**	82.62±	135.75±	6.11±	12.81±	18.70±	17.60±	226.95±
	10.73	11.55	25.06	2.82	0.89	1.75	0.10	11.71	1.93	1.08	79.23	23.40	**1.64**	14.83	7.69	2.10	5.52	4.18	3.10	100.67
VIII	48.60±	82.65±	148.20±	20.49±	5.49±	2.62±	1.29±	70.62±	11.95±	7.92±	382.48±	176.99±	16.02±	100.40±	138.30±	15.39±	35.89±	16.33±	14.63±	524.57±
	9.98	13.95	13.66	2.07	0.99	0.71	0.17	22.53	1.19	0.83	52.92	39.50	1.97	14.92	5.10	3.99	4.83	1.99	2.16	107.08
IX	49.35±	66.05±	172.23±	19.52±	4.07±	2.60±	1.05±	50.93±	11.03±	7.25±	237.17±	115.36±	11.84±	78.05±	120.91±	8.45±	23.07±	12.31±	11.51±	269.60±
	4.53	7.29	27.65	3.34	0.73	0.83	0.13	18.27	1.55	0.89	72.00	27.67	2.46	7.73	6.01	3.38	9.12	2.25	1.92	122.77
X	**70.50±**	90.00±	179.82±	22.83±	6.16±	**11.67±**	1.69±	173.98±	9.57±	5.94±	**859.33±**	**580.07±**	13.62±	104.00±	138.50±	5.86±	9.19±	15.08±	14.16±	141.52±
	9.19	9.19	21.59	0.74	0.37	**1.53**	0.28	38.29	1.53	1.83	**119.08**	**64.26**	0.28	19.80	7.78	5.52	4.36	3.32	4.99	107.08
XI	52.38±	66.62±	154.04±	21.30±	5.39±	2.91±	1.14±	71.42±	10.58±	6.72±	331.33±	150.23±	15.46±	78.62±	135.85±	**21.32±**	**44.70±**	14.87±	14.06±	**616.21±**
	6.18	4.33	24.38	3.17	1.30	1.06	0.11	18.04	1.00	0.82	54.19	25.44	3.19	6.25	6.95	**5.59**	**5.38**	2.92	2.82	**84.97**
XII	51.07±	73.36±	195.50±	25.00±	5.20±	4.02±	1.34±	78.56±	11.90±	7.26±	519.43±	246.61±	14.77±	80.71±	134.00±	12.84±	31.44±	16.79±	15.24±	484.92±
	7.11	11.39	13.77	2.67	1.04	1.33	0.23	8.97	1.71	0.86	97.66	53.58	3.26	12.34	7.66	3.66	5.50	2.76	1.93	82.65

Results and Discussion

On averaging data of both years, wide range of variation was observed for the various characters recorded. Twelve genotypes were erect type, 53 were semi erect, six were bushy, 27 were viny and 74 genotypes were spreading. The earliest flowering accessions were EC240564 and EC244979 (38 days) and most late flowering genotype was IL-181 in 88 days. Tallest genotypes were, HY-10P-10-2-4 (234.9 cm) followed by IL-99-171 (231.7 cm) and Local-1 (231.2 cm). Shortest were, IL-168 (105.9 cm) followed by NP-3-10 (113.0 cm) and HY 10P- 52-7 (115.3 cm). Accessions having more number of leaves per plant were IL-1177 (201); IL-1057 (185); and IL-1050-3 (158). Higher dry weight per plant was obtained for IL-1177 (625.51 g); IL-3171 (543.63 g); and IL-449 (345.94 g). Genotypes that showed higher dry leaf/stem ratio were [IL-160-A (1.02); IL-99-98-1 (0.97); and (IL-792 (0.94). Genotypes that had higher 100 seed weight were IL-181 (25.2 g); IL-4216 (22.6 g); and IL-156 (22.5 g). Genotypes that showed early maturity initiation in days after sowing were NP-3-10 (60 days); EC240782 (61 days); and EC240887 (62). Genotypes that took lesser number of days for total maturity of pod were EC244979 and IL 99-72 (113 days); EC240884 and IL 99-65 (115 days). The higher biomass was obtained for IL-1177 (943.5 g); IL-3171 (775.1 g); and IL-966-B (663.7 g). Higher leaf/stem ratios were for HY6P52-3 (1.04); IL-893 (1.01); and IL-99-171 (0.95). Genotypes that showed higher number of pods per plant were IL-3168A (53.2); IL-156 (51.3); and IL-2000-180 (50.5). Genotypes that had higher pod length were Local 1 (24.6 cm); IL-2000-182 (24.4 cm); and NP 3-7 (21.8 cm). Genotypes that showed higher number of seeds per pod were Local-2 (22.2); Local-1 (21.1); and IL-1057 (20.8).

The frequency distribution pattern of some morphological traits for the years 2004 and 2005 pooled data, varied from almost symmetrical to asymmetrical types and was in general of unimodal type.

Clustering pattern of pooled data over the years 2004 and 2005, showed 12 clusters for 20 variables as shown in Tables 1 and 2. Cluster V was the biggest with 26 lines and cluster IV was the smallest with only 1 member. The earliest flowering lines were grouped in cluster III. Cluster IV had one genotype with maximum values for plant height, number of nodes, number of primary branches, leaves/plant, leaf length, dry weight/plant, pod length and number of seeds/pod. Cluster X had higher fodder yielding lines with maximum value for number of secondary branches, leaf weight/plant, stem weight/plant and days to 50% flowering. Cluster VI had genotypes with maximum days to total flower and days to total maturity. Cluster XI had genotypes with highest number of pod clusters /plant, number of pods/plant, number of seeds/plant. Genotypes of Cluster VII showed maximum value for dry stem weight/plant. Genotypes of Cluster I showed maximum value for leaf width.

The maximum distance between cluster centroids was between cluster VII and X, *i.e.,* 11.781 followed by between clusters IX and X i.e. 11.589 and 11.054 between cluster X and XI (Table 2). Maximum average distance of cluster members from cluster centroids was 3.711 of cluster II.

Similarily, Henry and Mathur (2003) studied varietal divergence in cowpea where twenty three varieties of cowpea of different centers were evaluated under rain-fed conditions during monsoon season of 1997 and 1998. In their study, Wards method of hierarchical cluster analysis was applied to group the varieties. The quantum of rainfall received during the cropping season of 1997 and 1998 varied considerably. Twenty three cowpea varieties were classified into 4 clusters in 1997 and into 3 clusters in

Table 2. Distance between centroids of twelve clusters of the pooled data of years 2004-05 and 2005-06

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	0.000											
II	3.390	0.000										
III	2.638	3.602	0.000									
IV	8.384	7.501	7.423	0.000								
V	3.097	4.225	3.203	9.342	0.000							
VI	4.577	3.310	4.462	7.742	3.829	0.000						
VII	4.723	6.105	4.104	9.324	3.933	5.386	0.000					
VIII	4.296	5.004	3.434	6.605	4.921	4.716	5.411	0.000				
IX	3.216	5.132	3.753	9.565	2.949	5.525	4.496	4.968	0.000			
X	10.311	7.642	9.741	9.042	10.460	7.991	11.781	10.009	11.589	0.000		
XI	5.074	5.955	4.128	7.740	5.029	6.002	5.681	2.826	4.746	11.054	0.000	
XII	4.650	4.500	3.690	5.865	5.383	5.144	5.827	3.332	5.269	8.514	3.854	0.000

Table 3. Cowpea genotypes identified as potential parents for hybridization

Traits	Donors	Source
High biomass/plant	IL-1177; IL-3171 and IL-966-B	IGFRI Jhansi
High fresh leaf/stem ratio	HY6P52-3; IL-893 and IL-99-171	IGFRI Jhansi
Dry matter yield/plant	IL-1177; IL-3171 and IL-449	IGFRI Jhansi
Early flowering	EC240564 and EC244979 (38 DAS)	NBPGR New Delhi
High seed test weight	IL-181; IL-4216 and IL-156	IGFRI Jhansi
High number of pods /plant	IL-90; IL 3117 and EC240809	IGFRI Jhansi and NBPGR New Delhi
Long pod	Local 1; IL-2000-182 and NP 3-7	ICAR Research complex Barapani and IGFRI Jhansi
High number of seeds/pod	Local 2; Local-1 and IL-1057	ICAR Research complex Barapani and IGFRI Jhansi
High pod clusters/plant	IL-178-4, IL-622, IL-362	IGFRI Jhansi

1998. The maximum inter cluster distance was between cluster I and IV in 1997 and cluster I and III in 1998. The varieties falling in cluster I in both the environments were early in maturity and some were high yielding in stress environment of 1998. The high yielding varieties with earliness in maturity could be crossed with bold seeded varieties with medium late maturity of cluster IV in 1997 and cluster III in 1998 to get high yielding, early maturing and bold seeded varieties suitable for arid region / rainfed areas.

On the basis of clustering in the present study identification of donor sources in respect of forage was done, *i.e.,* for higher biomass/plant, IL-1177 (943.5 g); IL-3171 (775.1 g); and IL-966-B (663.7 g), higher fresh leaf/stem ratios, HY6P52-3 (1.04); IL-893 (1.01); and IL-99-171 (0.95), dry matter yield/plant, IL-1177 (625.51 g); IL-3171 (543.63 g); and IL-449 (345.94 g), earliest flowering, EC240564 and EC244979(38 days) lines were identified (Table 3).

In respect of grain yield identified donor sources were (Table 3), heaviest seed bearing lines, IL-181 (25.2 g); IL-4216 (22.6 g); and IL-156 (22.5 g), The lines with higher number of pod clusters/plant, IL-178-4, IL-622, IL-362, with a mean value of 15 pod clusters/plant. The maximum pod bearing lines IL-90, EC240809, IL-3117) with a mean value of 45 pods per plant, longest pod bearing lines, Local 1 (24.6 cm); IL 2000-182 (24.4 cm); and NP 3-7 (21.8 cm), highest number of seeds per pod bearing lines, Local-2 (22); Local-1 and IL 1057 (21).

Similarily, Misra *et al.,* (2003) evaluated a set of 740 germplasm accessions of cowpea including both indigenous and exotic origin at IARI during *kharif* 2001. A wide range of variation was observed in almost all the characters under study. Many promising genotypes have been identified which can serve as potential donors for major economic traits.

Thus the characterization of germplasm in to various clusters in the present study resulted in the useful information. Cluster X can be identified as having competent traits that can be utilized for improving fodder yield and cluster number XI has lines with potential for seed yield. Thus cluster analysis helped in drawing representative sample from various segments of genetic stock for further utilization in never ending process of genetic manipulation as earlier reported by (Kohli *et al*., 2000). Earlier, Shwe *et al.,* (1972) and Kumari *et al.,* (2000) observed better recombinants by crossing parents from clusters of high and low means for the characters under consideration. Therefore, it can be suggested that to have a better heterotic effect the genotypes from diverse clusters (identified sources) could be used for hybridization which may result in desired recombinants.

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Exploration and Collection of Crop Germplasm from Eastern Parts of Arunachal Pradesh

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Survey and collection of multi-crop germplasm from Arunachal Pradesh was executed in three different trips, during November to December to collect the indigenous crop germplasm diversity and other economic plants. These exploration trips concerted in East, West and Upper Siang districts of eastern part of Arunachal Pradesh. These explorations were conducted in a way keeping in view of the period of maturity and harvest of collected germplasm. These trips were yielded a total of 553 different crop germplasm collected from 49 different sites with an altitudinal variation between 183 to 1100 m above msl. The crop group wise break-up of collections is cereal (188), pseudocereals (51), grain legumes (78), vegetables (86), oilseeds crop (21), spices (66), tuber crop (22), fruit crops (38) and other crops (03). Local indigenous technical knowledge practiced by the farmers on some crops was also recorded during exploration. Extents of diversity with in the collected accessions have been summarized in this paper.

Key Words: Northeastern India, Siang district, Variability, Indigenous technical knowledge

Introduction

Arunachal Pradesh is located in the contiguity of the eastern Himalayan region, sharing international boundaries with China (North), Myanmar (South) and Bhutan (West). The state is situated in between $26^0$28' and $29^0$30' North latitude and $91^0$30' and $97^0$30' East longitude with an area of 83,743 km^2. A number of exploration and collection trips for the collection of crop germplasms have been conducted in this state since the colonial period, which was referred as *Abor* land. It is reported that about 134 plant species are consumed by the people of the state (Maikhuri and Ramakrishnan, 1992). However, many plant species and crop germplasm are still need to be collected, identified and assayed scientifically for potential use in future. Harnessing unknown/ underutilized natural resources and to bring them in agriculture will obviously uplift economic status of the local people. The important tropical semi evergreen tree species of Arunachal Pradeesh are *Terminalia myricarpa, Bombax ceiba, Canarium strictum, Alianthus grandis, Ammora wallichi, Toona ciliata, Juglans regia* etc. The coniferous forest containing *Pinus wallichi*, *Cedrus deodara*, *Abies pindraw*, *Picea* spp., *Quercus* spp. are other important temperate species found in higher altitudes of these areas. The farmers generally practice mixed type of farming system. Majority of crops are grow in spring season, autumn cultivation is very rare. Rice, finger millet and job's tear are grown as mixed crop in uplands (Burkill, 1978). Besides these, maize, foxtail millet, rice bean, soybean, *Perilla,* cucurbits, *Colocasia, Dioscorea,* ginger, etc are other commonly grown crops.

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The literature and demographical information available about the area coupled with its remoteness and less explored conditions has lead to undertake the explorations with the following objectives, *i.e.* inventorization and collection of crop landraces, their diversities, both inter and intraspecific level from three explored area, especially in eastern parts of Arunachal Pradesh.

Materials and Methods

The collection mission was planned meticulously with an aim to collect as many as the crop diversities of cultivated plants as well as their wild relatives, so that it covers and represent the genotypes of the particular crop within the districts. Three explorations were executed in East, West and Upper Siang districts (Fig. 1). The West and Upper Siang districts share international boundary with China in North. Altitudinal variations (350 – 4,500 m msl) of the area determine the vegetation type of the localities. The study area is characterized by their mountainous, undulating topography. Soils are fairly deep to very deep and well drained, whereas in the valley land and plains of East and west Siang are alluvial deposit favouring luxurious growth of plants. Hence rich soils, moderate temperature and plenty of rainfall (2,000-2,500 mm) are conducive for good agricultural harvest. The three explorations were executed separately in the months of November to December coinciding the period of crop maturity and harvest so that fresh, viable seeds could be collected. Standard practice and procedure of collection of germplasm developed by NBPGR was followed (Pareek *et al.,* 2000). Mostly the local landraces and primitive

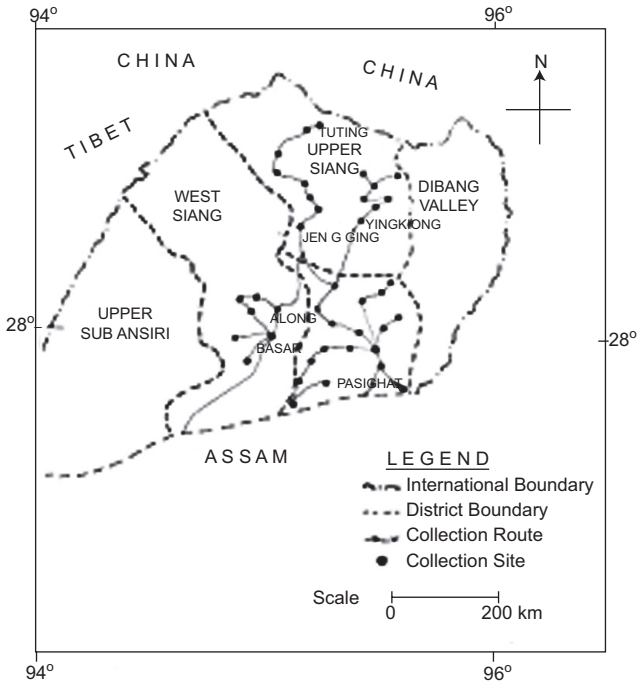

Fig. 1: Map showing explored areas in East, West and Upper Siang districts of Arunachal Pradesh

crop cultivars of germplasm were collected during this trip. Selective and bulk method was followed as per the population/quantity of germplasm material available. Sampling was made in fruit form in case of *Citrus* spp., which is recalcitrant in nature. Due attention was paid to collect the materials which are disease free, viable and confirm the standard for medium term storage, as voucher sample. Most of the materials were collected from wild habitat, farm store, and farmer's field. A few samples were collected from village markets, after ensuring the information from the place of cultivation from the retailers. Markets were surveyed, because they represent a large area where villagers from many nearby areas come to sale and purchase of their farm produce which gives broad idea of the type of crop variability represented in the area. The source of collected germplasm is mentioned in Table 1. Passport data on each accession was recorded at the time of collection, following the standard procedure.

Samples of collected plant species were identified with the help of relevant floras (Hooker, 1872-1897; Kanjilal *et al.,* 1934-1940; Burkill, 1978; Arora and Pandey, 1996; Hajra *et al.,* 1996; Chauhan *et al.,* 1996). The vegetatively propagated materials were retained at the NBPGR Regional Station, Umiam, Meghalaya for their multiplication, maintenance and subsequent characterization. The seed materials were sent to the National Gene Bank, NBPGR, New Delhi for medium term storage along with passport data.

Results and Discussion

Altogether 553 accessions of various crop genotypes were collected, covering 63 botanical species together with their variability. The break-up of collections is cereal (188), pseudocereals (51), grain legumes (78), vegetables (86), oil seed crop (21), spices (66), tuber crop (22), fruit crops (38), and other crops (03). The genotypes were collected either in seed form or as vegetative propagules as per the nature or method of reproduction of the respective crop. Primitive cultivars and landraces are dominant collection and this may be due to the isolation and remoteness of the area (Table 2, Figs. 2 and 3). The collection includes 84 rare genotypes indicating biodiversity richness of the area. The description and discussion of collected germplasm along with ITK is as under:

1. Cereal

A total of 188 collected accessions of cereals belong to 3 different genera (*Oryza, Zea* and *Sorghum*). Most of these collected samples were primitive cultivars occurring occasionally. Ten rare samples of rice landraces were collected from this belt. The diversity of rice and their presence of variations to a great number from the North eastern region of India can be traced way back to 1931 (Roschevioz, 1931) and Assam rice collection, where 6,730 rice races were collected from Northeast India, including Arunachal Pradesh. Sharma (2002) reported 105 rice landraces from this state and precisely 12 and 32 accessions from West and East Siang districts, respectively.

Table1. Sources of collected germplasm from Arunachal Pradesh

Source	Number of accessions	% Collected accessions
Farm store	437	79.1
Market (local weekly market)	16	2.9
Farmer's field	83	14.9
Homestead garden	2	0.4
Wild habitat	10	1.8
Institutional experimental field	5	0.9
Total	553	100.0

Table 2. Status and frequency of germplasm collected from Arunahal Pradesh

Crop group	Crop	Status of collections				Total	Frequency of collected accessions				Total
		Type of material	Primitive cultivar	Landraces	Genetic stock		Abundant	Occasional	Frequent	Rare	
Cereal	*Oryza sativa*	Seeds	135	7	0	142	5	70	57	10	142
	Zea mays	Seeds	38	4	0	42	0	18	17	7	42
	Sorghum sp.	Seeds	4	0	0	4	0	1	2	1	4
Pseudocereal	*Amaranthus* sp.	Seeds	2	0	0	2	0	1	0	1	2
	Elusine coracana	Seeds	26	6	0	32	0	13	18	1	32
	Setaria italica	Seeds	3	1	0	4	0	2	0	2	4
	Coix lacryma-jobi	Seeds	10	3	0	13	5	2	6	0	13
Grain legumes	*Phaseolus vulgaris*	Seeds	6	0	0	6	0	5	1	0	6
	Vigna unguiculata	Seeds	33	1	0	34	0	12	21	1	34
	Cajanus cajan	Seeds	1	0	0	1	0	1	0	0	1
	Vigna umbellata	Seeds	17	0	0	17	0	12	3	2	17
	Dolichos lablab	Seeds	5	0	0	5	0	4	1	0	5
	Glycine max	Seeds	9	2	0	11	0	4	2	5	11
	Vigna mungo	Seeds	4	0	0	4	0	2	0	2	4
Vegetables	*Benincasa hispida*	Fruits	6	0	0	6	1	3	1	1	6
	Momordica charantia	Seeds	2	0	0	2	0	0	0	2	2
	Lagenaria siceraria	Seeds	1	0	0	1	0	1	0	0	1
	Solanum melongena	Fruits	10	2	0	12	0	8	2	2	12
	Cucumis sativus	Seeds	17	0	0	17	0	9	4	4	17
	Lycopersicon pimpinelifolium	Seeds	2	0	0	2	0	1	0	1	2
	Raphanus sativus	Seeds	1	0	0	1	0	0	0	1	1
	Cucurbita moschata	Fruits	17	0	0	17	0	9	2	6	17
	Luffa acutangula	Seeds	2	0	0	2	0	1	0	1	2
	Trichosanthes anguina	Seeds	1	0	0	1	0	0	0	1	1
	Abelmoschus esculentus	Seeds	6	0	0	6	0	4	0	2	6
	Solanum gillo	Fruits	8	1	0	9	0	6	3	0	9
	Solanum indicum	Fruits	2	0	0	2	0	2	0	0	2
	Solanum spirale	Fruits	1	0	0	1	0	1	0	0	1
	Solanum spp.	Seeds	3	0	0	3	0	0	2	1	3
	Luffa cylindrica	Seeds	2	1	0	3	0	0	1	2	3
	Lycopersicon esculentum	Seeds	1	0	0	1	0	1	0	0	1
Oilseeds	*Brassica* sp.	Seeds	14	0	0	14	0	6	4	4	14
	Guizotia abysinica	Seeds	2	0	0	2	0	1	0	1	2
	Perilla frutescens	Seeds	2	0	0	2	0	0	1	1	2
	Sesamum indicum	Seeds	3	0	0	3	0	0	3	0	3
Spices	*Capsicum annum*	Fruits	37	4	0	41	4	13	21	3	41

	Allium schoenoprasum	Bulbs	1	0	0	1	0	1	0	0	1
	Coriandrum sativum	Seeds	4	0	0	4	0	4	0	0	4
	Curcuma caesia	Rhizomes	1	0	0	1	0	0	0	1	1
	Zingiber officinale	Rhizomes	14	0	0	14	0	5	9	0	14
	Illicium grifithii	Seeds	1	0	0	1	0	1	0	0	1
	Allium cepa	Bulbs	1	0	0	1	0	0	0	1	1
	Curcuma longa	Rhizomes	3	0	0	3	0	2	1	0	3
Tubers	*Colocasia esculenta*	Rhizomes	16	0	0	16	0	13	2	1	16
	Dioscorea sp.	Rhizomes	6	0	0	6	1	3	0	2	6
Fruits	*Musa* sp.	Suckers	2	0	0	2	1	1	0	0	2
	Citrus jambhiri	Fruits	7	0	1	8	1	6	0	1	8
	Citrus latipes	Fruits	1	0	0	1	1	0	0	0	1
	Citrus reticulata	Fruits	3	0	0	3	3	0	0	0	3
	Citrus spp.	Fruits	10	0	0	10	0	3	3	4	10
	Garcinia sp.	Fruits	0	0	1	1	0	0	0	1	1
	Artocarpus heterophyllus	Fruits	1	0	0	1	0	1	0	0	1
	Kinnow	Fruits	0	0	1	1	0	1	0	0	1
	Cucumis melo	Seeds	1	0	0	1	0	1	0	0	1
	Carica papaya	Fruits	4	0	0	4	0	4	0	0	4
	Citrus grandis	Fruits	2	0	0	2	0	2	0	0	2
	Poncirus trifoliata	Fruits	0	0	1	1	0	0	0	1	1
	Juglans regia	Seeds	1	0	0	1	0	0	0	1	1
	Citrullus lanatus	Seeds	1	1	0	2	0	0	1	1	2
Miscellaneous	*Canarium strictum*	Seeds	1	0	0	1	0	0	0	1	1
	Gossypium arboreum	Seeds	1	0	0	1	0	0	0	1	1

Wide variations were observed in characters like panicle type, presence or absence and size of awn, glume and kernel characteristics in the collected samples. Red and black kernelled rice was also observed. Tribal people usually prefer glutinous types of rice for food as well as to prepare the local beer (*Apong*). They have a preference of local rice landraces known as *Taker, Amsi, Amkel Ketsing* and *Umkel* for beer preparation. These variants were found to be growing in Karko (849 m), Nari (200 m), Linka (250 m) and Mariyang (1,100 m). Some farmers also grow lowland rice in terraces with 30-60 cm water depth under controlled water management. The farmers informed that there was very less incidence of crop failure due to pest or disease attack, which may be attributed to their mixed cropping system of cultivation. Similar observations were also reported in some of the earlier reports (Hore, 1999a).

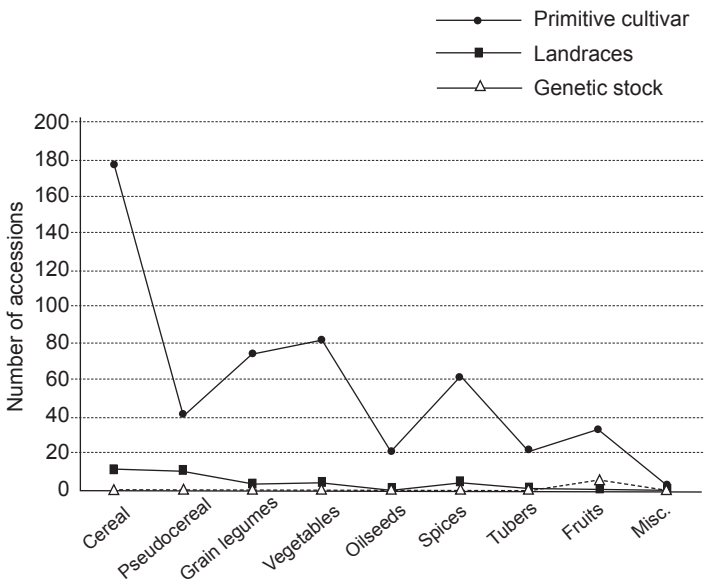

Fig. 2: Status of collected crop germplasm of Arunachal Pradesh

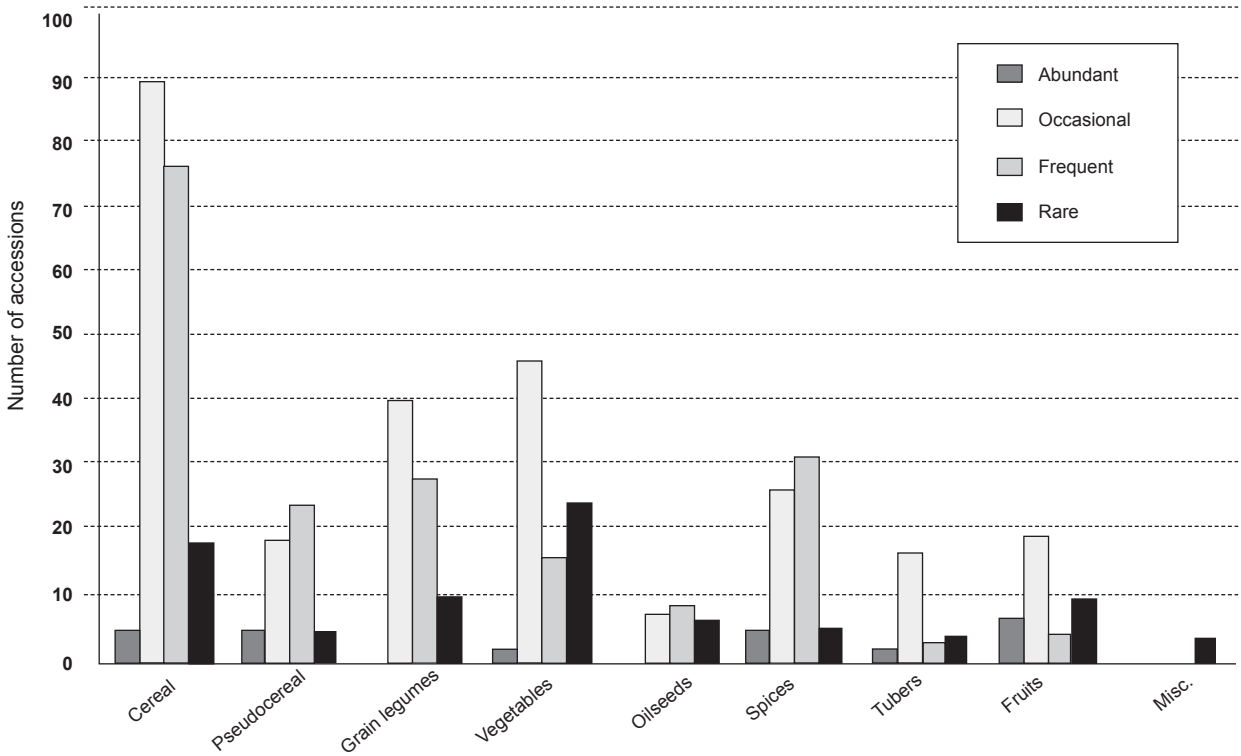

Fig. 3: Frequency of collected crop germplsm of Arunachal Pradesh

Ricebug (*Leptocorisa oratorius*) is one of the major pest of rice in these areas, which generally appears in the field during flowering. Farmers fix several wooden/bamboo sticks randomly at certain interval in the rice field (both in lowland and upland condition). Dead frog/crabs are placed on it for 5-6 days. The idea behind this is to attract the bugs to this rotten, foul smell emitting frog/crab deviating from crop. Meanwhile, the milk stage of rice grain is over and thus evades the pest attack. Farmers also apply other traditional method for control of pest and disease, such as application of ash from wood, rice husk, straw, cowdung slurry, cattle urine etc. Leaf and seed extracts of *Xanthoxylum* and *Nicotiana* are also used for the control of pest and disease attack.

Maize is another important crop for these areas, which is generally sown in April - May and the crop gets ready within 120-150 days. Variability was found with regard to cob especially in size, length, kernel size, row arrangement pattern, etc. Kernel colour was found to be varying to a great extent and it may be due to highly heterozygous nature of this crop and farmers are not aware to maintain the purity of the genotype by keeping isolation distance. This is in conformant of earlier report by Sharma (2002).

Villagers prefer to smoke the seeds by keeping them in the ceiling of kitchen for safe storing of seeds. Smoke makes the seeds dry and keeps free from insect and disease attack. But such system does not followed for bulk quantity of seeds. Singh and Bag (2002) reported such practices adopted specially by Adi tribe of the state.

2. Pseudocereal

Among the 51 collected pseudocereals samples, finger millet and job's tear had the largest share. The availability and occurance of these crops are frequent. Farmers use to grow primitive cultivars of these two crops. The main preference lies with these crops are for their brewing quality, which forms local beer (*Apong*). The finger millet accessions were found to vary in number of fingers, which ranges between 5 to10. The prominent types were *Tami* (10 fingers), *Taker* (8 fingers), *Kompo* (6 fingers) and *Marua* (5 fingers). Burkill (1978) also reported the preferences of local tribes for using finger millet and job's tear in local beer (*Apong*) preparation.

3. Grain legumes

A total of 75 diverse germplasm of seven grain legumes were collected. The local tribes grow various grain legumes like French bean, cowpea, rice bean, soybean etc. These are generally sown as mixed crop and left unattended,

until they are ready for harvest. Diversity was prominent particularly in soybean, cowpea, sembean, pigeon pea and rice bean. The variability in soybean was observed for growth habit, plant height, number of pods per plant, grain size and colour. Cowpea is generally grown for vegetable and their pod length varied from 8-25 cm. Soybean and rice bean is generally utilized as pulse crop. Variation in the number of seeds per pod and seed shape was found in the collected accessions.

4. Vegetables

A total of 86 accessions, covering 18 types of vegetables were collected. Among the solanaceous crops, a wild relative of tomato, *Lycopersicon pimpinelifolium* was collected. The fruits were rounded, barely 1 cm in diameter with innumerable tiny seeds. *Solanum spirale,* locally known as *Bangkho* in East Siang district, was also collected. The fruits are bitter in taste and used in folk medicines by the tribes. The variations were observed in *Solanum melongena*, involving the morphological characters like fruit size, shape and colour; plant characters such as thorny, thorn less, stem colour, carpel character and fruit taste. The people of these areas also grow *Solanum gillo* in their homestead area and use as medicine for various stomach ailments. Among cucurbits, the variability in terms of their fruit size, fruits skin colour and luster were found in bitter gourd (*Momordica charantia*). Oblong, round and oval shaped fruits of pumpkins (*Cucurbita moschata*) were collected with golden yellow to purple coloured skin. One accession of ash gourd (*Benincasa hispida*) locally known as *Joha lau*, was collected from West Siang district and it was found to possess distinctive pleasant aroma.

5. Oilseeds

At lower elevation (<300 m) oilseed Brassicae grows to a limited scale, though utilization of leafy brassicae is much more in practice. Sesame cultivation is not much popular in the area. However, indigenous *Perilla* was seen to cultivate as mixed crop with *Coix,* either in homestead area or in *jhoom* field. *Guizotia abysinica* was also grown in some pockets. A total 21 accessions of these four oilseeds were collected.

6. Spices

Variability in terms of fruit shape, size and level of pungency were observed in collected 41 accessions types of chilli. An accession of *Allium schoenoprasu* (chives) was collected from Karko village in Upper Siang district. The local tribe (*Adi*) of the area called it *Talap.* It has a characteristic bulb of 4-5 cloves remaining attached loosely from the base only. Besides these, the villagers also collect *Curcuma caesia* (black zedoary) and *Illicium griffithii* (a medicinal plant) from the forests, which they use as condiments and also for various medicinal purposes.

7. Tuber crops

The entire northeast belt of India is one of the centers of origin for *Colocasia* and *Dioscorea* (Plucknett, 1976). Six accessions of primitive type of *Dioscorea* were collected and variability was observed in rhizome shape and flesh colour (*viz.,* brown, white). Conical, round and oblong shaped tubers were seen in 16 *Colocasia* accessions.

8. Fruit crops

Chakravarty (1951) established that northeastern region may be the center of origin of cultivated banana and other taxonomic groups of the genus *Musa.* In all three districts, abundant populations of wild banana were observed, while most of them belong to *Musa balbisiaina* group. It is characterized by 6-8 m tall pseudostem with 1.5-2 m long drooping peduncles. During the exploration one accession each of *M. velutina* and *M. ornata* was collected. These accessions are having erect inflorescence with yellow and reddish coloured bracts, respectively.

Species of *Citrus, i.e., C. jambhiri, C. reticulata* and *C. grandis* were collected from farmers fields, while, *C. latipes,* Kinnow and *Poncirus trifoliata* were collected from Basar (West Siang). *C. reticulata* is characterized by upright trees, lanceolate leaves with narrowly winged petiole. Fruits globose, sweet and loose skinned. The trees of *C. grandis* are almost thornless with spreading habit. Lower surface of leaves are pubescent with characteristic broad wings in petiole. Fruits have thick spongy rind with bold seeds. Trees of *C. jambhiri* are medium spreading habit. It is widely used as rootstock and imparts resistance to tristeza and drought. *C. latipes* is also used as rootstock as it is resistant to greening disease and cold tolerant, but the fruits are not suitable for commercial use. *Poncirus trifoliata* is chiefly used for rootstock against frost resistance and tolerance to root knot nematode. Kinnow is a commercial hybrid and mainly introduced for large scale cultivation in these areas. The fruiting season of *C. jambhiri, C. reticulata, C. grandis* and *C. latipes* is in between September–December, April- May, October- February and December-January, respectively. Hore (1999b) reported the occurrence of wild population of *C. jambhiri* around Shimmong, Pugging, Ramshing and Gossang villages of Yingkiong area of Upper Siang

districts. Although, the plants of *C. jambhiri, Poncirus trifoliata* and *C. grandis* are being tried as rootstock for *C. reticulata* (Khasi mandarin), a local type found in this region, but the *Citrus* plantations of this area experiences substantial infestation of trunk borer, leaf miner, die back, lichens and mosses. These maladies finally made a major problem in these areas in *Citrus* production.

9. Other crops

The tribes grow opium in some pockets of these areas for consumption and other medicinal purposes. Tree cotton (*Gossypium arboreum*) is another crop, which is used by the villagers for household purposes. The seeds of *Canarium strictum* were collected and the dried gums/resin of these trees is used by the villagers as mosquito repellent. One accession each of these three species was collected during the exploration trip.

Conclusion

The explored areas of Arunachal Pradesh have vast potentiality of crop germplasm as these areas are in contiguity with Chinese center of origin. Looking to the cultivation practices of rice, maize and other crop the identification of cold tolerant and disease, pest resistant types cannot be denied. There is every possibility to occur more genotypes of *japonica* race of rice in this belt. The occurrence of banana and *Citrus* in various altitudes may also enrich our gene pool with biotic and abiotic stress resistant types. Local landraces of various crop germplasm of these areas are vanishing slowly as gradually these are being replaced by high yielding varieties. The changing socio-economic condition of the tribes, different development activities as well as climatic changes is leading to alterations in cropping pattern. The use of local landraces must be enhanced by educating the villagers at grassroot levels, about its benefits, which they have been practicing since ages without fail. There is a further scope to study the area more intensively in respect of the collection of plantation and forestry related plant species.

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Developing Core Set in Brinjal (*Solanum melongena* L.) with Limited Traits

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Large collections of genetic resources held in Gene Banks poses a challenge for the maintenance of both the accessions as well as the information documented for the germplasm characterized. The accessibility and knowledge of the landrace collections are the prerequisite for an efficient utilization of the genetic resources. Different sample sizes and sampling strategies, either random or non random, were proposed to obtain core sets in brinjal from entire collection of 622 landraces. The proposed strategy emphasizes on relatively smaller number (5) of highly variable descriptors for computing inertia score through Principal Component Score Strategy (PCSS) and thereby capturing maximum genetic diversity in the core set. This strategy is compared with three other strategies i.e. Random, Stratified and Principal Component Score Strategy based on the entire set (13) of quantitative descriptors. This strategy will help in developing core set with limited resources or when information on some descriptors is not available.

Key Words: Brinjal, Core set, Diversity, Principal component score strategy, Random sampling, Stratified random sampling

Introduction

Brinjal (*Solanum melongena* L.) is an important vegetable crop of Central, Southern and South-East Asia, and in number of African countries (Kalloo, 1988). It is a good source of minerals and vitamins and has several medicinal properties (Khan, 1979). India and Indo-China is considered to be the centre of diversity (Vavilov, 1951; Daunay *et al.,* 2001). The important brinjal growing countries are China, India, Egypt, Turkey, Japan, Italy, Sudan, Indonesia, Philippines and Spain. In India, it is grown in 0.5 million hectare area with a total production of over 8 million tons (FAOSTAT, 2007).

Ex-situ conservation of plant genetic resources can result in large collections that are difficult to characterize, evaluate, utilize and maintain. An important objective for curators is to find a way to preserve the widest range of genetic diversity within crop species as well as to improve the knowledge and utilization of the genetic resources. To overcome management difficulties, the identification and use of core collection has been suggested. The National Bureau of Plant Genetic Resources (NBPGR), New Delhi has the responsibility of collection, characterization and conservation of the brinjal diversity in the country and presently maintains over 2,500 accessions. Much of this diversity was augmented in the recent past during 1999-2005. The diversity was also enriched from exotic sources. Recently, Kumar *et al*. (2008) studied the morphological diversity of 622 accessions of brinjal germplasm comprising indigenous and exotic collections for 24 descriptors.

The essential features of a core collection are minimum redundancy and capturing maximum genetic diversity from entire collection of a crop species/ wild relatives. Some of the core collections in other crops have been developed under the Indian National Programme (Mahajan *et al.,* 1996; Bisht *et al.,* 1998) at NBPGR.

For the development of core set, several strategies have been proposed since Frankel first suggested the concept of a core collection in 1984 (Brown, 1989a). Brown (1989b) proposed the use of random sampling strategies among a stratified collection. He assumed that over 70% of the alleles would be retained in 10% of the total collection based on the theory of selectively neutral alleles. With the objective of retaining the maximum genetic diversity from the whole base collection in a manageable working collection, non random Principal Component Score Strategy (PCSS) has been suggested. This has been applied to identify a core set that will maximize the representation of the phenotypic variability of the base collection (Noirot *et al.,* 1996; Mahajan *et al.,* 1996; Sapra *et al.,* 2006). Sapra *et al.,* (2006) further discussed the issue of minimum sample size for capturing diversity. They suggested a clustering cum inertia score strategy which selects single entry from each group (cluster) having highest inertia score in the group and ensured higher diversity in terms of allelic evenness and richness in the sample. In the past the core sets were developed on the basis of inertia score computed from entire set of quantitative descriptors. The question here arises, can we take a subset of these descriptors for

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computing inertia score without compromising the genetic diversity in the core set. Such a situation may arise due to either non availability of the information for all the descriptors or to save the cost and time in recording the entire set of descriptors. It is quite logical that the highly variable descriptors play a significant role in computing inertia score in the PCSS in comparison to the low variable descriptors. Thus, the present study examines the merit of highly variable descriptors for computing inertia scores and compares the results with other strategies based on the entire set of descriptors.

Materials and Methods

The plant material consisted of 622 accessions of brinjal germplasm comprising 543 indigenous and 79 exotic accessions held at National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India. The region/ country wise grouping of the accessions is presented in Table 1. The accessions were grown in 6 m row plots, with 75 cm row to row and 60 cm plant to plant spacing. These accessions were evaluated for 24 morphological descriptors (13 quantitative and 11 qualitative) during kharif 2003 cropping season (July to December) and the quantitative traits were transformed into qualitative ones (Table 2).

Allelic Evenness was measured by Shannon-Weiner Diversity Index (H′) (Weaver and Shannon, 1949) while allelic richness was measured by counting the descriptor states without considering their individual frequencies for different descriptors.

$$H' = -\Sigma\, p_{ij} \log_e p_i$$

where p_i is the proportion of the accessions for the i^{th} descriptor state of the qualitative character. In order to keep the value of H′ in the range of 0-1 each value of H′ was divided by the maximum value, $\log_e n$ where n is the number of descriptor states. The pooled H′ was obtained by summing the individual H′ over the entire set of descriptors. The average diversity was computed as the total diversity divided by the number of qualitative descriptors. Three strategies namely, Simple Random Sampling without replacement (SRSWOR), Stratified Random Sampling (SRS) and Principal Component Score Strategy were used for selecting the accessions with varying sample sizes i.e. 5, 10, 20 and 30 per cent of the entire collection having 31, 62, 124 and 187 accessions respectively. Due to the complex nature of H′, the bootstrapping was performed to estimate the confidence intervals (CI). The technique resamples the original data large number of times before drawing sample. In our case, 500 samples were drawn to estimate the expected mean and variance of the pooled H′. The selection of accessions and the estimation of CI for the above mentioned three strategies are described below.

a) Simple Random Sampling without Replacement (SRSWOR)

A random sample of size n was drawn by SRSWOR from N accessions. Let p_{ij} (i=1,2,..,d; j=1,2,…,k) denote the sample proportion of accessions for j^{th} state of i^{th} descriptor. Then an estimate of pooled H' is

$$H' = \Sigma_i \Sigma_j\, p_{ij} \log p_{ij}$$

For computation of 95% CI of H′, 500 independent random samples of a given size were drawn from the population by SRSWOR and mean [E(H′)] and variance [V(H′)] of H′ were computed. The 95% CI was computed as $(x - 1.96s/\sqrt{m}) < H' < (x + 1.96s/\sqrt{m})$, where x = E (H′); s = V (H′) and m = 500.

Table 1. Region-wise number of accessions studied and their diversity indices

Group	Origin	No. of accessions	Average SDI (H′)
I	Zone I (North-western Himalaya)	17	0.56
II	Zone II (West Bengal and Assam)	141	0.59
III	Zone III (North-eastern region, Andaman & Nicobar islands)	28	0.51
IV	Zone IV (Indo-Gangetic plains)	49	0.58
V	Zone V (Eastern peninsular region)	160	0.58
VI	Zone VI (North-western plain and arid region)	33	0.61
VII	Zone VII (Central plateau region)	35	0.56
VIII	Zone VIII (Southern peninsular region)	80	0.66
IX	Bangladesh	22	0.55
X	Japan	7	0.45
XI	Sri Lanka	42	0.63
XII	Taiwan	8	0.44
	Total	622	

Table 2. List of descriptors studied and alongwith their diversity indices

Quantitative descriptors	Frequency class	SDI
1. Number of primary branches	1=<4; 2=4-8; 3=8-12; 4=12-16; 5=>16	0.55
2. Plant height	1=Small (<50 cm); 2=Medium (50-100 cm); 3=Tall (>100cm)	0.45
3. Plant spread	1=Very narrow (<30 cm); 2=Narrow (30-40 cm); 3=Intermediate (40-60 cm) 4=Broad (60-90 cm) 5=Very broad (>90 cm)	0.59
4. Petiole length	1=<4 cm; 2=4-8 cm; 3=8-12 cm; 4=12-16 cm; 5=16-20 cm; 6=>20 cm	0.41
5. Leaf blade length	1=<8 cm; 2=8-12 cm; 3=12-16 cm; 4=16-20 cm; 5=20-24 cm; 6=>24 cm	0.63
6. Leaf blade width	1=<10 cm; 2=10-15 cm; 3>15 cm	0.69
7. Days to 50% flowering	1=<40; 2=40-55; 3>55-70; 4=>70	0.48
8. Fruit peduncle length	1=<4 cm; 2=4-8 cm; 3>8 cm	
9. Fruit length	1=<8 cm; 2=8-13 cm; 3=13-18 cm; 4=18-23 cm; 5=23-28 cm; 6=28-33 cm; 7=>33 cm	0.61
10. Fruit width	1=<5 cm; 2=5-10 cm; 3>10 cm	0.61
11. Number of fruits/plant	1=<10; 2=10-20; 3=20-30; 4=30-40; 5=40-50; 6=50-60; 7=60-70;8=70-80; 9=80-90; 10=90-100; 11=100-110	0.48
12. Fruit weight	1=<100g; 2=100-200 g; 3=200-300 g; 4=300-400 g; 5=400-500 g; 6=500-600 g; 7=600-700 g; 8=>700 g	0.48
13. Days to first fruit set	1=<30; 2=30-45; 3>45-60; 4=60-75; 5=>75	0.43
Qualitative descriptors		
14. Plant growth habit	1=Upright; 2=Intermediate; 3=Prostrate	0.29
15. Petiole color	1=Green; 2=Greenish violet; 3=Violet; 4=Dark violet; 5=Dark brown	0.45
16. Leaf blade lobing	1=Very Weak; 2=Weak; 3=Intermediate; 4=Strong; 5=Very strong	0.72
17. Leaf blade color	1= Light green; 2= Green; 3= Dark green; 4= Greenish violet and 5= Violet	0.45
Calyx colour	1=Green; 2=Light Purple; 3=Dark purple	0.82
18. Calyx spininess	3= Smooth; 5= Medium thorny; 7= High thorny	0.54
19. Corolla color	1=White; 2=Greenish white; 3=Pale violet; 4=Light violet; 5=Bluish Violet	0.65
20. Fruit length/breadth ratio	1=Broader than long; 3=As long as broad; 5=Slightly longer than broad; 7=Twice as long as broad; 9=Several times as long as broad	0.73
21. Fruit shape	1=Long; 2=Round; 3=Oblong; 4=Oval	0.71
22. Fruit color	1=Milky white; 2=Green; 3=Deep yellow; 4=Purple; 5=Purple black; 6=Black; 7=Light purple	0.58
23. Fruit flesh density	1=Very loose (spongy); 2= Loose (crumbly); 3=Medium compact;4=Compact; 5=Very compact	0.57
24. Seediness	3= Low; 5= Medium; 7= High	0.88

b) Stratified Random Sampling (SRS)

A sample of size n was allocated to different groups in proportion to the diversity in the group. Let n_s be the sample size selected from s^{th} (s=1, 2,…, 12) group such that ($\sum n_s = n$). The samples from each group were selected by SRSWOR and an estimate of H´ was computed over the pooled set of accessions. CI was computed as mentioned in SRSWOR. Samples from different groups were retained for use in PCSS.

c) Principal Component Score Strategy (PCSS)

The entries from each group were selected by PCSS (Noirot *et al.,* 1996). The accessions were arranged in descending order in terms of inertia score and the top accessions having higher inertia scores were selected from each group. Two strategies of PCSS were designed, *i.e.* (i) entire set of 13 quantitative descriptors [PCSS(13)] and (ii) a sub set of 5 highly variable descriptors, namely, fruit weight, number of fruits/plant, fruit length, fruit width and peduncle length selected on the basis of high co-efficient of variation [PCSS(5)].

Results and Discussion

Among the total accessions, 88% were indigenous and 12% of exotic origin. The indigenous accessions were grouped into Zone I to Zone VIII whereas exotic accessions (Zone IX to XII) were from Bangladesh, Japan, Sri Lanka and Taiwan respectively. Zone V (160) followed by Zone II

(141) had maximum number of accessions while Japan (7) represented the least number of accessions. Among the indigenous accessions, the average maximum diversity was observed in Zone VIII (0.66) followed by Zone VI (0.61) while in the exotic group it was maximum in accessions from Sri Lanka (0.63) followed by Bangladesh (0.55). The diversity for quantitative descriptors ranged between 0.41 for petiole length to 0.69 for leaf blade width and between 0.29 for plant growth habit to 0.88 for seediness among qualitative descriptors (Table 2).

Allelic evenness and allelic richness are the most commonly used parameters for measuring diversity. It would be worthwhile considering both the parameters simultaneously while discussing the issue of diversity. Table 3 in general shows a less pooled diversity as well as richness for all the three strategies when a sample size of 5% is considered. However, when the sample size is increased from 5 to 10% there is considerable increase both in diversity as well as in richness. Further increase in sample size to 20% showed marginal increase in diversity and it was negligible beyond 20% sample size in all the strategies. The size of core collection has long been under discussion. Brown (1989b) proposed that a fraction of about 10% is an appropriate sample size for sampling core entries and suggested a log proportion strategy (L) or absolute proportion strategy (P) when the whole collection is composed of several groups. He further made calculations based on the Ewens (1972) theory under certain assumptions that at least 70% of the existing alleles could be drawn with 95% certainty if 10% or more of the plants are sampled from the population. Our findings support his view and 10% sample size was found to be efficient for all the sampling strategies employed. Hence, increasing the sample size beyond 10% may not be much advantageous in terms of enhancing both evenness and richness.

Figure 1 shows the relationship between the sample size and the pooled SDI corresponding to different strategies. All the four curves rise sharply when the sample size is increased from 5 to 10% and after that the curves rise slowly upto 20% of the sample size. However, when the sample size increases from 20 to 30% the curves become almost parallel to the horizontal axis indicating it would not be advantageous in terms of increasing diversity. Table 3 and Figure 1 indicate that the random strategy (SRSWOR) is the most efficient one as the average SDI is the lowest among all the strategies. The stratified sampling is slightly better than that of the random one. The PCSS strategy based on 13 and 5 descriptors resulted in higher SDIs as compared to SRSWOR and Stratified strategies. However, the proposed strategy, PCSS (5) based on limited number of traits resulted in higher SDI for all sample sizes when the accessions were selected from the top after arranging the accessions in terms of decreasing inertia score.

Figure 2 represents more or less similar behaviour as that of Figure1 except for stratified sampling strategy where it has been found to be less efficient compared to SRSWOR in terms of pooled richness. The proposed strategy, PCSS (5) could capture richness of 92.16 % even with a smaller sample size of 10%. This value is even higher than 91.18% obtained through PCSS (13) strategy for a sample size of 30%. The proposed strategy, PCSS(5) based on limited number of traits resulted in the highest pooled H´ and allelic richness for all sample sizes. This may be due to the selection of five most variable descriptors in PCSS (5).

In general in previous studies, the stratified sampling has been found to be effective and efficient as compared

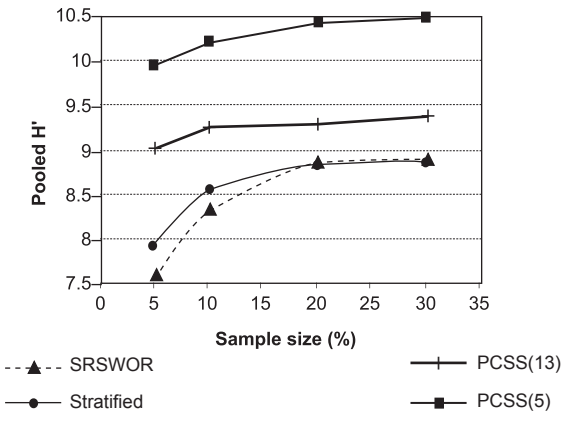

Fig. 1: Relationship between sample size and pooled H' for various strategies

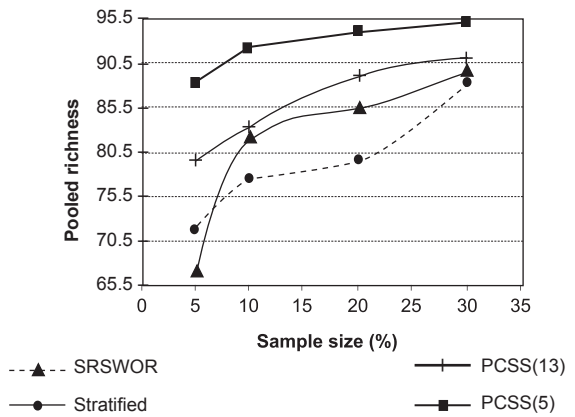

Fig. 2: Relationship between pooled richness and sample size for various strategies

Table 3. Comparison of Shannon-Weiner diversity index and pooled richness of selected accessions through various strategies

Sample size (%)	Number of accessions	SRSWOR (SDI)	Stratified (SDI)	PCSS (SDI)		SRSWOR (richness)	Stratified (richness)	PCSS (Richness)	
				13 Characters	5 Characters			13 Characters	5 Characters
5	31	7.606 [4.922-10.390]	7.920 [4.940-10.900]	9.031	9.932	66.67	71.57	79.41	88.23
10	62	8.334 [6.134-10.534]	8.563 [6.151-10.975]	9.240	10.211	82.27	77.24	83.33	92.16
20	124	8.862 [6.861-10.863]	8.845 [6.640-11.150]	9.271	10.430	85.58	79.50	89.22	94.12
30	187	8.870 [7.600-10.141]	8.846 [7.645-10.047]	9.379	10.481	89.72	88.24	91.18	95.10

Figures within parenthesis indicate the 95% confidence interval

to the random sampling in many of the cases and has been extensively used in developing the core sets. However, in our case also it has proved to be efficient for all sample sizes except for 5% and 10% where SRSWOR showed better results. The reason for this unusual behavior could be attributed to a chance factor. The relationship between sample size and the allelic richness showed similar pattern as in case of diversity except for stratified random sampling where it was found to be less efficient as compared to SRSWOR.

The results clearly indicate that the proposed strategy which uses limited number of traits has proven to be the most efficient in capturing both the pooled diversity as well as allelic richness for a given sample size. Thus, the strategy can be effectively utilized in developing core sets where the information is lacking, particularly for less heterogeneous traits and still ensuring diversity in the core set.

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Genetic Variation for Seed Proteins in Cultivated and Wild Species of Pigeonpea

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Electrophoretic analysis of seed protein of three cultivated varieties of *Cajanus cajan* and its three wild relatives were carried out to study variability in protein band expression. In all, 22 protein bands were identified ranging with molecular weight of 97.0 to 16.5 kD. Cultivated and wild species showed variability in protein band expression ranging from 6 in ICPL 84023 to 8 in UPAS 120 and Pant A 134 whereas in wild species 9 bands in *C.cajanifolius* and *C.acutifolius* and 8 bands in *C.scarabaeoides*. The differences were also observed for number, length and intensity of polypeptide bands of the protein. Band at 87.5 kD was common in all the cultivated and in wild species. In the cultivated lines, bands at 92.5 and 37.0 kD were common, whereas two bands at 87.5 and 74.0 kD were common among wild species.

Key Words : *Cajanus cajan*, Electrophoresis, Pigeonpea, Seed protein, Wild species of *Cajanus*

Introduction

Pigeonpea [*Cajanus cajan* (L) Millspaugh] is the second most important pulse crop of India. It is rich in protein which constitutes an important component of human diet in developing countries like India. Besides its main use as *dhal* (dehulled split seed), its immature green seeds and pods are consumed as vegetable. Pigeonpea seed is a rich source of protein, carbohydrates, vitamins and certain minerals (Srivastava and Srivastava, 2006). Varietal differences exist for the nutritional composition in pigeonpea seeds (Yadava, 1984). *C.cajanifolius* and *C.scarabaeoides* has high seed protein. Since genetic differences are reflected in shifts of seed protein patterns, the present study was undertaken on biochemical characterization of seed storage protein in order to assess variation for seed protein in cultivated lines *viz*., Pant A 134, UPAS 120 and ICPL 84023 and wild species *viz*., *C.cajanifolius*, *C.acutifolius* and *C.scarabaeoides.*

Materials and Methods

Three cultivated lines of pigeonpea *viz*., Pant A 134, UPAS 120 and ICPL 84023 along with three wild species *viz*., *C. cajanifolius, C. acutifolius* and *C.scarabaeoides* were raised at Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar during *kharif* 2003-04. Protein separation was carried out by SDS-PAGE according to the method of Laemmli (1970). The degree of electrophoretic similarity was calculated by pair wise comparison of the cultivated with wild species, cultivated lines with cultivated lines and wild species with wild species. Similarity index (SI) was also worked out following Mishra *et al*. (1996) *i.e.*

$$\text{Similarity Index (\%)} = \frac{\text{Number of similar bands in a sample}}{\text{Total number of bands for the two sample}} \times 100$$

Results and Discussion

The relative mobility (Rm) values for various seed protein bands of cultivated and wild species of pigeonpea used in the present study ranged from 0.03 to 0.74 suggesting a wide range of variability in protein band expression (Table 1). Among *Cajanus cajan* genotypes, Pant A 134 and UPAS 120 depicted highest number of bands (8) followed by 6 in ICPL 84023. Nine protein bands were observed in *C. cajanifolius* and *C. acutifolius* followed by 8 in *C. scarabaeoides*. One polypeptide band at 87.5 kD was noted in all the three cultivated lines *viz.*, Pant A 134, UPAS 120 and ICPL 84023 and two wild species *viz.*, *C. scarabaeoides* and *C. acutifolius,* which might be due to genetic relationship among them. The similarity in two polypeptide bands at 92.5 and 37.0 kD was noted in all the cultivated lines *viz*., Pant A 134, UPAS 120 and ICPL 84023, whereas one band at 74.0 kD was present in all the three wild species *viz*., *C. cajanifolius, C. acutifolius* and *C. scarabaeoides.* There was homogeneity of bands at 92.5, 87.5, 80.0, 71.5, 60.0, 49.5, 45.0, 35.0, 24.0 and 16.0 kD between cultivated lines and some wild species used in the present study.

All types of protein band intensity i.e. low, medium and high were observed in various cultivated and wild species of pigeonpea. However, in some varieties the quantitatively similar numbers of total protein bands were noted, but differences in presence and / or absence of particular band at particular position and their Rm

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values as well as different protein band intensity for common bands showed diverse nature of these varieties to each other. Though there were total 9 protein bands in electrophoregram of species *C. cajanifolius* and *C. aculifolius*, but band position was different. The bands at 97.0, 80.0, 45.0 and 24.0 kD were characteristically present in *C.cajanifolius* while missing in *C. acutifolius*. Similarly, bands at 71.5, 42.5, 39.0, 26.0 and 21.5 kD were present in *C. acutifolius* and missing in *C. cajanifolius*. Eletrophoregrams of ICPL 84023 and *C. scarabaeoides* indicating quantitatively different protein bands 9, 6 and 8 respectively, and showing some similarities and some diverse banding pattern revealed clear-cut resemblances and differences among them. Similar to the present study Sharma and Maloo (2006) also reported quantitatively similar numbers of total protein bands but differences in presence and/or absence of particular bands at their particular position in soybean.

Highest similarity index (58.82%) for *C. cajanifolius* was seen with Pant A 134 followed by UPAS 120 with Pant A 134 (50.00%) and *C. scarabaeoides* with *C. cajanifolius* (47.05%) and *C. cajanifolius* with UPAS 120 (47.05%). High order of similarity within cultivated lines was observed in UPAS 120 with Pant A134 (50.00%) followed by ICPL 84023 with UPAS 120 (42.85%) and Pant A 134 with UPAS 120. All the three wild species also shared good similarity index ranging from 23.52 – 47.05% within the species. All types of protein band intensity were observed (Fig.1). Maximum 9 bands were noted in *C. cajanifolius* and *C. acutifolius* followed by 8 in Pant A 134, UPAS 120, and *C. scarabaeoides* and lowest 6 in ICPL 84023.

The cultivated lines and wild species of pigeonpea had protein bands of both high as well as low molecular weight ranging from 97.0 to 16.5 kD. Similarly, Naik and Kole (1992) observed bands ranging from 17.4 to 75.0 kD in mungbean. Singh *et al*. (1992) and Roy *et al.* (2001) also noted differences in band mobility, width and intensity in legumes. Proteins being the direct gene products reflect the genomic composition of lines accurately to some extent and, therefore, are ideal for genomic distinctiveness.

In all, 22 protein bands observed in all the cultivated as well as in wild species seem to be very informative and useful in deriving qualitative and quantitative differences in various protein fractions. It was noted that a protein band of 87.5 kD was present in all the three cultivated lines as well as in wild species indicating that the genes controlling expression of these proteins bands appeared to behave as a single block. The observed differences in protein band intensity in cultivated and wild species could be utilized in identification of high protein lines and these lines could be directly used or may be used as protein rich parents in hybridization programme to transfer high seed protein quality trait in to desirable lines. Such types of

Table 1. Relative mobility values for various protein bands electrophoressed in seed protein extract of cultivated and wild species of pigeonpea

Protein Band #	Rm value	Mol.wt. kD	Cultivated / Wild species					
			Pant A 134	UPAS 120	ICPL 84023	*C. cajanifolius*	*C. acutifolius*	*C. scarabaeoides*
1	0.03	97.0	—	—	—	+	—	+
2	0.05	92.5	+	+	+	+	—	—
3	0.08	87.5	+	+	—	+	+	+
4	0.09	85.0	—	+	—	—	—	—
5	0.11	80.0	+	—	+	+	—	—
6	0.14	74.0	—	—	—	+	+	+
7	0.15	71.5	+	+	—	—	+	—
8	0.20	60.0	—	+	+	+	+	—
9	0.26	49.5	+	—	—	—	—	+
10	0.29	45.0	—	+	—	+	—	—
11	0.31	42.5	—	—	—	—	+	—
12	0.34	39.0	—	—	—	—	+	—
13	0.36	37.0	+	+	+	—	—	—
14	0.38	35.0	+	—	—	+	+	—
15	0.45	31.0	—	+	—	—	—	—
16	0.47	30.0	—	—	+	—	—	—
17	0.55	26.0	—	—	—	—	+	—
18	0.59	24.0	+	—	—	+	—	+
19	0.64	21.5	—	—	—	—	+	—
20	0.66	20.5	—	—	—	—	—	+
21	0.67	20.0	—	—	—	—	—	+
22	0.74	16.5	—	—	+	—	—	+

Note : Protein band Absent, + : Protein band Present, Rm : Relative mobility

Table 2. Quantitative and qualitative differences among cultivated lines and wild species of pigeonpea

Genotype	Qualitative differences Total no. of bands	Quantitative differences Specific band number	Thick	Medium	Thin	Faint (%)	Similarity Index(%)
Pant A134	8	71.5,49.5,37.0	2	1	—	5	—
C. cajanifolius	9	97.0,60.0,45.0	1	—	—	8	58.82
Pant A134	8	92.5,80.0,49.5,37.0,24.0	2	1	—	5	—
C. acutifolius	9	74.0,60.0,42.5,39.0,26.0,21.5	1	—	1	7	35.29
Pant A134	8	92.5,80.0,71.5,37.0,35.0	2	1	—	5	—
C. scarabaeoides	8	97.0,74.0,20.5,20.0,16.5	—	—	2	6	37.50
UPAS 120	8	85.0,71.5,37.0,31.0	1	1	—	6	—
C. cajanifolius	9	97.0,80.0,74.0,35.0,24.0	1	—	—	8	47.05
UPAS 120	8	92.5,85.0,45.0,37.0,31.0	1	1	—	6	—
C. acutifolius	9	74.0,42.5,39.0,35.0,26.0,21.5	1	—	1	7	35.29
UPAS 120	8	92.5,85.0,71.5,60.0,45.0,37.0,31.0	1	1	—	6	—
C. scarabaeoides	8	97.0,74.0,49.5,24.0,20.5,20.0,16.5	—	—	2	6	12.50
ICPL 84023	6	37.0,30.0,16.5	3	—	—	3	—
C. cajanifolius	9	97.0,80.0,74.0,35.0,24.0	1	—	—	8	40.00
ICPL 84023	6	92.5,80.0,37.0,30.0,16.5	3	—	—	3	—
C. acutifolius	9	87.5,74.0,71.5,42.5,39.0,35.0,26.0,21.5	1	—	1	7	13.33
ICPL 84023	6	92.5,80.0,60.0,37.0,30.0	3	—	—	3	—
C. scarabaeoides	8	97.0,87.5,74.0,49.5,24.0,20.5,20.0	—	—	2	6	14.28
Pant A134	8	80.0,49.5,35.0,24.0	2	1	—	5	—
UPAS 120	8	85.0,60.0,45.0,31.0	1	1	—	6	50.00
Pant A134	8	87.5,71.5,49.5,35.0,24.0	2	1	—	5	—
ICPL 84023	6	87.5,85.0,71.5,45.0,31.0	3	—	—	3	42.85
UPAS 120	8	80.0,30.0,16.5	1	1	—	6	—
ICPL 84023	6	37.0,30.0,16.5	3	—	—	3	42.85
C. cajanifolius	9	97.0,87.5,74.0,45.0,35.0,24.0	1	—	—	8	—
C. acutifolius	9	71.5,60.0,42.5,39.0,350.,26.0,21.5	1	—	1	7	44.44
C. scarabaeoides	9	97.0,49.5,24.0,20.5,20.0,16.5	1	—	—	8	—
C. cajanifolius	8	92.5,80.0,60.0,45.0,35.0	—	—	5	6	47.05
C. scarabaeoides	8	49.5,20.5,20.0,16.5	—	—	2	6	—
C. acutifolius	9	71.5,60.0,42.5,39.0,35.0,26.0,21.5	1	—	1	7	23.52

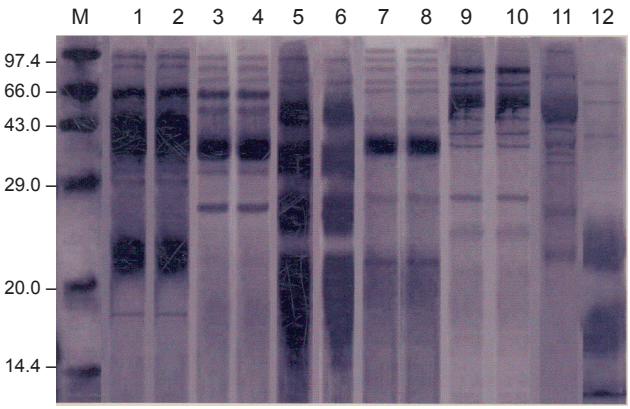

Fig. 1: Electrophoretic banding pattern of cultivated and wild species of pigeonpea
Lane No. 1 & 2 (Pant A 134), 3 & 4 (UPAS 120), 5 & 6 (ICPL 84023) 7 & 8 (*C. cajanifolius*), 9 & 10 (*C. acutifolius*) , 11 *C. scarabaeoides*

close relationships and / or minor variations were observed in chickpea also (Kharkwal, 1999). The present study is preliminary to assess the variation in seed protein banding patterns in order to identify the potential genotype(s) in pigeonpea and further study of seed protein fractions would be required for identifying the true high protein rich lines.

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Farmer's Criteria for Naming Crop Varieties: A Case on Rice Varieties in Kumaon Himalaya of Uttarakhand

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Kumaon Himalaya of Utatrakhand is a well known repository of local rice cultivars. A large number of local cultivars are managed and named by local farming communities. To maintain this large genetic stock, farmers have named them on the basis of certain characteristics features. In order to investigate the naming criterions, the investigators have surveyed 5 districts, 33 development blocks, 132 villages and 405 households of the Kumaon region during last ten years. A total of 84 different farmer named cultivars were documented for the study. The present paper reveals the different nomenclature criteria followed by farmers for maintaining the rice genetic wealth on farm. The naming parameters involve morphological traits, environmental adaptability, agronomic traits, local recipes, place of origin and local legendlores.

Key Words: Farmer named rice cultivars, Traditional rice cultivars, Rice cultivars of Kumaon Himalaya, Traditional rice nomenclature system

Introduction

Rice is the major food crop of entire Kumaon region during kharif. It is grown here since time immemorial in the region. Despite the spread of several high yielding varieties; several local cultivars are still grown in the region because of their well adaptability in various agro-climatic conditions (Bisht *et al.,* 2006). Local rice cultivars are mainly confined to rainfed as well as semi-irrigated areas in the region. Farming communities in the interior localities are completely dependent on local farmer named cultivars, which are also suitable for their environmental, socio-economic and ethnic requirements (Mehta *etl. al.,* 2008).

It is very difficult for farmers to maintain a large number of crop varieties without any name. Farmers even put the improved and high yielding varieties (HYVs) under some local naming words, which is convenient to them to call. Farmers maintain a large number of crops and their varieties without any mixture. Farmers varieties include crop population, which farmers have identified and named as units (Lando and Mark 1994). To maintain the separate identity of individual primitive cultivars of a crop, they need it's name for convenient identification. In order to maintain the separate identity of various crop primitive cultivars, farmers named them on the basis of some criterions and parameters. To study the nomenclature pattern of local cultivars of the crops, rice (*Oryza sativa* L.) was selected as it is a major crop grown worldwide. It is well known that rice emerged as staple food in South-East Asia that proliferated and subsequently dominated the world food bowl along with other food crops (Paroda 2004).

The old traditional rice landraces are also well known in the Gazetteer of Himalayan provinces (Atkinson 1882). In view of a large number of local farmer named rice varieties which are still under cultivation in Kumaon Himalaya, the present investigation of nomenclature of traditional varieties and their relationships with the certain characteristics of cultivars, environmental factors, habitats and other ethnic needs are studied thoroughly. The characteristic features, agronomic traits and cuisines are the major criterions of naming of crop varieties (Bhatt and Chauhan 1999) were also observed in the past.

Materials and Methods

For collection of data on traditional farmer named rice varieties grown in Kumaon Himalaya, a structured and un-structured questionnaire and interview schedule was developed. Data were collected from primary sources at individual farm household level during 1999 to 2008 cropping seasons. Sample households were randomly selected from all 33 development blocks of five districts of Kumaon region of Uttarakhand. Four villages were selected from each development block representing the distinct agro ecological niches. In each selected village 5%, households were randomly selected for interview. Lottery system was adopted for randomization at all levels. Thus a total of 405 respondent households were interviewed for documenting farmer named traditional rice

varieties. The district wise detail of development blocks, number of villages surveyed and respondent households are presented here (Table 1). Non-participant observation method was also used to collect information.

Using participatory rural appraisal, information was obtained on local rice varieties / cultivars grown in the villages and their nomenclature pattern. Respondent households were also asked to express the meaning of the local name of the varieties what they have revealed. All possible care was taken to determine the consistency in farmers naming and describing rice cultivars by comparing information from farm households and different social groups. After carefully recording the information the data were compiled and analyzed on the basis of various nomenclature parameters.

Results and Discussion

In the present investigation, a total of 120 traditional cultivars were recorded, 36 of them were repetitions of each other. Thus a net 84 different local varieties were found under cultivation. These 84 local farmer named varieties were subjected to analysis of the nomenclature pattern. Data of the study disclosed that farmers tested and evaluated the varieties for a long. After a careful evaluation of various characteristics of the varieties they were named after a certain distinct and prominent character or place of origin or local legendlores etc. There were nine parameters of nomenclature identified during the study. The nomenclature parameters identified were seed colour (25.30%) followed by seed shape and size (21.68%), plant habitats (18.07%), place/area of origin (9.64%), panicle characters (8.43%), suitability for particular cuisine (4.82%), local legendlores (4.82%), plant height (3.62%) and emergence of panicle and maturity period (3.62%) as mentioned in Table 2. There was no consistency in cultivars names and often it was difficult to ascertain that all farmer named varieties are genetically distinct (Bisht *et al.,* 2007). All care was however, taken to record only distinct cultivars based on farmers description of their varieties using distinct nomenclature criteria as listed (Table 2). It is interesting to note that farmers criteria of naming of varieties is based on some scientific features such as morphological characters (seed colour, plant height, vegetative traits), environmental adaptation (soil type, micro-econiches, tolerance of biotic/abiotic stresses, cropping system), agronomic traits (panicle emergence and maturity time, earliness, growth habit, grain yield), place of origin (region, village, farmer) and type of recipes (taste, ethnomedicinal values etc.).

It is very common to call the varieties on the basis of their seed colours. In case of rice, there are a large number of local varieties which are known after their seed colour such as *Laldhan* (red), *Kaladhan* (black), *Pyolia* (yellow), *Dhaulia* (White), *Anjan* (black), *Kalthunia* (black tipped)

Table 1. Number of districts, development blocks, villages and households surveyed for collection of information on traditional rice varieties

District	Development blocks	No. of villages selected for the study	Number of households surveyed
Almora	11	44	128
Bageshwar	03	12	36
Champawat	04	16	51
Nainital	07	28	89
Pithoragarh	08	32	101
Total	**33**	**132**	**405**

Table 2. Farmers parameters of nomenclature of local rice cultivars

S. No.	Parameters of nomenclature	Characteristic features	Percentage of varieties responsible for naming
1	Morphological traits	Seed colour	25.30
		Seed shape and size	21.68
		Panicle character	8.43
		Plant height	3.62
2	Environmental adaptation	Plant habitats	18.07
3	Place of origin	Village and area	9.64
4	Type of recipes/uses	Cuisines	4.82
5	Local legendlores	King, queen, goddesses and other personaties	4.82
6	Agronomical traits	Maturity period	3.62

etc. The maximum number of local varieties are named after their seed colour. It is not certain that all these varieties of a single name are genetically same. It may be genetically different from one another, but it is a popular naming criterion in the region. Farmers also maintain the population of each variety with its colour (Table 3a).

Seed shape and size is also an important seed character, which is considered for selection of a variety. On the basis of seed shape rice varieties were named like *Patoli* (thin), *Sweedi* (Needle pointed), *Binduli* (Round), *Jeeruli* (Cumin shaped), *Nan basmati* (small scented rice) etc. The names of traditional rice varieties mentioned in Table 3b are different varieties. They differ in seed shape and sizes. The name of a particular variety reveals itself the character of the seed. Seed shape and size is a very important parameter of nomenclature of the varieties in Kumaon Himalaya. Several varieties are named after seed shape, size and other characteristics like scent, shattering habit, threshing, dehusking qualities etc.

In Kumaon Himalaya, there are various types of topographic climatic conditions and micro-econiches. Farmers of the region have identified the rice varieties in order to suit their conditions, 18.07% traditional varieties are named after the various agro-econiches ranging from rainfed (dry/wet) to irrigated areas, from low land to hilltops and various other climatic and environmental conditions of the hills (Table 3c).

For naming of the local varieties, the place/areas of origin of seed material also play an important role. There were 9.64% rice varieties, which are named after the place or area of origin. *Kapkoti, Katyuri, Dotiyali, Askotiya* and *Ramgarhi* are the farmer named varieties, which are popular in another region of the Kumaon hills, hence named after the place or area of their origin. *Kashimiri, Punjabi* and *Jorhati* are the varieties carried by some army service personnel in the region and became very promising for yield point of view. Similarly, an important and promising landrace *Thapachini* is considered brought by *Thapa* people, who intruded into the region from China. Chinese people locally called as *Chini* in the Kumaon. Hence the rice brought by them is called *Thapachini* in Kumaon hills (Table 3d). The exchange of seed material within a region and inter regional system helps farmers to introduce the seed material. After getting a seed popularized in the area, it was named after the area or place of its origin. It is also observed in the study area that sometimes a married daughter carries the seed material from parental house to her in-laws house and visa-versa.

Similarly some service personnel like military men and others collected the seed material from very far-flung regions like Punjab, Kashmir and Jorhat. After observing their performance. After successful cultivation and acclimatization of these varieties in the area where they were introduced, they are named after their place of origin (Mehta *et al.,* 2008). Several studies have also documented the flow of local seed material of different landraces among small farmer (Sperling and Loevinshon, 1993).

Farmers also name varieties on the basis of panicle characters and 8.43% local varieties are named accordingly. Drooping, erect, long panicle fingers, long and thick panicles, long awns and hard threshability are the major features of panicles, which are used by the local farmers to name the varieties. *Jhakai, Jhumariya, Badtiya, Sirmodiya, Lamadiya, Jhusia* and *Lathait* are the varieties, which were named after their panicle characters (Table 3e).

Distinct using qualities of a particular variety are known for that cuisine. *Jaulia* is best known for its *Jaula* (a local cuisine) quality. *Jaula* is a popular local recipe of Uttarakhand hills. A large population prepare and consume it. A local rice variety, which is coarse grained is very useful for making *Jaula* and its taste qualities. Similarly a local rice, which is suitable for its *khaja* and popping quality is named as *Khajia* or *Khasiyari* by the local communities *Naula* (plant biomass) is required to feed the domestic animals. Since animal husbandry is also an integral part of farming system in Kumaon hills, farmers have identified good biomass yielding rice cultivars they named them as *Naula*. These cultivars are well known in the region for their distinct quality traits (Table 3f). These cultivars are very popular among local folks. Apart from the cuisine qualities, rice varieties were also named after their plant height. There are some popular varieties like – *Nandhani* (dwarf rice), *Chhotia* (small plant/dwarf) and *Thang* (Tall and strong stem) are named on the basis of their plant height (Table 3g) an important morphological trait.

Duration of emergence of panicles and maturity is very important features used for nomenclature of cultivars by the farming communities. In Kumaon hills 3.62% local varieties are identified their names with their duration of panicle emergence and maturity. *Timasia* means matures in three months. *Taoli* and *Utaoli* also express the meaning early in maturity (Table 3h). Farming communities have also given the due respect to their

Table 3. Criterions followed by local farmers for naming their rice cultivars

S. No.	Vernacular/local name of the varieties	Common meaning of the naming words (Characteristics description)
a)	**Nomenclature on the basis of seed colours**	
1	Lalsal	Red shawl (Red seeded)
2	Kalthudia	Black tips (Black tipped seeds)
3	Ratdhan	Red paddy (Red seeded)
4	Dudh	Milky white (White seeded)
5	Sunkhar	Pure gold (Golden seeded)
6	Pyolia	Yellow (Yellow seeded)
7	Matiya	Like soil (Brown seeded)
8	Ram manua	Blackish finger millet (Round fine blackish seeded)
9	Lali	Reddish (Reddish seeded)
10	Pingau	Yellow (Yellowish seeded)
11	Khardudh	Pure milk (White seeded)
12	Mail	Dirty (Brownish fine seeded)
13	Suntola	Gold weighing (Golden fine seeded)
14	Kaidhan	Blackish paddy (Black seeded)
15	Kalisal	Black shawl (Black seeded)
16	Bhuria	Brownish (Brown seeded)
17	Kalparia	Black husk (Black seeded)
18	Dhaulia	White (White seeded)
19	Musia	Colour like rat (Brown seeded)
20	Kalasyot	Black pine (Blackish in colour seeds like pine seeds)
21	Anjan	Black (Blackish seed corners)
b)	**Nomenclature on the basis of seed characters**	
22	Patoli	Thin (Fine seeded)
23	Sweedi	Like needle (Sharp pointed tips and hard awns)
24	Binduli	A round mark made on the forehead (Round seeded)
25	Jeeruli	Like cumin (*Jeera*) (Seeds like cumin-*Jeera*)
26	Akadi	Tight (Hard dehusking like leather)
27	Nanbasmati	Small scented (Small scented seeds)
28	Thulbasmati	Bold scented (Bold scented seeds)
29	Goldhan	Round paddy (Round seeded)
30	Chamari	Hard (Hard dehusking)
31	Chinburi	Small brown (Small brown seeded)
32	Jhadua	Shattering (Shatters on maturity)
33	Bhadgar	Stout (Stout seeded)
34	Jawan	Caraway-*Ajwain* (Seeds fine and caraway shaped)
35	Masur	Lentil (Seed round like lentil)
36	Dhania	Coriander (Stout seeds like coriander)
37	Ghesu	Rubbing (Needs more rubbing for dehusking)
38	Bakul	Broad bean (Seed thick like broad beans)
39	Basmati	Scented (Local scented rice)
c)	**Nomenclature on the basis of plant habitats**	
40	Dhurbasmati	Forest edges/hillocks, scented (Scented rice grown in forest and hillocks areas)
41	Boran	Rainfed (Suitable for rainfed conditions)
42	Gadayai	Near rivulets (Grown in marshy land)
43	Gajai	Marshy land (Grown in marshy land)
44	Gajla	Marshy land (Grown in marshy land)
45	Jangloi	Near forest (Suitable for forest areas)
46	Dangajai	Hill top marshy land (Grown in hill top marshy land)
47	Jamoli	To transplant (Transplanting rice)
48	Banpas	Near forest (Grown near forest land)
49	Jamal	To transplant (Transplanting rice)
50	Jungle dhan	Forest rice (Suitable for nearby or close to forest areas)
51	Danisanw	Hill top stout rice (A coarse rice grains suitable for hill tops)
52	Rokhyal	Dry land (Suitable for dry areas)
53	Kirmiti	Tight soil (Suitable for hard or clay soil)
54	Thai	Hill top plain (Suitable for hill top plains)
d)	**Nomenclature on the basis of place or area of origin**	
55	Thapachini	Thapa community people of Chinese origin (The Chinese people living in the Kumaon hills with their surname Thapa. It is considered that they brought this variety with them from adjoining areas of China and Tibet.)

S. No.	Vernacular/local name of the varieties	Common meaning of the naming words (Characteristics description)
56	Kapkoti	Belongs to Kapkote area of Bageshwar district (Brought from Kapkote area)
57	Katyuri	Belongs to Katy ur area of Bageshwar district (Brought from Katyur)
58	Dotiyali	Nepalese are known as Dotyal (Nepalese brought it in Kumaon from district Doti in Nepal)
59	Askotiya	Belongs to Askote area of Pithoragarh district (Brought from Askote area)
60	Kashmiri	Belongs to Kashmir in J&K (Brought from Kashmir by some one military person)
61	Ramgarh	Belongs to Ramgarh area of Nainital district (Brought from Ramgarh)
62	Jorhat	A place in Assam (Brought from Jorhat by any service person)
63	Punjabi	Punjab origin (Brought from Punjab)
e) Nomenclature on the basis of panicle characters		
64	Jhakai	Long hairs (Long awned rice panicles)
65	Jhumariya	Drooping (Drooping panicles)
66	Badtiya	Erect (Erect panicles)
67	Sirmodiya	Drooping panicles (Drooping panicles)
68	Lumadiya	Drooping thick panicle (Drooping thick panicles)
69	Jhusia	Awned (Long awned rice panicles)
70	Lathait	Needs more beating (Hard threshability)
f) Nomenclature on the basis of local use/recipes		
71	Jaulia	A local recipe (a local recipe) prepared from rice, curd, black soybean)
72	Khajia	Uncooked rice eating (Suitable for eating uncooked) and popping
73	Khasiyara	Uncooked rice eating (Suitable for eating uncooked)
74	Naulia	Straw for animals (More straw yielding rice, tall)
g) Nomenclature on the basis of plant height		
75	Nan dhani	Dwarf rice (Dwarf plants)
76	Chhotia	Dwarf rice (Dwarf plants)
77	Thang	Tall and strong (Tall and strong stem)
h) Nomenclature on the basis of crop maturity		
78	Timasia	Three monthly (Matures in three months)
79	Taoli	Early (Early maturing)
80	Utaoli	Early (Early maturing)
i) Nomenclature on the basis of local legendlores		
81	Rajdhan	King's rice (Preferred by the Kumaoni kings (Raja) because of fine grain rice)
82	Rajmati	Queen's rice (Preferred by the Kumaoni queens (Rani) because of its fine grain)
83	Parvati	Lord Shiva's wife (Sacred, named after Parvati)
84	Rajula	The queen of *Bairath* in Kumaon and heroin in the drama '*Kumaon ke Samrat'* –Hindi (Sacred, named after Rajula–a fine rice)

local legends such as Kumaon's king, queen, Parvati (Lord Shiva's wife) and *Rajula* (the queen of *Bairath* in Kumaon region). Four fine grain rice varieties were named after them (Table 3i).

Naming of varieties is very important in view of their separate identity. The origin of naming words is based on seed colour, seed size, place of sowing, recipes, persons and distinct properties of rice in Kumaon Himalaya were observed earlier also (Bhatt and Chauhan 1990). After its satisfactory yield, they name the varieties for their future use. For naming, farmers carefully study the characteristic features of the variety and distinct features are taken into consideration. The distinct characteristic feature may be its morphological character, environmental adaptability, agronomic trait, place or area of origin, cuisine quality etc. Naming of a local and promising cultivar is also very important in view of its identity, exchange, potential utilization, conservation and sustainable agricultural development. Plant breeders may select the different cultivars of their choice on the basis of this compendium. The present study may be very useful for those who are involved in varital development and breeding programmes.

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Combining Ability Studies in Cucumber (*Cucumis sativus* L.) under Salinity Condition

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A field study with diallel analysis (excluding reciprocals) in cucumber using cross combinations of salinity-tolerant and -sensitive inbreds indicated that the mean square due to gca and sca were significant in desirable direction for all the characters. The higher sca values than gca and, PR and ADD values <0.5 and >1, respectively indicates the predominance of non-additive gene effects in the expression of characters and accordingly hybrids development was rewarded. The potential cucumber hybrid CRC-8 x Pusa Uday and CHC-2 x Pusa Uday were found superior for earliness, yield and its attributing traits based on high sca effects and could be exploited in saline areas of our country.

Key Words: *Cucumis sativus*, **Salinity, Combining ability, Gca, Sca**

Introduction

Cucumber is one of the most important cucurbits grown throughout the country for its tender fruits. Low fruiting ability and yield suppression are due to its inherent habits. Development of high yielding varieties mainly depends upon the extent of genetic variability and superiority of parents, coupled with suitable breeding methodology. Combining ability analysis is one of the powerful breeding tools available which give the estimates of general combining ability (gca) for selecting desirable parents and specific combining ability (sca) for hybrids selection which are necessary for devising an effective and efficient breeding methods. Therefore, selection of suitable parents with high gca is most crucial and critical aspect of any breeding programme for hybrids development (Sprague and Tatum, 1942).

In India, 8.5 m ha areas are affected by salinity and around 27 per cent of cultivable land in the state of Punjab, Haryana, Uttar Pradesh, Gujarat, Rajasthan, West Bengal, Maharashtra, Orissa, Andhra Pradesh, Karnataka and Tamil Nadu comes under salinity. India possesses vast genetic variability for vegetative and fruit characters of cucumber due to being its native place. Unfortunately, cucumber can not tolerates salinity. Therefore, cucumber production under saline soil requires salinity tolerant varieties. In this regard, present study was undertaken to select better combiner parents among saline-tolerant and -sensitive inbreds of cucumber and consequently hybrid development from them to exploit the hybrids in salt affected areas of our country.

Materials and Methods

The present study was carried out at research farm of Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi during 2006-07. Six cucumber inbreds namely P_1 (CRC-8), P_2 (CHC-2), P_3 (G-338), P_4 (CH-20), P_5 (Pusa Uday) and P_6 (DC-1) were used for experimentation after 5 generation of selfing. Among these inbreds, three parents namely P_1, P_2 and P_3 had salinity tolerance upto 4dSm^{-1} whereas P_4, P_5 and P_6 were sensitive to salinity (Kumar, 2007).

The salinity-tolerant and -sensitive inbred lines were crossed in 6 x 6 half-diallel fashion [n(n-1)/2] (Hayman, 1954) to obtain 15 F_1 hybrids. All the hybrids and parents (inbreds) were grown in Randomized Block Design with three replications. The crops were sown at the spacing of 1.5 m between rows and at 50 cm between plants. All the recommended package of practices was followed to grow a successful crop. Out of 10 plants per hybrid in each replication, 8 plants were marked for observations and 2 border plants were rejected to minimize the error. Observations on individual plant basis were recorded for seven quantitative characters *viz.* days to first female flower anthesis, days to first fruit harvest, fruit weight (g), number of fruits per plant, fruit length (cm), fruit diameter (cm) and fruits yield per plant (g). The combining ability analysis was estimated according to Method-2, Model 1 of Griffing (1956) in which parents (inbreds) and hybrids are included without reciprocals using SPAR1 programme developed by IASRI, New Delhi. For Standard error of an estimate was calculated by square root of variance of that

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estimate. Critical difference was calculated as a product of standard error and 't' value for error degree of freedom at 5% and 1% level of significance. Genetic component of variance i.e. $\sigma^2g = [(Mg-Ms)/n+2]$, $\sigma^2s = Ms-Me$ and $\sigma^2e = Me$ were estimated where, σ^2g and σ^2s are variance due to gca and sca, respectively; Mg, Ms and Me are mean sum of square due to gca, sca and error; and n is number of parents used i.e. six. The relative importance of gca and sca effects was determined by the Predictability Ratio (PR) $[2\sigma^2g/(2\sigma^2g+\sigma^2s)]$ and the Average Degree of Dominance (ADD) $[\sigma^2s/2\sigma^2g]$, where σ^2g and σ^2s also denote the additive and non-additive components of variance, respectively (Baker,1978). If the PR value is <0.5 and ADD value is >1, it indicates the predominance of non-additive components of variance. While if the PR value is >0.5 and ADD value is <1, it indicate the predominance of additive components of variance.

Results and Discussion

The mean square due to gca and sca were highly significant for all the characters indicated importance of both additive and non-additive gene effects in the expression of the characters (Table 1). Estimates of gca effects of the parents (inbreds) and sca effects of the hybrids are presented in Table 2 and Table 3, respectively. Table 2 reveals that sca components of variance were higher than gca components of variance for days to first female flower anthesis, days to first fruit harvest, number of fruits per plant and fruit production per plant, in addition the PR and ADD values were also estimated <0.5 and >1, respectively. The above traits indicating the preponderance of non-additive variance of gene action. Hence, heterosis breeding is rewarded for the improvement of days to first female flower opening, days to first fruit harvest, number of fruits per plant and fruit production per plant in cucumber. While gca components of variance were higher than sca components of variance for fruit weight, fruit length and fruit diameter, besides the PR and ADD values were also estimated >0.5 and <1, respectively for these traits which indicates the predominance of additive variance of gene action. These differences may be due to the difference in the genetic materials studied. Therefore, simple selection procedure is rewarded for the improvement of fruit weight, fruit length and fruit diameter in cucumber.

The significant gca value in desirable direction was estimated in the cucumber parents (inbreds) and showed them as the better combiner parents namely P_1 for days to first female flower anthesis (-1.98) and days to first fruit harvest (-1.97), P_5 for number of fruits per plant (0.46), fruit diameter (0.31), and fruit production per plant (382.41) and P_6 for fruit weight (13.82) and fruit length (1.20) for breeding cucumber in Table 2. Since

Table 1. Analysis of variance for combining ability for seven characters in 6 × 6 half-diallele cross of cucumber

Source	d. f.	Days to 1st female flower anthesis	Days to first fruit harvest	Fruit weight (g)	Number of fruits per plant	Fruit length (cm)	Fruit diameter (cm)	Fruit production per plant (g)
Gca	5	3.11 **	5.01 **	528.39 **	1.27**	7.39**	1.31**	97723.29 **
Sca	15	12.05 **	10.16 **	92.74 **	1.68**	0.91**	0.21**	255584.35 **
Error	40	0.15	0.17	18.05	0.06	0.24	0.03	2739.17
σ^2g		1.12	0.64	54.46	0.05	0.83	0.14	19732.63
σ^2s		11.90	9.99	74.69	1.62	0.67	0.18	252845.18
PR		0.23	0.15	0.59	0.06	0.71	0.60	0.14
Add		5.31	7.80	0.68	16.2	0.41	0.64	6.40

$\sigma^2g = [(Mg-Ms)/n+2]$, $\sigma^2s = Ms-Me$ and $\sigma^2e = Me$; Predictability ratio (PR) $= 2\sigma^2g/2\sigma^2g + \sigma^2s$; Average degree of dominance (ADD) $= \sigma^2s/2\sigma^2g$; *Significant at 5% level, **Significant at 1% level

Table 2. Estimates of general combining ability (GCA) of the parents for different characters in 6 × 6 half-diallele cross of cucumber

Inbred lines	Days to 1st female flower anthesis	Days to 1st fruit harvest	Fruit weight (g)	Number of fruits	Fruit length (cm) per plant	Fruit diameter (cm)	Fruit production per plant (g)
P1	-1.98**	-1.97**	-5.77**	0.14**	0.25	0.05	-98.25**
P2	-0.52**	-0.48**	-7.54**	-0.33**	-0.33**	-0.06	-54.42**
P3	0.71**	0.72**	-9.42**	-0.80**	-0.84**	-0.12*	-171.66**
P4	1.16**	1.25**	-2.89*	-0.43**	-0.74**	-0.10	-74.60**
P5	0.27*	0.38**	11.81**	0.46*	0.46*	0.31**	328.41**
P6	0.41**	0.10	13.82**	0.31**	1.20**	0.17	267.52**
S.E. (gi)	0.13	0.14	1.37	0.08	0.16	0.06	8.78

the parents (inbreds) P_1, P_2 and P_3 had salinity tolerance and high yield components attributes as well, they could be used to breed high yielding cucumber hybrids for salt affected areas of our country.

Table 3 shows the estimates of sca effects of 15 F_1 cucumber hybrids obtained through cross combination of better combiner salinity tolerant parent *viz.*, P_1, P_2 and P_3 and salinity sensitive parent *viz.*, P_5, P_6 and P_4 for earliness, yields and its components. Table 3 demonstrates that the significant sca value was estimated in the 10 hybrids for days to first female flower anthesis, among which the hybrid P_1 x P_5 (-3.07) showed maximum negative sca effect followed by P_1 x P_6 (-2.97). Among the 9 highly significant hybrids for days to first fruit harvest, the hybrid P_2 x P_5 (-2.82) was estimated maximum negative sca effects value followed by P_2 x P_6 (-2.64). Thus, the cucumber inbreds-hybrids P_1 x P_5 and P_2 x P_5 were found to be superior for earliness characters. Highly positive significant sca effects were exhibited by 8 hybrids for fruit weight among which the hybrid P_1 x P_6 showed maximum (25.80) sca effects followed by P_2 x P_5 (22.95). For number of fruits per plant, among 6 positively significant hybrids, maximum highly significant sca effects was observed in cross P_2 x P_5 (1.68) followed by P_1 x P_5 (1.64). Analysis of sca effects for fruit length revealed that 9 hybrids showed highly significant values, in which maximum positively highly significant sca effects recorded in P_2 x P_5 (2.91), followed by P_1 x P_5 (2.67). Fruit diameter was observed significant in 7 hybrids, among which P_2 x P_6 (0.68) revealed maximum sca effect for followed by P_1 x P_6 (0.63).

A perusal of Table 2 reveals that fruit production per plant was found positively significant sca effects in 7 hybrids, among which maximum sca effects was observed in P_1 x P_5 (420.38) followed by P_3 x P_5 (399.86) and P_1 x P_6 (380.94), and minimum positive sca effect was noted in P_2 x P_4 (302.80). These results were very much similar to the finding of Shushir *et al.* (2005) and Sreevani (2005) who observed the high gca effects for parents and high sca effects in hybrids coupled with non-additive component of variance in cucumber. Yudhvir and Sharma (2006) and Munshi *et al.* (2006) also opined the pre-dominance of non-additive genetic variance and low narrow sense heritability in cucumber for the days to first fruit harvest, number of fruits per plant and yield per plant and suggested the heterosis breeding for the improvement of these traits.

The saline-tolerant and -sensitive inbreds with its high gca values and higher genetic base -due to diverse source from different parts of the states in India- produced hybrids with higher sca effects for faster and higher magnitude of success. The advance inbred lines -produced through 5 generations of selfing to attain a level of homozygosity- were used for hybrids production. The gca effect of parent is primarily a function of additive and additive × additive gene effect and it determines the breeding value of the parent. Besides, gca effects are more stable due to polygenic fixable components of genetic variation and therefore, it is of more use for breeders (Griffing 1956). Though, cucumber is cross-pollinated crop in which hybrid development is possible through crossing of inbred lines.

Table 3. Estimates of specific combining ability (SCA) for different characters in 6 × 6 half-diallele cross of cucumber

Hybrids	Days to 1st female flower anthesis	Days to 1st fruit harvest	Fruit weight (g)	Number of fruits per plant	Fruit length (cm)	Fruit diameter (cm)	Fruit production per plant (g)
P_1 x P_2	0.88	0.16	1.97	0.09	-0.68	0.33*	-137.05
P_1 x P_3	0.67	-0.09**	4.13	0.03	0.10	0.42*	-146.75
P_1 x P_4	-2.05**	-1.87**	9.51*	-0.33	-0.24	0.23	12.79
P_1 × P_5	-3.07**	-2.60**	22.70**	1.64**	2.67**	0.49**	420.38**
P_1 x P_6	-2.97**	-2.25**	25.80**	1.12**	1.09*	0.63*	380.94**
P_2 x P_3	-0.11	0.34	1.15	-0.25	1.15*	-0.04	331.66**
P_2 x P_4	-1.21**	-0.93*	9.32*	0.02	-0.54	-0.08	302.80**
P_2 x P_5	-2.61**	-2.82**	22.95**	1.68**	2.91**	0.51**	363.06**
P_2 x P_6	-2.50**	-2.64**	22.41**	1.42**	2.37**	0.68**	345.62**
P_3 x P_4	-0.44	0.46	4.37	0.41	1.19*	0.40*	-69.61
P_3 x P_5	-2.33**	-2.49**	16.56**	1.08**	1.15*	0.29	399.86**
P_3 x P_6	-0.09	-0.41	1.79	-0.63	-0.05	0.06	14.11
P_4 x P_5	-0.68*	1.31	-4.33	-0.71	1.18*	-0.06	-87.23
P_4 x P_6	-0.95*	1.63	0.59	0.03	0.31	0.25	-73.14
P_5 x P_6	-1.17*	-0.12**	14.72**	1.18**	1.02*	0.13	29.21
S.E. (sij)	0.34	0.37	3.77	0.22	0.45	0.16	24.10

Thus, results demonstrate that the significance of gca and sca effects of parents (inbreds) and hybrids, respectively in favorable direction for earliness, yield and its components in cucumber. Accordingly inbred-hybrids P_1 x P_5 for days to first male flower anthesis and fruit production per plant, P_2 x P_5 for days to first fruit harvest, number of fruits per plant and fruit length and fruit diameter and P_5 x P_6 for fruit weight were found to be suitable for further exploitation in salinity affected areas of our country.

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Interception of Scale Insects and Mite Pests in Imported Vegetative Germplasm during 2007-08

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Quarantine examination of 3,028 exotic vegetative samples of various crops during 2007 and 2008 revealed infestation of insect and mites in 193 samples. These included five species viz., *Aceria tulipae* in *Allium sativum* from Kazakhstan and USA, *Amphitetranychus viennensis* in *Pyrus communis* from USA, *Polyphagotarsonemus latus* in *Persea americana* from Vietnam and *Oligonychus peruvianus* in *P. americana* from USA and also four species of scale insects, *Aonidiella orientalis* in *Vitis vinifera* from Brazil, *Aspidiotus nerii* in cuttings of *P. communis* from USA, *Chrysomphalus dictyospermi* and *Hemiberlesia lataniae* in *P. americana* from USA and *Parasaissetia nigra* in *P. americana* from Vietnam. All the infested samples were salvaged using suitable pesticidal dip treatment.

Key Words: Quarantine, Germplasm, Vegetative propagules, Detection, Salvage

Introduction

The import of small samples of plant/ planting material meant for research in various crop improvement programmes is a potential and inadvertent source of introducing exotic pests into new areas which may cause severe threat to crop production and economy of a nation. There are several glaring examples of pests introduced along with imports, which have resulted in enormous crop losses over the past several decades such as fluted scale *(Icerya purchasi*), a serious pest of citrus and native of Australia was introduced into India before 1928 from Sri Lanka probably on *Acacia* sp. which later became a serious pest on citrus in south India. Another example is that of San José scale (*Quadraspidiotus perniciosus*), a pest of apple introduced into India in 1930s which causes enormous losses in apple orchards in Himachal Pradesh (Khetarpal and Gupta, 2008).

Several insects and mites of economic significance have been intercepted at National Bureau of Plant Genetic Resources (NBPGR) from time to time, many of which have yet not been reported from India. NBPGR is the nodal agency to undertake the quarantine processing of germplasm including transgenic planting material introduced into the country for research purposes. Few of the exotic pests intercepted over the years include *Acanthoscelides obtectus* intercepted in *Cajanus cajan* introduced from Brazil and Colombia; *Anthonomus grandis* in *Gossypium* spp. from USA; *Ephestia elutella* in Macadonia (nuts) and *Vigna* sp. from USA; *Pachymerus lacerdae* in nuts of *Orbynya phalerata* from Brazil; *Quadrastichodella eucalyptii* in *Eucalyptus* spp. from Australia (Khetarpal *et al.*, 2006; Gupta *et al.*, 2005).

Materials and Methods

During the years 2007 and 2008, a total of 3,028 samples of exotic vegetative planting material of various crops were processed for quarantine. These samples included rooted plants, cuttings, rhizomes, suckers, bulbs, nuts and tissue culture tubes of different crops. The various vegetative material imported include bulbs of *Allium sativum*, cuttings of *Carya illinoensis*, *Fragaria ananossa, Malus* spp., *Olea europaea, Persia americana, Prunus armeniaca, Theobroma cacao* and *Vitis vinifera* rooted plants of *Phoenix dactylifera* and sets of *Saccharum officinarum.* All the planting material were inspected by naked eye or with the help of magnifiers for the detection of external symptoms of damage i.e. holes, rotting, swelling, deformity, etc. or presence of dead or alive insects/ mites, eggs/ egg shells, immature stages, exuviae or excreta thereof.

The insects were retrieved from the material in water or 70% alcohol. The mites and scales thus retrieved were stained, slide mounted and identified on the basis of identification keys (Keifer 1938, Pritchard and Baker, 1955, Williams and Watson, 1990) and reference collection at NBPGR.

All the infested samples were salvaged using pesticidal dip/ spray treatment. Curative dip/ spray treatment with an acaricide, Kelthane @ 0.035% and insecticide, Malathion @ 0.05% or a combination of both was given to 193 samples

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of infested material comprising *Allium sativum*, *Persia americana, Pyrus communis, Saccharum officinarum,* and *Vitis vinifera* and 2,835 samples were given prophylactic treatment with Malathion and Kelthane as above.

Results and Discussion

The quarantine processing of 3,028 samples of imported germplasm revealed infestation in 193 samples and the pests intercepted during quarantine processing are presented in Table 1.

Aceria tulipae intercepted in *Allium sativum* is a mite belonging to family Eriophytidae; a pest restricted to genus associated with bulbs of liliaceous plants and is reported from several countries in Europe, South Asia including India, northern Africa, Central America and USA. Eggs, nymphs and adults survive in the bulbs for long period both in soil and in storage, and are the main source of infestation and spread (Wahba *et al*., 1984). Estimates of economic losses caused by *A. tulipae* are few, but reductions in yield of 23% reported in garlic due to mite infestation (Larrain, 1986) and combined loss of upto 40% has been reported by mites and *Garlic mosaic virus* (Ahmed and Benigno, 1984). *Amphitetranychus viennensis* intercepted in *Pyrus communis* from USA is generally considered as a pest of Rosaceae and is an important pest of apple, peach, pear, apricot, plum, hawthorn, cherry, sweet cherry and raspberry in China, Georgia, Japan, Russia, Turkey, Ukraine and other European countries. Adult females are ovoid, dark-red, diapausing individuals are bright red, approximately 0.36 mm in width, 0.54-0.59 mm in length. Adult males are smaller, approximately 0.31 mm in length, with a hysterosoma that narrows posteriorly (CAB International, 2007). *A. viennensis* may cause serious damage in dry years (Chepurnaya and Myalova, 1981), and mite damage affects the photosynthesis of the plants consequently resulting in reduction in fruit size and weight, but not in the number of fruits produced (Cai *et al*., 1992). It is widely distributed in several countries of Europe and Asia but not yet reported from India and is on the quarantine pest list in Australia and in USA.

Mites of the genus *Oligonychus* intercepted on *Saccharum officinarum* from USA are recognized by having a well developed empodial claw, with six to twelve hairs proximoventrally and by the absence of the caudal pair of para-anal setae, while *O. peruvianus* intercepted on *Persea americana* from USA is easily recognized by the short, lanceolate and nearly nude body setae on dorsum (Pritchard and Baker, 1955). *O. peruvianus* occurs along with other spider mites, and is known to cause serious injury to host plants in South America. It is known to be present in few countries in Central and South America and the Caribbean, Mexico, Spain and USA and is yet not reported from India. The fourth mite species *Polyphagotarsonemus latus* intercepted in *Persia americana* from Vietnam is a polyphagous species and has been found on hosts species belonging to over 60 different plant families worldwide (Gerson, 1992). Adult females of *P. latus* are small (200 µm) and have an unornamented dorsal shield. Dorsal idiosomal setae are short. Males have four pairs of setae on the dorsum of propodosoma with tibia and tarsus IV fused bearing a button-like claw. The mite is a serious pest of tea, chilli pepper and aubergines in China (Li *et al.*, 1985). It was reported to have destroyed 50% of the bean crop in New Guinea and of the lemon crop in parts of South Africa. It is a pest of cotton in tropical Africa and Brazil. Damage by *P. latus* was 100% on sweet peppers (*Capsicum* sp.) grown in a screen house in Taiwan, while aubergines, Datura, chilli pepper and Gerbera were severely damaged (Liu *et al*., 1991).

Table 1. Scale Insects and Mites Intercepted in the Exotic Vegetative Germplasm during 2007-08

Pest	Host	Samples Received (Infested Samples)	Source/ Country
Mites			
Aceria tulipae	*Allium sativum*	201 (22)	Kazakhstan, USA
Amphitetranychus viennensis	*Pyrus communis*	48 (10)	USA
Oligonychus peruvianus	*Persea americana*	82 (3)	USA
Oligonychus spp.	*Saccharum officinarum*	3 (1)	USA
Polyphagotarsonemus latus	*Persia americana*	21 (21)	Vietnam
Scale insects			
Aonidiella orientalis	*Vitis vinifera*	64 (8)	Brazil
Aspidiotus nerii	*Pyrus communis*	48 (12)	USA
Chrysomphalus dictyospermi	*Persia americana*	84 (10)	USA
Hemiberlesia lataniae	*Persia americana*	30 (2)	USA
Parasaissetia nigra	*Persia americana*	21 (12)	Vietnam

Aonidiella orientalis intercepted on *Vitis vinifera* from Brazil is an armoured scale with adults covered with a scale or cover that is morphologically separate from the body. The adult female is less strongly reniform than typical for its genus, with less developed prosomatic lobes. It is a tropical and subtropical species with a wide distribution, including the West Indies, Middle East, India, East Africa and South Africa, southern Asia and northern Australia (CAB International 2007). It has been accidentally distributed worldwide on host plants and also occurs in greenhouses in temperate areas. It is highly polyphagous, can attack almost any host except conifers and is an economic pest of citrus, *Ficus*, mango, papaya, banana and other fruits; palm trees, including coconut, arecanut and tea (Rajagopal and Krishnamoorthy, 1996). It is also a serious pest on coconut in Malaysia and Sri Lanka, mango in the Philippines and Israel, papaya in Malaysia and Australia, and guava in India (Rosen, 1990).

Aspidiotus nerii in cuttings of *Pyrus communis* from USA is also an armoured scale with female grey-white, circular, slightly convex and 2 mm long with almost central yellow exuviae. Adults remain under the scale armour and are yellow, broadly ovoid or circular and membranous except for parts of the pygidium. *A. nerii* is highly polyphagous and has been recorded on hundreds of host species in over 100 plant families (Beardsley and Gonzalez, 1975). Although the pest is of worldwide distribution, it is considered to be native to the Mediterranean area and is usually only a minor or non-economic pest on most of its hosts (DeBach and Rosen, 1991). However, it is particularly important where aesthetic value of the crop is high where its presence makes them unmarketable.

Chrysomphalus dictyospermi and *Hemiberlesia lataniae* intercepted on *Persea americana* from USA are both highly polyphagous scales recorded on hosts belonging to >70 plant families. *C. dictyospermi* can be easily confused with *A. aurantii,* however, adult female *C. dictyospermi* can be distinguished from *A. aurantii* in slide mounts because they possess perivulvar pores, and lack prosomal lobes expanded postero-laterally to partially enclose the pygidium (the latter is a prominent feature of mature female *A. aurantii*). The species is probably native to southern China; widespread in tropical and subtropical regions, and occur in glasshouse in temperate areas (Gill, 1997). It is distributed predominantly in Turkey, Syria, and Iran. *H. lataniae* was first described from a very popular ornamental palm distributed worldwide and is considered to be a serious pest in many areas of the world, including Israel, Palearctic Regions, the former USSR and USA (Miller and Davidson, 1990). Both the scales are important from quarantine viewpoint as they get transported and introduced to new countries often via importation of infested plant material, especially ornamental plants.

Parasaissetia nigra intercepted in *Persea americana* having the diagnostic characters of adults - presence of dorsal reticulations and cylindrical or capitate dorsal setae; the absence of tibio-tarsal scleroses and free tibio-tarsal articulation; and the absence of large discal setae from the anal plates. *P. nigra* is polyphagous and has been recorded on 240 hosts from 81 plant families, especially field crops, fruit trees and ornamental plants of tropical origin. *P. nigra* probably originated in Africa but is presently occurring all over the world. It is speculated that its geographical range in temperate areas is likely to increase as a result of global warming. It is widely distributed in Africa, India, Sri Lanka, Malaysia, Indonesia, Central and South America; rubber trees in Sri Lanka, India, Malaysia, Indonesia and South America; cotton in Africa, Sri Lanka, India, China, Taiwan, Japan, South Pacific islands, Hawaii and South America; sandal trees in India; cherimoya in Sri Lanka, Australia and the West Indies; guava in Taiwan, Australia, USA and West Indies; mango in South Africa, Hawaii, California and Florida; and papaya in Australia, USA and West Indies. However, major outbreaks and serious damage in these countries have been avoided mainly as a result of natural enemy activity (CAB International, 2007).

The importance of plant quarantine is clearly indicated by the interception of few economically important quarantine pests not yet reported from India. Although some of the pests intercepted are already known to occur in the country, they are important from quarantine point of view because of their economic impacts and the increasing number of strains of species being reported (Wadhi, 1980). Moreover, due to the perishable nature of the vegetatively propagated material they are immediately planted in the field which increases the chances of associated pests finding suitable conditions for survival and establishment. Their repeated interception year after year warrants proper detection and salvaging of infested material for pest-free release of vegetative germplasm for crop improvement programmes.

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Evaluation and Identification of Suitable Maize Cultivars for Baby Corn Productivity Traits

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Twenty cultivars of maize were assessed for their suitability for baby corn cultivation on the basis of different characteristics relevant for baby corn production relating to productivity traits, viz. flowering, as well as ear and plant characteristics (days to first cob picking, fodder etc.), during *kharif* 2007 and *rabi* 2007-08 seasons. HM 4 and HQPM 1 were found superior for most of the important productivity traits for cultivation, viz. husked cob yield per plant, HM 4(174.8g), HQPM 1 (169.9g); de-husked cob yield per plant, HM 4 (30.4g), HQPM 1 (26.0g); number of cobs picked per plant, HM 4 (3.3), HQPM 1 (2.7) and fodder yield per plant, HM 4 (522.3g), HQPM 1 (650.6g). Vivek Hybrid 17 and Vivek Hybrid 9 were found 10-14 days early for number of days to first cob picking and number of days to last cob picking compared to other cultivars. On the basis of overall characteristics, two elite hybrids HM 4 and HQPM 1 were identified for baby corn purpose. Many genotypes with specific characteristics can serve as potential genetic resources for effecting further development of new genotypes useful for baby corn improvement.

Key Words: Maize cultivars, Baby corn, Productivity, Ear characteristics, Hybrids

Introduction

Maize is unique among the cereals for its amenability to diverse uses and specialty corns attract utmost attention especially under Indian context. Specifically, baby corn is very relevant on account of a wide range of factors including enormous potentiality, multiple benefits to many stake holders etc. Baby corn is a young finger like unfertilized cob of maize harvested early within 1-3 days of silk emergence depending upon the growing season (Yodpetch, 1979; Yodpetch, and Bautista 1983). The ears are hand picked after the cob emerges from the ear tips, or a few days later. Being tender, it is eaten as whole cob in various forms (raw and cooked), and cooking does not change its culinary and physical properties significantly. Growing maize cultivars for baby corn has several advantages over other options like green ears or grain purpose, compared to other vegetable crops. Baby corn is a good option for crop diversification (Dass *et al.,* 2008) and it suits to peri-urban agriculture. Being a short duration crop (60-70 days during *kharif,* 120-140 days in winter- *rabi* and 75-90 days in spring), 3-4 crops of baby corn can be taken in a year, fitting well into the need to diversify the cropping system which is more remunerative to farmers (Kumar *et al.* 2001).

There is a great potential to earn foreign exchange through export of fresh/canned baby corn and its processed products, apart from increasing demand to meet local requirement within the country (Paroda, 2001). The major importing countries are USA, Japan, Hong Kong, Singapore, Australia, Malaysia, Canada, Saudi Arabia, New Zeeland, European countries and India. Thailand is major baby corn producing and exporting country in the world (Chutkaew, 1989), but India is emerging as one of the potential baby corn producing countries due to low cost of production and high demand within the country. Further, it is a dairy promoting crop as tassels (male part, consisting of pollens which are rich in protein and sugar contents), green sheathes, stalks and the other crop residues which are obtained as byproducts after picking of baby corn could be used both as fodder and silage for livestock production. Even from value-addition point of view, baby corn finds its way in to an array of preparations of several recipes like soup, raita, pakoras, chutney, pickles sour and sweet, cutlets, chat, mixed vegetable, kofta curry, baby corn masala, manchurian, baby corn chilli, jam, murabba, halwa, laddoo, burfi, kheer, candy, south Indian dishes etc. It is used as an ingredient in Chop-Suey (chinese dish), deep fried baby corn with meat and rice and mixed with other vegetables (Thakur and Jamwal, 2001). Baby corn is also very remunerative if it is cultivated with intercrop especially during winter. Since the winter season is long, farmers can utilize this lean period and get additional

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income through intercropping in baby corn. Intercropping of baby corn with pulse crops improves the soil fertility (Dass *et al.,* 2008). Thus, baby corn is a potential crop to generate income and employment for the rural poor, youth, women throughout the year, facilitating human welfare, sustainable development and best use of available resources in rural areas.

Despite such enormous prospects and potentialities, research initiatives are very much lacking in India. Very few studies are undertaken systematically to evaluate, identify or develop maize cultivars specifically suitable for baby corn usage across the seasons in Indian context. Usually early maturing maize cultivars primarily developed for grain yield are also cultivated for baby corn purpose. Specific features indicate desirability or otherwise of a maize cultivar for use at tender ear stage (Kumar and Kalloo, 2000). However, detailed information regarding productivity and ear aspects of most of the popular maize cultivars at the stage amenable for consumption as baby corn is scarce, necessitating systematic evaluation. Hence the present investigation was undertaken to assess the productivity traits and critically evaluated 20 diverse genotypes of maize aiming to identify potential cultivar(s) more suitable for utility as baby corn.

Material and Methods

The material for the present study consisted of a set of 20 maize cultivars comprising six single cross hybrids, four double cross hybrids, one three-way cross hybrids as well as nine composites (Table 1). These genotypes were obtained from the Directorate of Maize Research, Pusa Campus, New Delhi, and evaluated in two diverse seasons, viz. *kharif 2007* and *rabi 2007-08*. The experiment was laid in a Randomized Block Design with three replications in both the years at the experimental farm of Janta Vedic College, Baraut, Baghpat (Uttar Pradesh). The plot size for each genotype was 3 m X 1.2 m, with two rows of 3 m length, at a spacing of 60 cm between rows and 15 cm between plants. Recommended agronomic practices and plant-protection measures were adopted to raise a healthy crop. Observations were recorded on 10 randomly selected plants of each genotype in each replication on 20 characteristics pertaining to maturity, economic yield, biological yield etc. (Table 2). The analysis of variance was carried out according to the method suggested by Panse and Sukhatme (1985).

Table 1. Maize genotypes studied, their source, and main features

Genotype	Source/Centre	Main features (Maturity; type of cultivar)
Kiran	PAU, Ludhina	Early; composite
Parkash	PAU, Ludhina	Early; single cross hybrid
X 3342	Pioneer Seeds (Pvt. Seed comp.)	Early; double cross hybrid
HIM 129	VPKAS, Almora	Early; three way cross hybrid
Vivek hybrid17	VPKAS, Almora	Early; single cross hybrid
FQH 4567 (Vivek QPM 9)	VPKAS, Almora	Early; single cross hybrid
Vivek hybrid 9	VPKAS, Almora	Early; single cross hybrid
Pargati	GBPUT, Pantnagar	Early; composite
HQPM 1	CCS HAU, Karnal	Late; single cross hybrid
HM 4	CCS HAU, Karnal	Medium; single cross hybrid
BIO-9637	Bio-Seeds (Pvt. Seed comp.)	Late; double cross hybrid
Comp R-2005-2 (Chandramani)	CSAUAT, Kanpur	Early; composite
D 131 (Pant Sankul Makka 3)	GBPUT, Pantnagar	Early; composite
L 201	R.S., Bajaura, CSK HPKVV, Palampur	Early; composite
PRO 311	Bio-Seeds (Pvt. Seed comp.)	Late; double cross hybrid
Seed Tech 2324	Bisco Seed Tech. (Pvt. Seed comp.)	Late; double cross hybrid
Navjot	PAU, Ludhina	Early; composite
Surya	GBPUT, Pantnagar	Early; composite
L 166	R.S., Bajaura, CSK HPKVV, Palampur	Medium; composite
MS Pool C 7	PAU, Ludhina	Late; composite

Results and Discussion

The analysis of variance for both the seasons, viz. *kharif* (2007) and *rabi* (2007-08) revealed significant differences among genotypes for all the 20 productivity traits in 20 baby corn genotypes, indicating genetic diversity of material chosen for the present studies. For identifying suitable genotypes of maize to be used as baby corn comparative assessment was done on the basis of a total twenty characteristics related to productivity, maturity, cob and plant during *kharif*, *rabi* and both seasons (Table 2 and Table 3). On the basis of mean and other characteristics, overall performance of all the 20 genotypes were ascertained. While six traits were considered in detail for broad grouping to identify elite cultivars, the remaining 16 characteristics could be used for determining additional specific attributes. As for instance, the cultivar HM 4 exhibited highest values for trait number 14 referring to tassel weight/plant (26.4 and 27.12 g during *kharif* and *rabi* seasons respectively) implying that stout tassel was characteristic of this genotype.

Table 2. Performance of maize cultivars for different productivity traits during *kharif* season (2007)

Genotypes	Characteristics																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Kiran	48.23	52.44	56.70	53.59	57.80	4.21	2.43	45.66	9.22	111.16	22.45	20.18	116.67	17.03	36.44	88.71	348.62	454.36	476.81	4.70
Parkash	47.39	50.79	53.47	52.02	54.60	2.58	2.33	35.21	8.41	82.12	19.62	23.90	144.40	17.07	26.37	62.50	375.69	455.25	474.87	4.12
X 3342	48.15	52.29	59.07	53.71	60.09	6.38	2.00	38.72	9.29	77.45	18.60	24.01	126.73	13.47	29.42	58.85	365.34	437.66	456.26	4.08
HIM 129	45.53	48.98	56.79	50.80	58.13	7.33	2.83	44.62	9.52	126.18	26.97	21.37	107.20	14.30	35.10	99.41	229.97	343.68	370.65	7.27
Vivek Hybrid 17	41.43	45.34	52.96	47.26	54.19	6.92	2.10	34.97	9.55	73.34	20.04	27.32	116.27	15.27	25.41	52.05	260.99	328.30	349.33	5.73
FQH 4567	42.51	46.66	53.38	48.58	54.65	6.07	2.07	35.29	10.32	72.86	21.32	29.25	128.20	17.20	22.36	53.08	349.92	420.20	439.99	4.84
Vivek Hybrid 9	43.90	48.18	54.84	50.00	55.34	5.35	1.97	39.33	11.19	77.15	22.00	28.54	136.80	16.07	27.84	50.05	301.59	367.74	395.04	5.57
Pargati	44.23	48.10	55.79	49.76	56.66	6.89	2.50	38.08	8.42	95.12	21.05	22.12	113.80	18.17	29.65	74.07	246.27	338.51	359.56	5.85
HQPM 1	53.24	57.46	60.41	58.66	61.50	2.84	2.72	49.06	9.56	133.19	25.98	19.50	117.03	16.57	33.51	91.15	399.41	523.19	549.17	4.72
HM 4	50.08	53.85	58.79	55.40	60.28	4.88	3.10	46.47	9.53	143.79	29.53	20.58	103.20	26.40	35.94	113.96	348.60	488.96	518.79	5.69
BIO 9637	52.75	57.15	60.75	58.25	61.82	3.57	1.83	48.96	9.71	89.75	17.82	19.86	119.47	18.17	37.57	71.93	389.83	479.93	497.75	3.58
Comp R-2005-2	48.29	51.90	58.59	53.46	59.73	6.27	2.37	48.69	9.04	115.22	21.40	18.58	139.80	20.47	38.98	93.82	437.73	552.01	573.41	3.73
D 131	45.10	49.11	56.24	50.63	57.38	6.74	2.10	36.19	9.57	75.96	20.08	26.44	121.40	18.47	26.29	55.88	287.33	361.68	381.76	5.25
L 201	45.49	48.94	55.10	50.37	56.21	5.84	2.13	41.04	9.57	87.55	20.41	23.32	124.70	16.80	31.14	67.14	326.58	410.52	430.93	4.73
PRO 311	56.47	60.00	63.26	63.25	64.37	1.12	1.90	39.86	9.55	75.75	18.18	24.06	142.53	13.33	26.64	57.58	373.96	444.87	463.05	3.92
Seed Tech 2324	59.45	64.31	66.49	65.73	67.51	1.78	1.93	34.65	9.28	67.02	17.95	26.80	128.87	17.13	25.37	49.07	359.07	425.28	443.22	4.04
Navjot	47.43	51.69	56.17	53.60	57.17	3.57	2.00	46.33	8.68	92.60	17.36	18.77	142.53	19.23	36.65	75.24	374.28	468.75	486.12	3.57
Surya	43.74	47.37	52.91	48.75	54.07	5.32	2.40	39.29	8.62	94.30	20.68	21.96	126.77	22.13	26.34	73.62	274.90	370.65	391.33	5.28
L 166	45.61	49.97	55.55	51.12	56.64	5.52	2.33	40.81	9.88	95.18	23.05	24.22	142.20	20.50	30.10	72.13	330.90	423.54	446.58	5.16
MS Pool C 7	57.62	57.62	60.74	58.99	61.90	2.90	2.23	49.17	9.69	109.86	21.63	19.70	114.10	20.37	27.66	88.23	359.56	468.15	489.78	4.41
Mean	**48.33**	**52.11**	**57.40**	**53.70**	**58.50**	**4.80**	**2.26**	**41.62**	**9.43**	**94.78**	**21.31**	**23.02**	**125.63**	**17.91**	**30.44**	**73.24**	**337.03**	**428.18**	**449.72**	**4.81**
SEm±	1.02	0.93	0.79	0.82	0.78	0.99	0.078	0.96	0.23	3.07	0.83	0.69	1.28	0.23	1.04	3.25	3.42	4.21	3.98	0.17
Range	**41.43-**	**45.34-**	**52.91-**	**47.26-**	**54.07-**	**1.12-**	**1.83-**	**34.65-**	**8.41-**	**67.02-**	**17.36-**	**18.58-**	**103.20-**	**13.33-**	**22.36-**	**49.07-**	**229.97-**	**328.30-**	**349.33-**	**3.57-**
	59.45	64.31	66.49	65.73	67.51	7.33	3.10	49.17	11.19	143.79	29.53	29.25	144.40	26.40	38.98	113.96	437.73	552.01	573.41	7.27
CD at 5%	2.04	1.86	1.58	1.64	1.56	1.98	0.16	1.92	0.46	6.14	1.66	1.38	2.56	0.46	2.08	6.50	6.84	8.42	7.96	0.34

1. Number of days to tasseling, 2. Number of days to first cob silking, 3. Number of days to last cob silking, 4. Number of days to first cob picking, 5. Number of days to last cob picking, 6. Number of days interval to first and last cob picking, 7. Number of cobs picked/plant, 8. Single husked cob weight (g), 9. Single de-husked cob weight (g), 10. Husked cob yield/plant (g), 11. De-husked cob yield/plant (g), 12. De-husked to husked cob yield ratio 13. Plant height (cm), 14. Tassel weight/plant (g), 15. Husk (green sheath) weight/cob (g), 16. Husk (green sheath) yield/plant (g), 17. Stalk (picked plant) weight/plant (g), 18. Fodder yield/plant (g), 19. Biological yield/plant (g), 20. Harvest Index

Table 3. Performance of maize cultivars for different productivity traits during rabi season(2007-08)

	Characteristics																			
Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Kiran	123.82	128.22	132.10	130.52	134.18	3.67	1.97	48.53	8.67	95.49	17.35	18.17	106.33	20.38	39.87	78.14	316.50	415.02	432.37	4.01
Parkash	121.91	126.83	129.33	128.83	130.73	1.90	2.13	50.29	9.08	107.31	19.36	18.05	133.87	24.85	41.21	87.90	347.94	460.74	480.09	4.03
X 3342	119.00	124.43	128.28	126.43	130.27	3.83	2.35	53.49	9.33	125.63	21.90	17.44	108.70	13.57	44.36	104.25	312.78	430.61	451.99	4.84
HIM 129	114.50	120.09	128.27	121.53	128.93	7.40	2.10	47.07	9.36	98.83	19.63	19.89	92.33	22.33	37.71	79.07	197.78	299.19	318.95	6.15
Vivek Hybrid 17	113.50	118.44	125.82	120.18	127.49	7.32	1.93	47.21	9.05	91.33	17.48	19.17	99.73	18.25	38.16	73.85	222.42	314.51	331.99	5.26
FQH 4567	120.80	125.95	128.24	128.51	130.88	2.37	1.90	44.75	10.15	85.00	18.31	21.61	112.47	18.56	34.60	66.68	306.74	391.98	410.30	4.46
Vivek Hybrid 9	120.16	125.92	128.61	125.02	130.80	5.79	1.83	47.01	9.98	86.13	18.29	21.28	133.93	14.10	37.03	67.84	295.70	377.65	395.93	4.62
Pargati	127.70	129.95	132.55	131.58	134.29	2.71	2.20	47.68	8.90	105.04	19.59	18.66	110.30	22.45	38.78	85.46	233.36	341.27	360.85	5.42
HQPM 1	129.18	134.20	138.20	135.47	139.87	4.40	2.69	59.31	9.08	169.97	26.02	15.31	142.20	21.90	50.24	135.14	484.77	650.62	676.64	3.84
HM 4	126.93	132.25	137.60	134.03	139.47	5.43	3.30	52.94	9.21	174.80	30.40	17.42	103.80	27.12	43.72	144.40	350.79	522.31	552.71	5.50
BIO 9637	128.63	134.27	138.13	135.67	139.73	4.07	2.60	55.72	8.61	144.74	22.29	15.41	125.20	20.57	47.11	122.45	408.40	551.42	573.71	3.89
Comp R-2005-2	123.69	128.27	133.63	129.85	135.32	5.47	2.27	53.29	8.93	120.75	20.24	16.75	136.27	23.49	44.07	100.51	425.93	549.93	570.17	3.54
D 131	124.33	129.53	133.22	131.20	135.07	3.87	2.40	51.39	9.07	126.66	21.76	17.24	118.67	25.37	42.32	104.90	280.23	410.50	432.26	5.03
L 201	120.21	125.82	129.19	127.39	131.30	3.91	1.60	50.79	9.54	81.17	15.27	18.78	124.93	19.35	41.25	65.90	327.04	412.29	427.56	3.56
PRO 311	124.63	130.03	133.60	132.24	135.32	3.08	2.60	57.76	9.96	150.21	25.83	17.18	144.13	22.15	47.80	124.38	377.91	524.45	550.27	4.69
Seed Tech 2324	125.50	130.60	136.40	132.48	138.15	5.67	2.33	50.24	10.02	117.25	23.38	19.94	131.13	21.90	40.22	93.87	365.07	480.84	504.22	4.63
Navjot	123.22	128.13	132.07	130.00	133.68	3.68	1.80	49.50	9.28	89.07	16.67	18.75	141.20	20.23	40.22	72.40	365.21	457.85	474.52	3.51
Surya	118.39	123.43	130.47	126.09	132.22	6.13	1.87	49.15	8.68	91.79	16.20	17.67	123.40	22.28	40.48	75.59	270.73	368.60	384.80	4.21
L 166	125.95	131.40	133.73	132.98	135.48	2.50	2.67	58.54	8.70	156.08	23.17	14.86	141.07	21.46	49.84	132.92	328.17	482.55	505.71	4.58
MS Pool C 7	127.77	133.25	136.53	134.98	138.22	3.23	2.50	52.72	9.50	131.80	23.78	18.03	113.60	22.36	43.22	108.02	357.75	488.13	511.91	4.64
Mean	122.99	128.05	132.30	129.75	134.07	4.32	2.25	51.37	9.26	117.45	20.85	18.08	122.16	21.13	42.11	96.62	328.76	446.52	467.35	4.52
SEm±	1.27	1.67	1.97	1.72	1.79	1.27	0.130	1.05	0.27	6.01	1.11	0.86	1.17	0.51	1.09	5.38	2.05	6.38	7.02	0.20
Range	113.50-	118.44-	125.82-	120.18-	127.49-	1.90-	1.60-	44.75-	8.61-	81.17-	15.27-	14.86-	92.33-	13.57-	34.60-	65.90-	197.78-	299.19-	318.95-	3.51-
	129.18	134.27	138.20	135.67	139.87	7.40	3.30	59.31	10.15	174.80	30.40	21.61	144.13	27.12	50.24	144.40	484.77	650.62	676.64	6.15
CD at 5%	2.54	3.34	3.94	3.44	3.58	2.54	0.26	2.10	0.54	12.02	2.22	1.72	2.34	1.02	2.18	10.76	4.10	12.76	14.04	0.40

1. Number of days to tasseling, 2. Number of days to first cob silking, 3. Number of days to last cob silking, 4. Number of days to first cob picking, 5. Number of days to last cob picking, 6. Number of days interval to first and last cob picking, 7. Number of cobs picked/plant, 8. Single husked cob weight (g), 9. Single de-husked cob weight (g), 10. Husked cob yield/plant (g), 11. De-husked cob yield/plant (g), 12. De-husked to husked cob yield ratio 13. Plant height (cm), 14. Tassel weight/plant (g), 15. Husk (green sheath) weight/cob (g), 16. Husk (green sheath) yield/plant (g), 17. Stalk (picked plant) weight/plant (g), 18. Fodder yield/plant (g), 19. Biological yield/plant (g), 20. Harvest Index

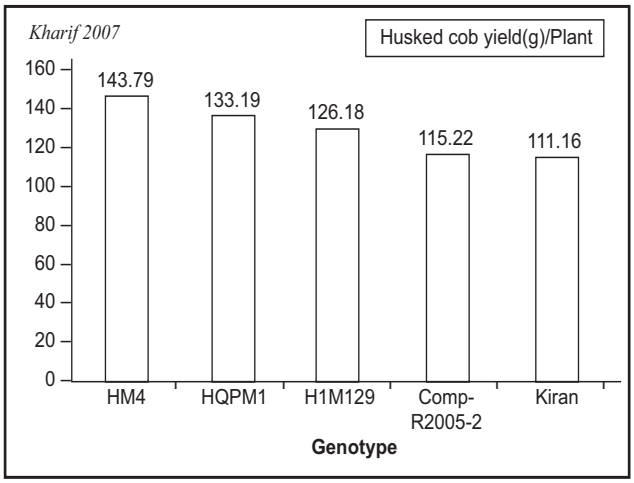
The six important yield traits directly contributing to baby corn production comprised husked cob yield per plant, de-husked cob yield per plant, number of cobs picked per plant, fodder yield per plant, number of days to first cob picking and number of days to last cob picking during *kharif* / *rabi* / both the seasons. Five top performing genotypes for husked cob yield (g) included HM 4 (143.8), HQPM 1 (133.2), HIM 129 (126.2), Comp R 2005-2 (115.2) and Kiran (111.2) during *kharif* and HM 4 (174.8), HQPM 1 (169.9), L-166(156.1), PRO-311(150.2) and BIO 9637(144.7) during *rabi* season (Table 4). For de-husked cob yield (g) five superior genotypes included HM 4 (29.5), HIM 129 (26.9), HQPM 1 (25.9), L166(23.0) and Kiran(22.4) during *kharif* and HM4(30.4), HQPM1 (26.0),PRO 311(25.8),M.S. Pool C 7(23.7) and L-166 (23.2) during *rabi* season (Fig. 3 and 4). The cultivars HM4 (3.1), HIM 129(2.8), HQPM 1(2.7), Pargati (2.5) and Kiran (2.4) during *kharif* and HM 4 (3.3), HQPM 1(2.7), L 166(2.7), PRO 311(2.6) and BIO 9637 (2.6) were found superior during *rabi* for the number of cobs picked per plant (Fig. 5 and 6). Comp R 2005-2 (552.0), HQPM 1 (523.2), HM 4 (488.9), BIO 9637 (479.9) and Navjot (468.7) during *kharif* and HQPM 1 (650.6), BIO 9637 (551.4), Comp R 2005-2(549.9), PRO 311 (524.4) and HM 4 (522.3) during *rabi* were found superior for the fodder yield (g) per plant. Five promising genotypes for number of days to first cob picking, Vivek Hybrid 17 (47.3), FQH-4567 (48.6), Surya(48.7), Pargati (49.7) and Vivek Hybrid 9 (50.0) during *kharif* and Vivek Hybrid 17 (120.2), HIM 129 (121.5), Vivek Hybrid 9(125.0), Surya (126.1) and X-3342 (126.4) during *rabi* were found superior. For the number of days to last cob picking, Surya (54.1), Vivek Hybrid 17 (54.2), Parkash (54.6), FQH 4567 (54.6) and Vivek Hybrid 9 (55.3) during *kharif* and Vivek Hybrid 17 (127.5), HIM 129 (128.9), X-3342 (130.3), Parkash (130.7) and Vivek Hybrid 9 (130.8) were found superior during *rabi* (Table 4).

Comparison among elite cultivars across the traits indicated that HM 4 and HQPM 1 gave superior performance for four important productive traits, viz. husked cob yield/plant, de-husked cob yield/plant, number of cobs picked/plant and fodder yield/plant during both the seasons, viz. *kharif* (2007) and *rabi* (2007-08) (Table 4). These two single cross hybrids were released in Haryana for grain cultivation and are having high protein content**.** Prasanna *et al* (1995) emphasized that genotypes for baby corn should have cylindrical and long ears, uniform ear size and properly developed ovule rows. The present study indicates that HM 4 possessed majority of the desirable traits for high yield in baby corn.

The HQPM 1 was found to be the next best hybrid for baby corn cultivation. This single cross maize hybrid belongs to high quality protein maize (QPM) (Dass *et al.* 2004) and has also shown good performance for majority of the important productivity traits for baby corn cultivation. For characteristic relating to maturity, Vivek Hybrid 17, Vivek Hybrid 9 and composite Surya were identified for early baby corn pickings during both the seasons. Similarly, Vivek Hybrid 17 and Vivek Hybrid 9 and Parkash were identified for days to last cob picking during both the seasons which could facilitate early vacating of field. Minimum number of days required for last cob picking was observed in Vivek hybrid 17, Vivek hybrid 9 and Parkash. Though HM 4 and HQPM 1 took about a week more extra for last cob picking as compared to other early maturing single cross hybrids, viz. (Vivek hybrid 17, Vivek hybrid 9 and Parkash), but both of them gave 30% higher yield in both the seasons, viz. *kharif* (2007) and *rabi* (2007-08). Therefore, for cultivation of maize genotypes for baby corn it is necessary to take in to account all aspects, so that they are economical to the farmers.

Among elite cultivars identified on the basis of important traits, hybrids were predominantly represented in the elite group for each trait in general, implying superiority and desirability of maize hybrids for baby corn usage, compared to composites. This feature is especially evident when performance of the genotypes in both the seasons is taken in to account (Table 4 and Fig. 1).These hybrids were also good for fodder yield, which is obtained as a byproduct after picking baby corn and could be used as fodder or silage purpose. As the emphasis on single cross hybrids as a strategy in the field corn since last few years in India has been instrumental in realizing higher production and productivity, similar approach in baby corn could be relevant and fruitful.

It is pertinent to note that critical assessment of various characteristics in the maize cultivars would be fruitful in selecting most desirable genotypes as indicated by studies in different countries (Bar Zur *et al*. 1990; Zhao, 1991; Fongmance and Soonsuwan, 1998; Almeida *et al.* 2005, Itala Paula de *et al.* 2005; Rodrigues *et al*. 2003 and Silva Le *et al.* 2006). Most appropriate baby corn genotypes identified by the farmers out of the available cultivars played significant role in popularization and spread of baby corn cultivars in some countries like Thailand, Brazil etc. This benefited various stake holders and strong drive for



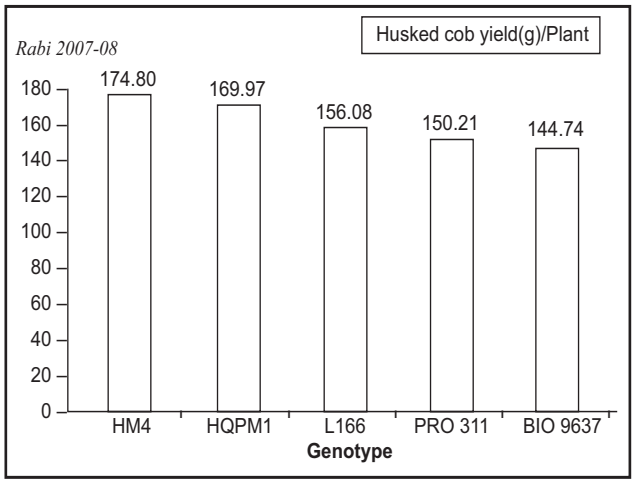
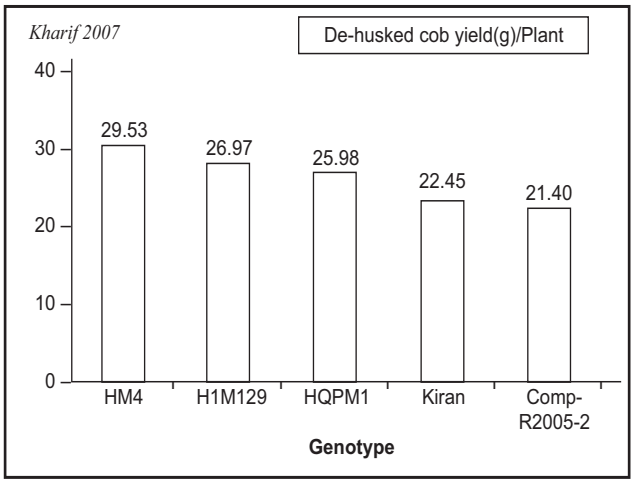


Fig. 1 and 2: Husked cob yield



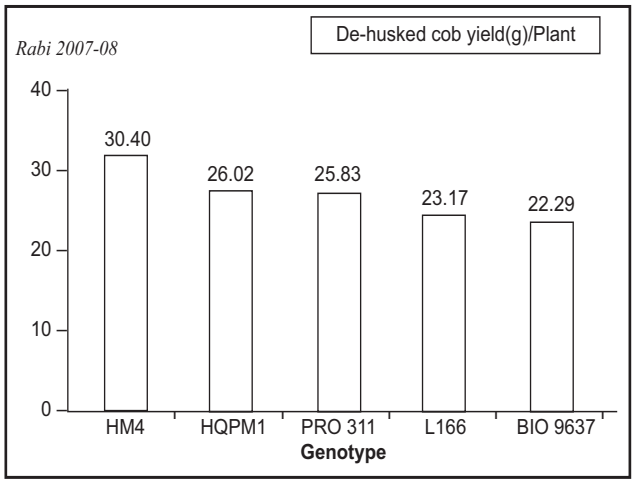
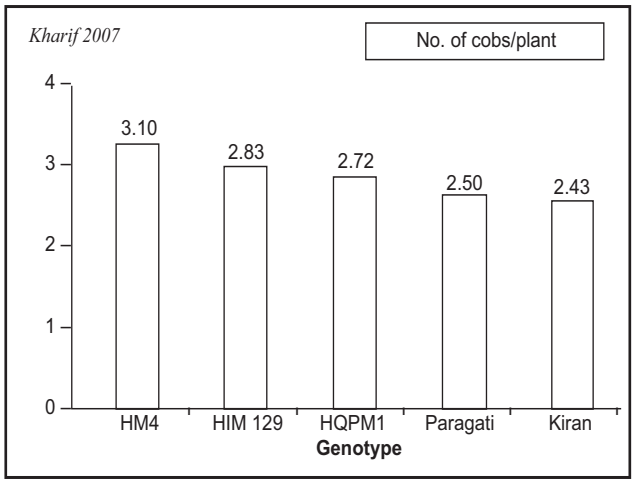


Fig. 3 and 4: De-husked cob yield (g)/Plant



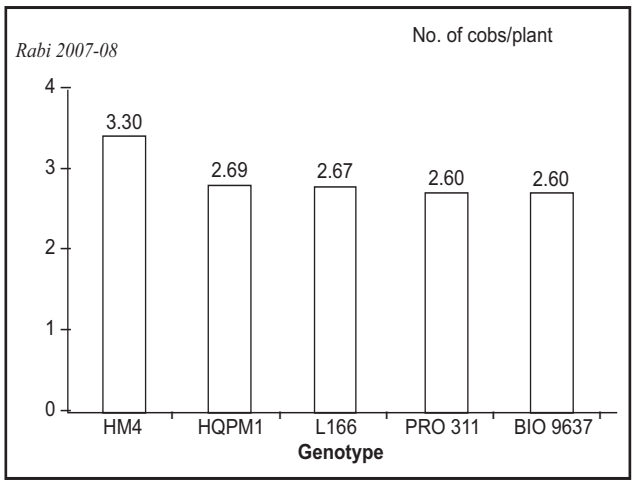
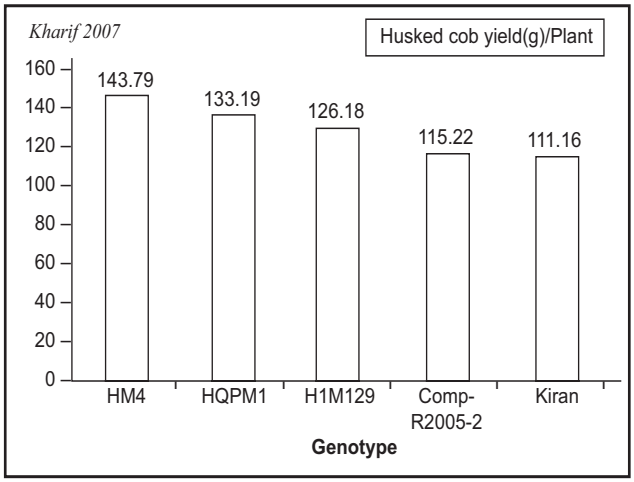


Fig. 5 and 6: Husked cob yield



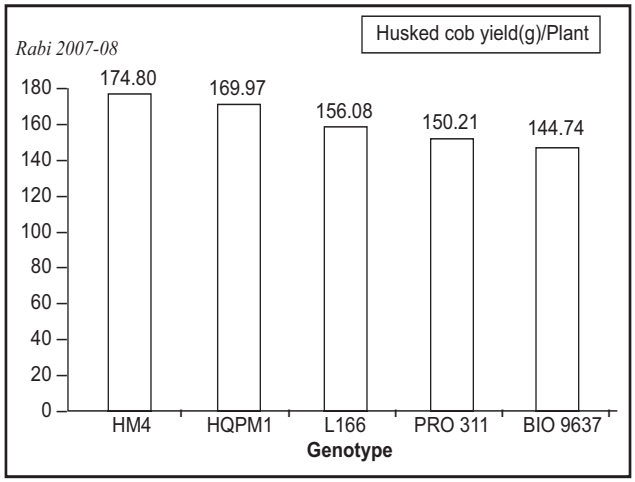
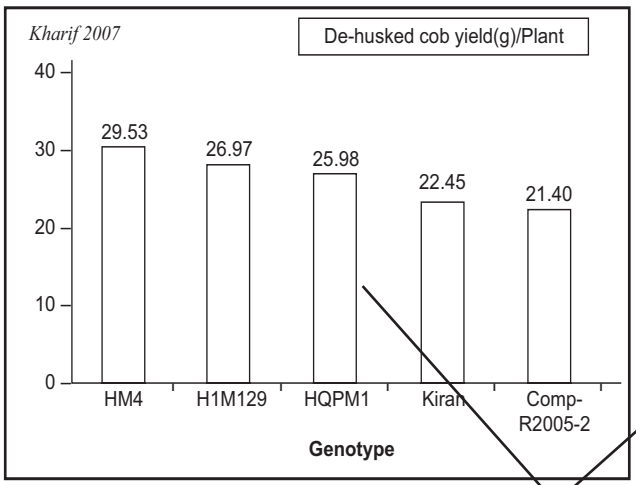


Fig. 1 and 2: Husked cob yield



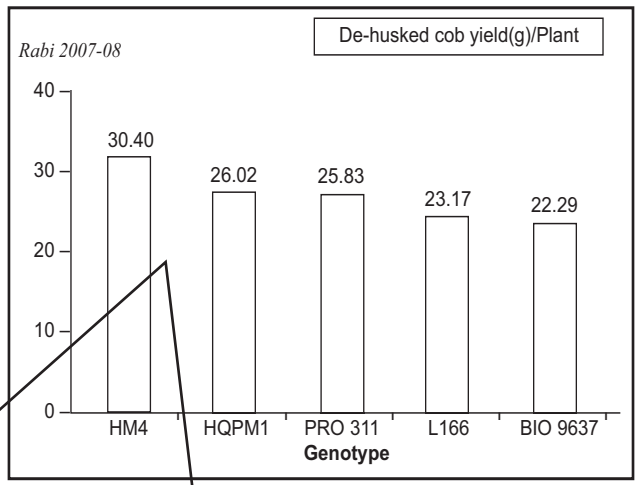
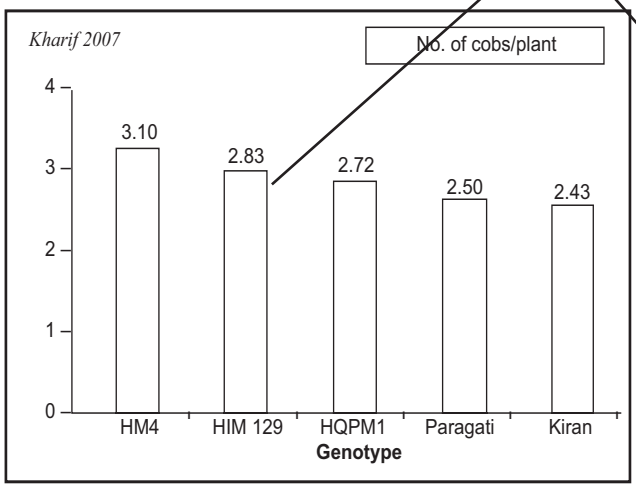


Fig. 3 and 4: De-husked cob yield (g)/Plant



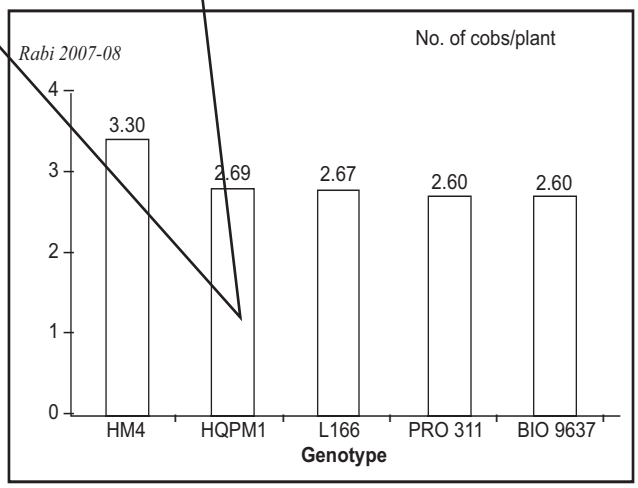


Fig. 5 and 6: Husked cob yield

Plate I: Field view

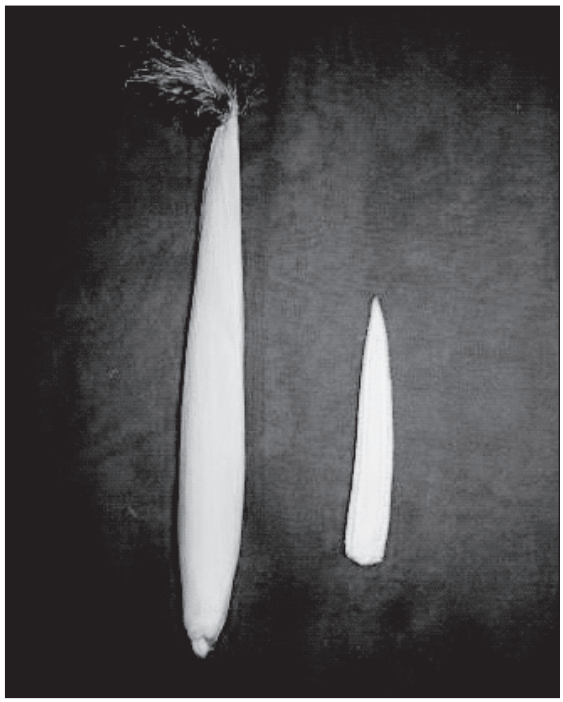


Plate II: Husked and de-husked cobs

HM 4

Plate III: Field view

Plate IV: Husked and de-husked cobs

HQPM 1

Table 4. Superior genotypes of baby corn identified for important productivity traits

Productivity traits	Superior genotypes under different seasons *Kharif* (2007)		Elite genotypes in both seasons *Rabi* (2007-08)		
Husked cob yield/plant (g)	HM 4	(143.8)	HM 4	(174.8)	HM 4
	HQPM 1	(133.2)	HQPM 1	(169.9)	HQPM 1
	HIM 129	(126.2)	L-166	(156.1)	
	Comp R 2005-2	(115.2)	PRO-311	(150.2)	
	Kiran	(111.2)	BIO 9637	(144.7)	
De-husked cob yield/plant (g)	HM 4	(29.5)	HM 4	(30.4)	HM 4
	HIM 129	(26.9)	HQPM 1	(26.0)	HQPM 1
	HQPM 1	(25.9)	PRO 311	(25.8)	L 166
	L 166	(23.0)	M.S.Pool C 7	(23.7)	
	Kiran	(22.4)	L-166	(23.2)	
Number of cobs picked/ plant	HM 4	(3.1)	HM 4	(3.3)	HM 4
	HIM 129	(2.8)	HQPM 1	(2.7)	HQPM 1
	HQPM 1	(2.7)	L 166	(2.7)	
	Pargati	(2.5)	PRO 311	(2.6)	
	Kiran	(2.4)	BIO 9637	(2.6)	
Fodder yield/plant (g)	Comp R 2005-2	(552.0)	HQPM 1	(650.6)	HM 4
	HQPM 1	(523.2)	BIO 9637	(551.4)	HQPM 1
	HM 4	(488.9)	Comp R 2005-2	(549.9)	BIO 9637
	BIO 9637	(479.9)	PRO 311	(524.4)	
	Navjot	(468.7)	HM 4	(522.3)	
Number of days to first cob picking	Vivek Hybrid 17	(47.3)	Vivek Hybrid 17	(120.2)	Vivek Hybrid 17
	FQH-4567	(48.6)	HIM 129	(121.5)	Vivek Hybrid 9
	Surya	(48.7)	Vivek Hybrid 9	(125.0)	Surya
	Pargati	(49.7)	Surya	(126.1)	
	Vivek Hybrid 9	(50.0)	X-3342	(126.4)	
Number of days to last cob picking	Surya	(54.1)	Vivek Hybrid 17	(127.5)	Vivek Hybrid 17
	Vivek Hybrid 17	(54.2)	HIM 129	(128.9)	Vivek Hybrid 9
	Parkash	(54.6)	X-3342	(130.3)	Parkash
	FQH 4567	(54.6)	Parkash	(130.7)	
	Vivek Hybrid 9	(55.3)	Vivek Hybrid 9	(130.8)	

export was manifested. This further triggered intensive research towards improvement and development of new cultivars specifically for baby corn cultivation, meeting both high productivity and quality standards.

In India, a few researchers (Verma *et al.*, 1998; Verma 2001; Prodhan *et al.* 2007a and Sharma *et al.*, 2002) have attempted to evaluate the available genotypes for their suitability for baby corn. In addition to productivity, need for emphasis on economic returns highlighted by Prodhan *et al.* (2007b). There are also parallel and complementary efforts towards highlighting finer cultivation and technological aspects to facilitate better general awareness and popularization of baby corn cultivation (Kalloo and Kumar, 1999; Nirmal De *et al.* 2005 and Thakur and Jamwal, 2001). In present study, two single cross hybrids viz. HM 4 and HQPM 1 (Plates: I-IV) were found to be superior for majority of important productivity traits and hence can be recommended for commercial cultivation of baby corn in Western Uttar Pradesh and adjoining areas. On the basis of further extensive multi-location trials their cultivation could be readily extended to larger areas and zones.

Further, in view of large amount variability for various productivity, ear and plant as well as flowering characteristics exhibited in these cultivars could serve as useful genetic resources and be effectively utilized as base material in deriving better and useful genotypes by hybridization and directional selection. This would be

instrumental in developing new cultivars including single cross hybrids for specific use as baby corn, fulfilling the needs and requirements of different stake holders.

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Genetic Divergence for Yield Contributing Traits in Winged Bean [*Psophocarpus tetragonolobus* L. (DC)]

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Genetic divergence in 30 indigenous and exotic collections of winged bean was studied by Mahalanobis D^2 statistic for days to flowering, days to maturity, plant height, pods per plant, pod length and number of seeds per pod. Significant variations were recorded among the genotypes for all the characters. The genotypes were grouped into nine different clusters. The clustering pattern of the genotypes indicated that genetic diversity was uncorrelated with geographic diversity. IC95234 was the best genotype for early maturity, plant height and more number of pods per plant. Days to maturity and plant height contributed maximum towards the genetic divergence. Hybridization of IC95234 with either of IC112416, IC27885-1, EC142654-4 and EC142667 for early maturity and inter crossing among EC038955, EC178331, EC178288 and IC95234 to get dwarf types have been suggested.

Key Words : Winged bean, Genotypes, Genetic divergence, Earliness, Non- staking types

Introduction

Winged bean [*Psophocarpus tetragonolobus* (L.) DC], also known as Goa bean, four angled bean, asparagus pea and princess pea, is a perennial but usually grown as an annual vine. It has climbing habit, attains height of about 2-3 m and requires staking for proper growth and development. It is primarily cultivated for its immature edible pods which are cooked and eaten as a vegetable. It grows abundantly in hot, humid equatorial countries, from Philippines to Indonesia to India, Burma and Sri Lanka. This bean has been referred as "one species supermarket" because practically the whole plant is edible. While the beans are used as a vegetable, the other parts (leaves, flowers, and tuberous roots) are also edible. Dried seeds are generally eaten as roasted or sprouted, can be used as flour and also to make a coffee-like drink. Being a leguminous crop, all parts are rich in protein, vitamin A and other vitamins. Being an under utilized legume very little work has been done on its genetic improvement.

Only one variety AKWB 1 has been released from germplsam selections. For its wider adoption and easy cultivation selection and development of non staking, non shattering varieties with determinate habit and uniform maturity are required. For that matter it is essential to screen the existing material and efforts be made to undertake hybridization programme among the diverse parents. In this direction an effort has been made to evaluate and classify the available indigenous and exotic material with respect to their divergence for various traits.

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Materials and Methods

The material comprised of 30 strains of indigenous and exotic collections and were grown in complete Randomized Block Design with three replications at main research farm at Birsa Agricultural University, Ranchi during *Kharif*, 2005. The plot for individual genotype comprised single row of 5 m length with intra and inter row spacing of 30 cm and 60 cm respectively. Observations were recorded for six yield attributing traits namely days to flowering, days to maturity, plant height (cm), pods per plant, pod length (cm) and number of seeds per pod from 5 randomly selected competitive plants. The replicated data were subjected to analysis of variance followed by multivariate analysis of D^2 statistic according to Mahalanobis (1936). The genotypes were grouped on the basis of minimum generalized distance using Toucher's method as described by Rao (1952).

Results and Discussion

The analysis of variance revealed significant differences among genotypes for all the six characters (Table 1). The mean values in respect of all the genotypes for all the characters along with SE and CD (5%) have been given in Table 2. As per diversity analysis, 30 genotypes were grouped into nine clusters (Table 3). Cluster III was the largest with 12 genotypes followed by cluster II with 8 genotypes. Cluster V and cluster I had 3 and 2 genotypes respectively, while clusters IV, VI, VII, VIII and IX had only one genotype each. Seven indigenous collections were grouped in three different clusters along with other exotic accessions. These were IC95236, IC95248 and

IC95248 in cluster II, IC95222, IC45229-1 and IC 112416 in cluster III and IC 95234 in cluster VI. This indicated that the geographic diversity is not an indication of genetic diversity. Such information that genetic diversity is not necessarily correlated with eco-geographical distribution has been indicated in other crops as well (De and Rao. 1987; Mishra and Dash,1997; Katiyar, *et al.,* 1998; Appalaswamy and Reddy, 2002; Reddy, *et al.,* 2004; Katiyar, et.al., 2005). Arunachalam and Bandyopadhayay (1984) indicated that the genetic drift and selection in different environments could cause greater diversity than geographic distances. This emphasizes the significance and importance of studying genetic diversity in germplasm irrespective of their geographic diversity in indigenous as well as exotic material.

The inter and intra-cluster D^2 values (Table 4) showed that there was very little diversity within a cluster, cluster III with 12 genotypes having D^2 value 3.46, followed by cluster V with 3 genotypes having D^2 value 2.96 and cluster II with 8 genotypes having D^2 value 2.88. The diversity was maximum between clusters IV and VI (D^2 13.23), followed by between clusters VII and VIII (D^2 12.79) and between 1 and VI (D^2 12.03).

The knowledge of the characters contributing to divergence is an important factor. This helps the breeder to choose parents with highly variable traits to seek

Table 1. ANOVA in respect of six characters in winged bean

Source	d.f.	Days to flowering	Days to maturity	Plant height	Pods/plant	Pod length	No. of seeds/pod
Reps	2	4.48	1.21	270.93	0.41	1.30	1.10
Genotypes	29	146.09**	329.52**	4086.10**	45.86**	8.81**	1.53*
Error	58	6.04	2.85	242.59	6.32	2.54	0.85

* Significant at P= 0.05, ** Significant at P= 0.01

Table 2. Mean values of different characters in respect of 30 winged bean genotypes

Acc.	Days to flowering	Days to maturity	Pl.height(cm)	Pods/plant	Pod length (cm)	No. of seeds /pods
IC45229-1	80.00	169.67	189.00	16.00	19.00	5.50
IC95222	75.00	165.00	213.00	18.00	16.33	6.67
IC95234	66.00	**153.00**	**170.00**	**19.67**	17.33	6.17
IC95236	83.00	179.67	210.00	15.00	14.00	5.13
IC95248	86.00	176.33	230.00	14.00	17.00	5.10
IC112416	78.00	**157.00**	250.00	9.67	14.67	5.07
IC112417	88.00	183.00	187.00	8.33	12.67	6.00
EC21904	72.00	160.00	193.00	18.00	15.00	5.13
EC27885-1	69.33	**155.00**	208.00	12.67	16.33	6.73
EC27886	78.00	162.67	**176.00**	11.00	17.00	6.97
EC27886-A2	89.00	169.33	210.00	9.00	16.67	5.60
EC114273-B	85.00	187.33	181.00	12.00	19.00	6.13
EC116887	76.00	168.00	**176.00**	14.67	13.67	5.07
EC116889	73.67	163.00	230.00	8.00	16.33	6.73
EC121918	76.00	166.67	205.00	9.33	17.00	6.63
EC121919-A	82.00	183.00	245.00	11.33	15.33	6.70
EC142654	80.00	175.00	178.00	10.33	13.00	6.40
EC142654-4	75.00	**157.67**	230.00	16.00	14.33	6.60
EC142662	79.00	162.00	208.67	14.00	15.00	5.50
EC142667	72.00	**159.67**	278.67	13.33	18.33	6.57
EC178266	79.00	170.00	282.67	18.00	15.67	7.07
EC178269	86.00	181.67	241.67	12.00	15.00	5.60
EC178287	90.33	184.00	286.00	8.33	14.33	6.80
EC178288	83.67	175.00	**168.33**	14.00	15.00	6.77
EC178296	88.33	179.33	195.00	12.33	12.00	6.93
EC038955	71.00	176.00	**138.33**	**21.00**	17.00	6.83
EC142665	67.00	180.00	195.00	14.00	15.00	7.00
EC178271	68.33	173.00	181.67	15.67	15.00	7.00
EC178313	72.67	188.00	**170.33**	**21.33**	15.33	6.33
EC178331	71.33	187.33	**161.67**	**20.33**	15.67	7.33
SE	1.42	0.98	8.99	1.45	0.92	0.53
CD(5%)	4.02	2.76	25.46	4.11	2.61	1.50

Table 3. Cluster composition in winged bean

Cluster group	No. of genotypes	Genotypes
I	2	EC178313, EC178331
II	8	EC121919-A, EC178269, IC95236, IC95248, EC178296, EC142654, EC178288, IC112417
III	12	EC116889, EC121918, EC142662, EC27886, IC95222, EC116887, IC45229-1, EC21904, EC142654-4, EC27885-1, IC 112416, EC 142667
IV	1	EC178287
V	3	EC142665, EC178271, EC038955
VI	1	IC95234
VII	1	EC178266
VIII	1	EC114273-B
IX	1	EC27886-A2

genetic improvement through hybridization. The relative contribution of each character towards divergence has been given in Table 5. A perusal of the data (Table 5) indicated that days to maturity contributed maximum (66.21 %) to the genetic divergence followed by plant height (12.41%). Number of seeds per pod and pod length contributed least towards genetic diversity having values 0.69 and 0.92 % respectively. Since plant height and days to maturity are the two important traits in winged bean for development of early maturing and indeterminate type of varieties, the selection of parents for hybridization from different clusters with respect to these traits will be desirable. The perusal of data in Table 3 showed that parents IC95234, IC112416, EC27885-1, EC142654-4 and EC142667 were earlier in maturity (< 160 days). Amongst them IC95234 belonged to cluster VI, whereas IC112416, IC27885-1, EC142654-4 and EC 142667 belonged to cluster III. Therefore, hybridizing IC95234 with either of IC112416, IC27885-1, EC142654-4 and EC142667 could give better early maturing genotypes in segregating generations. Similarly genotypes EC038955, EC178331, EC178288, IC95234, EC 178313, EC27886, EC116887 and EC142654 were short (< 180 cm height) in height. Among them EC 038955 in cluster V was the shortest (138 cm) followed by EC 178331 (161.67 cm) in cluster II, EC178288 (167.33 cm) in cluster I and IC95234 (170 cm) in cluster VI. Therefore, inter crossing of all these divergent genotypes could give still better segregates in respect of short height for easy handling in cultivation of this crop. Exotic genotypes EC178313, EC038955, EC178331 had maximum no. of pods per plant (> 20). Of these genotypes, EC178313 and EC178331 were in cluster I and EC038955 in cluster V. Therefore, inter crossing EC038955 with either of 178313 and EC178331 may throw good segregates in respect of pods per plant. Among the available genotypes IC95234 was the best in respect of early maturity, lower plant height and more number of pods per plant. Therefore this genotype appeared promising and needs multi-location evaluation before recommending for cultivation.

From this study it became evident that wide variations existed among genotypes in respect of plant height, days to maturity and pods per plant. Apart from IC95234 being a promising genotype, hybridizing IC95234 with either of IC112416, IC27885-1, EC142654-4 and EC142667 for early maturity, intercrossing amongst EC038955, EC178331, EC178288 and IC95234 for dwarfing and hybridizing EC038955 with either of EC178313 and EC178331 for more no. of pods per plant can be useful

Table 4. Average intra (in bold) and inter cluster distance (D^2)values in winged bean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	0.85	6.03	9.69	7.69	4.40	12.03	7.78	4.81	9.21
II		2.88	7.00	4.16	5.40	10.65	5.43	3.96	4.43
III			3.46	9.06	6.35	5.18	4.49	9.37	5.24
IV				0.00	7.84	13.23	6.41	4.86	5.97
V					2.96	8.32	5.28	6.16	7.07
VI						0.00	7.56	12.79	8.93
VII							0.00	7.71	5.34
VIII								0.00	6.59
IX									0.00

Table 5. Contribution of different characters towards genetic divergence in winged bean

SI. No.	Characters	Contribution (%)
1	Days to flowering	10.57
2	Days to maturity	66.21
3	Plant height (cm)	12.41
4	Pods per Plant	9.20
5	Pod length (cm)	0.92
6	No. of seed per pod	0.69

in selecting desirable non staking plants with in winged bean for higher productivity and early maturity.

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Status of Genetic Resources of Forage Crops in India: A Review

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Dairy industry and animal rearing have opened up new market avenues and Indian farmers are taking up fodder production in a much bigger way. Forage crops occupy an important position across the world. For developing varieties resistant to various pests and diseases and to improve forage quality and quantity, there is a continuous need of diverse genetic resources. Acquisition of diverse and superior forage germplasm plays an important role in the development of varieties. Keeping this in mind, the Germplasm Exchange Division played the pivotal role and introduced a total of 13,181 accessions of forage crops into India mainly from Australia, Italy, USA, UK, Brazil, Germany, Egypt, Ethiopia, Bulgaria, Philippines, Singapore, Costa Rica, Zimbabwe, Japan, Russia and New Zealand. Most of the introduced germplasm was supplied to Indian Grassland and Fodder Research Institute and All India Coordinated Research Project on Forage Crops located at Jhansi, Uttar Pradesh. Some promising varieties introduced into India were directly used for cultivation. Forage species of *Sesbania rostrata, Sesbania aculeata, Pennisetum squalatum* and *Pennisetum pedicellatum* from different Institutes were registered for various traits and their seeds have been deposited for long-term storage in National Gene Bank. Details of trait specific germplasm, wild germplasm introduced and conserved in forage crops in India are highlighted.

Key Words: Forage crops, Germplasm introduction, Conservation

Introduction

India is an agricultural based country and about 70 per cent of its people live in villages. Their livelihood is dependent mainly on agriculture and animal husbandry. India holds one-fourth of the total cattle population of the world, but is highly deficient in various livestock products. The analysis of the situation revealed that one of the main reasons for the low productivity of our livestock is malnutrition, under-nutrition or combination of both, besides the low genetic potential of the animals (Anonymous, 2007). Global demand for meat, milk and other animal products is growing dramatically and so is our need for improved forages. There is a huge gap between demand and supply of all kinds of feeds and fodders in India as seen from the figures of availability, *vis-a-vis* the requirement of green-fodder crops, crop residues and concentrates (www.Krishiworld.com).

Forages comprise of grasses, legumes and other herbaceous species. Most forage grow in grasslands or produced by fodder crops and provided by fodder crop residues also as reviewed from literature (Bennett 1999, 2001 Bounejmate *et al.* 1999, Charlton 1981, Dhillon *et al.* 2001, Gladstones 1975, Maxted and Bennett 2001, Singh *et al.* 2006, Perry 1990, Plucknett *et al.* 1987, Williams 1983) and existent web sites of major forage genebanks at CIAT Columbia; ICARDA Syria; ILRI, Nairobi; CSIRO-Australia, IGER-UK, USDA-Fort Collins and EMBRAPA-Brazil.

Origin and Distribution of Forages

Grass Forages

Grasses belong to a wide range of genera and over 600 species are currently used for grazing and livestock feeds from about a total of 10,000 grass species that occur in the world. Grasses are distributed along the main climatic belts and are classified into major groups, the tropical grasses (Africa is the most important centre of variation in the Gramineae) (Clayton 1983) and the Mediterranean and temperate grasses (most current utilized grass species were originated from Eurasia, East Africa and South America) (Knight 1983). Wild species have been distributed widely into South America (*Brachiaria decumbens*) and Australia (*Stylosanthus* sps). They vary from annual to perennial or summer-growing to winter-growing ecotypes. Forage grasses are mostly used as cut fodder (often also using remaining from cereal food crops) or grazed pasture and also as harvested seed crops (generally from dual purpose food and feed crops). Over 1,500 species of legumes (from about a total of 17,000 legume species worldwide) can be used as forage, although only about 60 species have been developed and widely used as forages. Although forage legumes have been used for many years they have only been under cultivation for as little as 75 years. Tropical legumes are possibly originated from tropical forests and are currently found from the tropics to the Arctic regions, from high rainfall regions to deserts and from rocky slopes and sand dunes to swamps (Williams 1983). Sometimes

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they are also used for human consumption (i.e. crops with dual purpose for food and feed). The use of forage legumes is estimated to be as old as 11,000 years, with some species being first used as grain for human consumption and latter on switched to be only used for fodder or pasture, or vice versa (Mathison 1983).

Legume Forages

Globally several large, perennial, tropical grasses are grown for forages in various parts that include: Elephant grass (*Pennisetum purpureum),* cultivars of Guinea grass (*Panicum maximum)* and Guatemala grass (*Tripsacum laxum)*, annual tropical or hot-season grasses teosinte (*Zea mexicana),* Sudan grass (*Sorghum* x *drummondii),* Columbus grass (*Sorghum almum)* and Johnson grass (*Sorghum jwlepenset).* Forage legumes include pea (*Pisum sativum),* guar (*Cyamopsis tetragonaloba),* pigeon pea (*Cajanus cajan),* soybean (*Glycine max),* hyacinth bean (*Lablab purpureus),* cowpea (*Vigna unguiculata),* groundnut (*Arachis hypogaea),* and fenugreek (*Trigonella foenum-graecum).* Fodder cereals including oats (*Avena sativa* and *A. strigosa*, maize (*Zea mays*), sorghum (*Sorghum bicolor*), pearl millet (*Pennisetum americanum*), barley (*Hordeum vulgare)*, rye *(Secale cereale*), proso millet (*Panicum miliaceun)* and finger millet (*Eleusine coracana)* and sugarcane *(Saccharum officinarum).* There has been a great expansion in the use of fodder oats recently, in sub temperate areas.

Other Forages

Perennial legumes used as fodder crops (Duke 1981, Frame *et al.* 1998) include alfalfa/lucerne (*Medicago sativa*), sainfoin (*Ollobrychis viciifolia)*, red clover (*Trifolium pratense)*, and Alsike clover (*Trifolium hybridum)*. Annuals and short-lived perennials include Egyptian clover (*Trifolium alexandrinum)*, crimson clover (*Trifolium incarnatum)*, Persian clover (*Trifolium resupinatum)*, sulla (*Hedysarum coronarium)*, vetches (*Vicia* spp.), Chinese milk-vetch (*Astragalus sinicus)*, seradella (*Ornithopus* spp.), sweet clover (*Melilotus alba*) and yellow sweet clover (*Melilotus officinalis)*. Root crops are also very important in humid temperate agriculture, but have been largely replaced by maize and grass silage. Besides, the members of the Brassicacae namely turnips (*Brassica rapa* var. *rapifera)*, swedes (*Brassica napus* var. *napobrassica)*, kale (*Brassica oleracea)*, cabbage (*Brassica chinensis*), (*B. oleracea),* forage radish (*Raphanus sativus)*, fodder beet (*Beta vulgaris)* and carrot (*Daucus carota*) also serve as important forage crops.

Arora *et al.* (1975) analysed the distribution pattern of Indian grasses, falling in seven phyto-geographic zones of India and concluded their distribution in tropical humid belt of south- western India for tropical types; north-west arid/semi arid belt and north-eastern moist belt for subtropical species and western Himalayan tract for the temperate species. Thus, these agroclimatic regions offer great opportunity for the collection of indigenous grasses as well as legume species for forages and pasture lands. This paper discusses the status of genetic resources of forage and fodder crops, the major issues related to their introduction, conservation and importance of their biodiversity.

Status of Introduction

The work on collection, introduction, domestication and utilization of fodder crops in India was initiated in 1970 in the PL-480 Scheme (Anonymous, 1984). To procure diverse genetic resource- promising genetic stocks, improved varieties and wild relatives international obligations for import and export of germplasm are observed. India is a party to relevant international agreement on access to PGR and sharing of benefit arising out of their use including Convention of Biological Diversity (1992) and International treaty on plant Genetic resources for Food and Agriculture (2001). As envisaged under the Treaty, the exchange of genetic resources of the Annex 1 crop of the Treaty (35 food crop genera and 29 forage crops) would be under the conditions of a standard material transfer agreement (SMTA) formulated by the Governing Body of Treaty in June 2006. The Treaty signifies wide international commitment that both traditional and modern technologies should serve humanity, in particular to alleviate hunger and promote sustainable development in developing countries (Anonymous 2007).

The national gene bank at NBPGR, New Delhi, conserves germplasm of forage crops including landraces, breeding lines, traditional varieties, released varieties, wild and weedy types, elite lines, improved cultivars and other genetic stocks at -18^{0}C for long term storage. As the forage grasses have low viability, therefore, the maximum viability limit in case of grasses is 20-40%. A minimum of 2000 seeds should be submitted in self-pollinated forage crops whereas 4000 seeds are required in cross pollinated crops. Seed moisture content should be in the range of 5-7%.

The germplasm introduced into India is being

multiplied, characterized, evaluated and conserved at different NBPGR regional stations located in different agro-climatic zones and also at Indian Grassland and Fodder Research Institute (IGFRI), Jhansi. IGFRI networks with its three Regional Centers and All India Coordinated Research Projects (AICRP) on forages with 18 coordinated centers under ICAR system and seven Regional Stations on Forage Production and Demonstration and one Fodder Seed Production Farm under Department of Animal Husbandry is the National Active Germplasm Site for forages. Significant headway has been made in varietals development at IGFRI, Jhansi. One hundred and eighty eight varieties of 30 fodder crops, range legumes and grasses(Annual Report, IGFRI, 1980-2008) have been released (Table 1) and notified through IGFRI. The function of the AICRP is to coordinate multi –location testing programmes at the national level for identification of appropriate varieties and production technologies for different agro-ecological conditions.

Status of Development of varieties of forage crops in

Table 1. Important high-yielding varieties of fodder crops

	(A) Northern region
Jowar (*Sorghum vulgare*)	
'J.S.-20', 'J.S.-29/1', 'J.S.-263', 'J3/53', 'Swarna', 'M.P. chari', 'S.L.-44', 'Pusa chari', 'Haryana chari'	Punjab, Haryana, Delhi
'T-3', 'T-4', '8B', 'M.P. chari', 'S-700', 'H1', 'H2', 'Rio'	Uttar Pradesh, (B) Western region
'Sundhia 1049', 'Chhastia 10-2', 'Dudhia'	Gujarat
'Red Khaki', 'Nilwa', 'Nandyal', 'M-35-1'	Maharashtra, (C) Central region
'Gwalior-82', 'Gwalior-304', 'Vidisha 60-1', '	Madhya Pradesh
Ujjain-6', 'Ujjain-8', 'J-195'	(C) Southern region
'K 3', 'Co 11', 'Co 18', 'Co 19', 'Rungu 1', 'M.P. chari'	Andhra Pradesh and Tamil Nadu
Maize (*Zea mays*)	
Hybrids-- 'Ganga-Safed-2', 'Ganga-3', 'Ganga-5', 'Ganga-7'	
Composites--'Jawahar', 'Amber', 'Kissan', 'Vijay', 'Sona', 'Vikram'	
Open-pollinated--'N.P. Yellow-2', 'K-41', 'Bassi', 'Jaunpur'	
'Emenillo de cuba', 'Kalimpong	West Bengal
Bajra (*Pennisetum typhoides)*	
'A-1/3', 'H.B.3', 'S-530', 'T-55' 'D 1941', '2291'	
Oat (*Avena sativa*)	
Early varieties--'Western-11'	
Mid-season varieties--'Kent', 'Craig', 'Afterlee', 'Green Mountain', 'A-17', 'Flaminagolds', 'Fulgham', 'Bamboo-966', 'IGFRI-Soil-3021', 'IGFRI-Soil-2688'	
Late varieties--'Algerian', '37/14', 'FOS-1/29', 'Kharsai'	
Cowpea (*Vigna sinensis*)	
'FOS-1', 'FOS-10', 'K-395', 'K-585', 'EC4216', 'IGFRI-S-450', 'IGFRI-S-457	Haryana, Punjab and Delhi
'Russian Giant', 'IGFRI-S-978', 'IGFRI-S-985', 'Russian Giant'	Uttar Pradesh and Karnataka
'E.C. 4216', 'Russian Giant', 'Chhrodi 14-20', 'Chhrodi 26-28'	Gujarat
'Co 1', 'Russian Giant', 'E.C. 4216'	Southern states
'Co 1', 'E.C. 4216'	West Bengal
Guar (*Cyamopsis tetragonoloba*)	
'FOS 1', 'FOS 2', 'E.C. 4216F.S. 277', 'IGFRI-S 212', 'No. 2'	Punjab, Haryana, Delhi, Uttar Pradesh
'Durgapura safed'	Rajasthan
Velvet bean (*Stizolobium niveum*)	
'IGFRI-S 2276-5'	Uttar Pradesh, Rajasthan, Andhra Pradesh, Madhya Pradesh and Haryana
Field bean (*Dolichos lablab* var. *lignosus*)	
'IGFRI-S 2214-II',--Broad leaf, erect	
'IGFRI-S 2218-1',--Medium leaf, decumbent	
Berseem (*Trifolium alexandrinum*)	
'Meskawi-Diploid', 'Pusa giant-Tetraploid', 'IGFRI-S-29-1', 'Chhindwara'	
Lucerne (*Medicago sativa*)	
'Type-8', 'Type-9' ,'Anand II', 'IGFRI-S-244', 'Moopa', 'IGFRI-S-54', N.D.R.I.-1	

(A) Northern region

Senji (*Melilotus parviflora*)
'FOS-1', 'F.S. 14', 'F.S. 18'

Methi (*Trigonella foenum graecum*)
'FOS-8'

Hybrid Napier
'Pusa Giant Napier', 'NB 21', 'EB 4', or 'Gajraj', 'N.B. 5', 'Coimbatore'

Sudan grass (*Sorghum Sudanese*)
'SS-59-3', 'G 287', 'Piper', 'J-69'

Dinanath grass (*Pennisetum pedicellatum*)
'Type-3', '10', '15', or 'IGFRI-S-3808', 'G-73-1', 'T-12', 'IGFRI-S-866-1'

Blue panicum (*Panicum antidotale'*)
'S-297'

Anjan or Buffel (*Cenchrus ciliaris'*)
'Pusa Giant Anjan', 'IGFRI-S-3108', 'IGFRI-S-3133', 'C-357', 'C-358', *Cenchrus glaucus*

Bird wood (*Cenchrus setigerus'*)
'Pusa yellow Anjan'

Marvel (*Dichanthium annulatum*)
'M-8', 'IGFRI-S-495-1', 'IGFRI-S-495

Mustard (*Brassica*) spp.
'Japan sarson', 'IM-98', 'IM-100', 'Laha 101', 'Chinese cabbage'

Stylos (*Stylosanthes*) spp.
Butterfly pea (*Clitoria ternatea'*)
'IGFRI-S-23-1', 'IGFRI-S-12'

Turnips
'Green Top', 'Purple Top', 'Kenshin--Kaba'

(http://www.krishiworld.com/html/for_crop_grass1.html)

India

Germplasm is a vital resource in generating new plant types having desired traits that help in increasing forage crops production and thus improve the level of nutrition for animal/ cattle population. Number of varieties were developed (Table 1) by ICAR in forage crops (Annual Report, IGFRI, 1980-2008; Annual Reports AICRP on Forage Crops 1980-2008) utilising exotic and indigenous germplasm. Some important varieties include Giant Bajra (evolved through a cross between Australian bajra and local bajra of *Pennisetum americanum*) Pusa Deenanath Grass a selection from African material of *Pennisetum pedicellatum;* Punjab Guinea Grass-1 an introduction from Australia under the name CPI-59985 of *Panicum maximum*, Nandi selection from African germplasm of *Setaria anceps;* Marwar Dhaman a clonal selection from exotic material EC017655 of *Cenchrus setigerus;* Marwar Anjan a clonal selection from exotic material EC14369 of *Cenchrus ciliaris;* Kent an introduction from USA of *Avena sativa*, UPO-90 a single plant selection from American material of *Avena sativa;* Mescavi and Fahl introductions from Egypt, BL-1 a selection from mescavi of *Trifolium alexadrium;* Kohinoor a selection from material obtained from Iran and UPC-5286 a single plant selection from germplasm line 5286 of *Vigna unguiculata* etc.

Exotic Introductions made in Forages

A total of 13,181 forage introductions were made by the Germplasm Exchange Division during last 33 years (Annual Reports, NBPGR, 1976-2008). Major genera introduced were *Agropyron, Amblyopyrum, Austialopyrum, Avena, Cliotoria, Cnidoscylus, Corymbia, Dasypyrum, Desmanthus, Desmodium, Elymus, Elytrigia, Eragrostis, Eremspyrum, Eucalyptus,Festuca, Enradia, Hordelymus, Lespedeza, Leymus, Lotus, Macroptilum, Medicago, Pascopyrum, Poa, Psarhyrostachys, Sorghum, Thinopyron, Trifolium* and *, Triticale* through its linkages with over 115 countries and eight IARC's.

A total of 10, 049 samples in sorghum (*Sorghum bicolor*) and 20,085 were introduced in pearl millet (*Pennisetum americanum*) for dual purposes. Many other important wild species of *Pennisetum* were also introduced from Nigeria, UK, USA and Zambia. In oats (*Avena sativa*), the genetic resources of grain and fodder types comprising of 1,827 accessions were procured. Several

promising introductions of fodder type were EC22017 and EC107536 from Australia, EC108586 and EC108602 from UK, EC10068 from Russia. Dual- purpose variety Rapida of oats from USA is suitable for malting industry. Another promising introduction Kent (from Australia) was released during 1970s. It has stiff straw, medium early and dual- purpose type and continues to be a popular variety. It was released directly as commercial variety. Another promising accession of oat used as donor for development of new variety PO-94 was a single plant selection from American material. This is a mulicut variety resistant to lodging, frost and shattering and also free from stem rust, crown rust, leaf blight and smut, grasshopper, cutworms, aphids and mites.

Trait Specific Introductions

Targeted and trait specific introductions, for nutritional quality and value addition are important. In the present scenario, where the access to germplasm is restricted due to many national and international treaties/ Acts, it is very important to search for and introduce trait specific germplasm for use in various crop breeding programmes. NBPGR continued its efforts and the trait specific germplasm introduced in forages in past ten years are presented in Table 2.

New Forage Crops and Wild Species Introductions

New forage crops and wild species introductions were also made at NBPGR. *Atriplex* sp. was introduced from

Table 2. Trait specific introductions in forage crops

Crop/EC No. and Source country	Traits	Distribution
Brachiaria hybrid variety Mulato EC 549024-25 USA	Stoloniferous growth, excellent forage production, vigorous regrowth, excellent palatability, drought tolerant, and produces forage round the year	IGFRI Regional Station, Dharwad, Karanataka
Deschampsia antarctica Antartic hair grass EC631954, Chile	New crop, native to Antarctica	Avesthagen Limited, Bangalore
Elytrigia repens EC586940 USA	Var. Eversett, advanced generation synthetic cultivar for high rhizome production ability to spread by rhizomes and used for land stabilization and reclamation	IGFRI, Jhansi
Medicago sativa EC499771-72 USA	Highly resistant to Aphanomyces root rot and northern root knot nematode, resistant to Phytopthora, pea aphid, spotted aphid and moderately resistant to Verticillium wilt, anthracnose race 1 and stem nematode, High forage yield under dry land condition	IGFRI, Jhansi
Medicago sativa EC596671 USA	Var. OK 190, unique combination of broad genetic base, resistance to blue alfaalfa aphid, spotted alfaalfa aphid & Phytopthora rot	IGFRI, Jhansi
Medicago sativa EC596673 USA	Var. OK 207, broad genetic base population provide resistance to blue alfa alfa aphid biotype BAOK 90 & spotted alfaalfa aphid	IGFRI, Jhansi
Medicago spp. EC271425-29, USA	Produce high forage, cold tolerant and resistant to aphids	IGFRI, Jhansi
Pennisetum typhoides ssp ***montana*** EC473259, USA	Potential for increase growth rate, resistance to rust, smut and leaf spot	NBPGR, Regional Station, Jodhpur
Trifolium pratense E560447-448, USA	Short internodes, plants usually present a rosette appearance but flower sparingly under long day conditions	IGFRI, Jhansi
Trifolium pratense EC578957, USA	Var. Freedom, free from pubescence, good for hay making as it permits faster drying and reduces dustiness	IGFRI, Jhansi
Trifolium pratense EC560447-448, USA	Short internodes, plants usually present a rosette appearance but flower sparingly under long day	IGFRI, Jhansi NBPGR RS, Bhowali
Triticale EC537921, Mexico	Hexaploid winter triticale, good forage quality	IGFRI, Jhansi
Triticale EC537922, Mexico	Hexaploid intermediate triticale, good forage quality	GCD, NBPGR
Triticale EC534274, USA	High yielding, superior forage quality	IGFRI, Jhansi
Triticale EC467937, Canada	Variety Bobcat, sprouting tolerant and resistant to stem rust and leaf rust	NBPGR, Regional Station, Bhowali

Tunisia for arid zones, it is a perennial, evergreen and salt tolerant. Promising introductions in *Atriplex* (Dhillon et al. 2001) include are *A.. halimus* (EC129767), *A. canescens* (EC129768) and *A. nummularia* (EC129766). Subabool (*Leucaena leucocephala)* was introduced from Australia, Philippines, Colombia, France, Malawi, Sierra Leone, UK and USA. This fast growing tree provides fodder, green manure and fuel and can withstand drought also. An introduction K-8 (EC124343) from Philippines performed well at Jodhpur for fodder purpose and variety EI Salvador (EC123866) from Australia proved superior for fodder and fuel. Other new species are *Brachychiton populneum* (drought tolerant, provides fodder and useful as wind breaker) from Tunisia, *Cassia sturtii* (fodder crop adapted to semi- arid habitats) and *Casuarina equisetifolia* (fodder for wastelands and alkaline soil) from Australia. Two new grass species introduced from USA for tropical and temperate areas are *Brachiara hybrid* and *Deschampsia antarctica,* respectively.

Wild species are generally more variable than the corresponding crop. Plant breeders utilize wild species mainly for sources of resistance to biotic and abiotic stresses as well as in breeding for genetic enhancement. NBPGR has introduced 986 wild forage species (Anonymous, 2007) in different forage crops. These genetic resources have been introduced with the efforts of scientist of NBPGR as well on requests from several scientists working at different research institutes, SAU's and other organization with R & D facilities. However, 11 genera of exotic wild forage germplasm representing 67 species have been introduced into India (Table 3).

Forage Germplasm Conservation

For conservation of PGR at national level, a network approach is being followed. It consists of the National Gene bank situated at the NBPGR headquarter, New Delhi, primarily responsible for conservation of collection on long-time basis for posterity and to support regeneration or restoration activities of active collections at National Active Germplasm Sites (NAGS). The germplasm introduced/imported into India is being multiplied, characterized, evaluated and conserved at different NBPGR regional stations located in different agro-climatic zones and also at Indian Grassland and Fodder Research Institute (IGFRI), Jhansi.

A total of four thousand five hundred and ninety four accessions of forage cereals (1167), grasses (1116), range legumes (1443), forage millets (781) and others (87) have been conserved at NBPGR in long term storage in the National Gene bank. The germplasm comprised of 4 species of of forage cereals, 63 species of grasses, 40 species of of range legumes, 20 species of forage millets and 19 species of others. Eighteen released varieties are also conserved in long term storage at National Gene Bank, NBPGR, New Delhi. The lists of released varieties and forage species conserved in NGB are listed in Table 4 and 5, respectively.

Registration of Germplasm

With the objective of giving credit to these scientists who have developed or identified promising experimental materials (including parent or inbred lines) or promising germplasm, and to facilitate flow of germplasm among the scientists working in the crop improvement programme,

Table 3. Wild species introduced in forage crops

Genera	Species
Agropyron	*A. cimmericum*
Brachiaria	*B. ruziziensis*
Clitoria	*Clitoria ternetea*
Desmodium	*D. intortum* and *D. uncinotum*
Elymus	*Elymus haffmannii*
Lotus	*L. conimbricensis, L. coribricensis, L. ornithopodioid, L. pendunoulatus, L. purshianus* and *L. uliginosus*
Macroptilium	*M. atropurpureum* and *M. axillare*
Medicago	*M. arabica, M. Ciliaris, M. coronata, M. intertexta, laciniata, M. littoralis, M. lupulina, M. minima, M. orbicularis, M. polymorpha, M. radiata, M. rigidula, M. rugosa, M. scutellata, M. tornata, M. truncatula, M. turbinate, M.liciruata* and *M.littoralis*
Melilotus	*M. indicus, M. messanensis, M. officinalis, M. segetalis,* and *M. sulcatus*
Stylosanthes	*S. scabra* and *S. viscosa*
Trifolium	*T. alpestre, T. angustifolium, T. arvense, T. aureum, T. baccarinii, T. balansaa, T. billardiari, T. campestre, T. clypeatum, T. dasyurum, T. diffusum, T. fomentosum, T. fragiferum, T. grandiflorum, T. incarnatum, T. lappaceum, T. leucanthum, T. ligusticum, T. michelianum, T. nigrescens, T. pilulare T. scabrum, T. squamosum, T. striatum, T. striatum* var. *spinescens, T. subterraneum* and *T. tomentosum*

Table 4. Status of Released Varieties in National Gene Bank

Botanical Name	Donor Identity	Var. No.
Avena sativa	SABZAAR, Jawahar Oat-1,OS-7,OS-6, JHO- 813, JHO- 816, JHO-2001-3,KENT, JHO 99-1,IC449066	10
Cenchrus ciliaris	IGFARI- 727, IGFARI-3108, IC526313	03
Chrysopogon fulvus	IGC 9903 (BUNDEL DHARSELU GRASS-1)	01
Cyamopsis-tetragonolobus	BUNDEL GUAR-1, BUNDEL GUAR-2, BUNDEL GUAR-3	*03*
Heteropogon contortus	IGHC 03-4	01
Medicago sativa	ANAND-3, ANAND-6, ANAND-2, ANAND-1, GAUL-1, GAUL-2	06
Panicum maximum	JHGG 04-01 (Bundel Guinea-2)	01
Pennisetum glaucum	GIANT BAJRA,IC526299	02
Pennisetum typhoides	GFB-1	01
Sehima nervosum	IGS-9001(Bundel Sain Ghes -1)	01
Stylosanthes hamata	PHULE KRANTI-95	01
Trifolium alexandrinum.	JAWAHAR BERSEEM-5, BL-180, CV.MASCAVI,	03
Sorghum bicolor	CO(FS)29, PC-23, PC-9, IGFARI/PC-23,C-10-2, S-1049, GFS-3, UTMCH1302(CSH 24 MF)H, ICSA467 (FEMALE), ICSA467 (MAINTAINER), PANT CHARI-6, SPV 1595 (CSV 18), SPH 1567, PMS28A (O PARENT OF SPH 1567)	14
Vigna unguiculata	UPC-607, C-30 (GFC-4), C-26 (GFC-3), C-14 (GFC-1),(GFC-2)	06
Zea mays	AFRICAN TALL	01

ICAR constituted Plant Germplasm Registration Committee (PGRC) with Deputy Director General (Crop Science) as the Chairman, to register such promising germplasm. NBPGR would be the nodal agency for registration of material which will receive applications, process the same and carry out the validation (if required). The decision of the committee must be finalized within one year of the submission of the proposal. In case the validation test by NBPGR is required, the proposal would be received at least two months prior to the normal crop sowing season i.e. Rabi and Kharif so that validation tests are made within the 1st crop season itself. In addition to long term storage of the registered material by NBPGR, working stock for supply to users would be maintained by the institution associated with the development of the material.

The information about registered germplasm is also published in Indian Journal of Plant Genetic Resources, various newsletters viz., ICAR Newsletter, NBPGR Newsletter and Seed News etc. to disseminate information among scientists. Thus, putting the information regarding these germplasm in public domain has become a mandatory requirement to safeguard the national resources with respect to intellectual property rights. The guidelines were developed for plant germplasm registration and were widely circulated among the scientists. Till 2009, seven forage species (15 accessions) have been registered for various traits as detailed in Table 6.

Conclusion

Conserving species biodiversity permits the conservation of a genetic heritage that might be necessary for future livestock production systems. International cooperation is necessary for efficient monitoring of forage crops, pasture and grassland genetic resources and their use. Many wild grassland species are not yet in gene banks; they remain widespread in low- input grasslands around the world and their contribution to animal feeding is important.

Introduction of wild relatives need to be emphasized for broadening of genetic base. The utilization of the genetic diversity is a critical factor in enhancing productivity on a sustainable basis. Though improved varieties have been released in forage crops, attention is required to register the unique forage germplasm for further utilization in breeding programmes. Emphasis should be on collections from areas left unexplored and having maximum diversity after the gap analysis. Based on available passport and evaluation data, and the information to be generated in future, enrichment of existing genepools and development of new pools for groups of important characters would be useful in easy and effective germplasm management and use. Awareness generation of the people at various levels (policy makers, scientific, administration, farmers etc.) about the value of PGR wealth and its protection is essential. Further, there is an urgent need to increase the interaction between plant breeders and PGR workers. The interface among different stakeholders is likely to bring

Table 5. List of Forage Species in the NGB

Acrachne racemosa Ohwi	*Canavalia ensiformis* (L.) DC
Ailanthus excelsa Roxb.	*Capillipedium hugelii* Stapf
Alloteropsis cimicina (L.) Stapf.	*Capillipedium parviflorum* Stapf.
Alysicarpus vaginalis Wall	*Cardiocrinum giganteum* Makino
Andropogon pumilus Roxb.	*Cassia rotundifolia* Pers.
Apluda mutica L.	*Ceiba pentandra* (L.) Gaertn.
Aristida adscensionis L.	*Celosia argentea* L.
Arthraxon prionodes (Steud.) Dandy	*Cenchrus biflorus*
Atriplex hortensis L.	*Cenchrus ciliaris* L.
Atylosia platycarpa Benth	*Cenchrus prieurii*
Atylosia scarabaeoides (L.) Benth.	*Cenchrus setigerus* Vahl
Avena fatua L.	*Chloris barbata* (L.) Nash
Avena sativa L.	*Chloris dolichostachya* Lag.
Boerhavia diffusa L.	*Chloris gayana* Kunth
Bothriochloa pertusa (L.) A.Camus	*Chrysanthemum morifolium* Ramat.
Brachiaria ramosa (L.) Stapf	*Chrysopogon fulvus* (Spreng.) Chiov.
Brachiaria setigera (Retz.) C.E.Hubb.	*Cichorium intybus* L.
Coix lacryma-jobi L.	*Echinochloa colonum* Beetle
Crotalaria retusa	*Echinochloa stagnina* P.Beauv.
Cyamopsis tetragonolobus (L.) Taub.	*Eleusine flagellifera* Nees
Cymbopogan martnii	*Elionurus royleanus* Nees ex A.Rich.
Cymbopogon flexuosus	*Eragrostiella bifaria* (Vahl) Bor
Cymbopogon jwarancusa Boiss.	*Eragrostis ciliaris* Link
Dactylis glomerata L.	*Eragrostis diarrhena* Steud.
Dactyloctenium aegyptium (L.) K.Richt.	*Eragrostis unioloides* Nees ex Steud.
Descuriana sophia	*Eriochloa procera (Retz.)* C.E.Hubb.
Desmodium Gangeticum DC.	*Eulalia argentea* Brongn.
Desmodium gyrens	*Festuca arundinacea*
Desmodium triquetrum	*Hackelochloa granularis* Kuntze
Desmostachya bipinatata Stapf.	*Heracleum candicans* Wall
Dichanthium annulatum Stapf	*Heteropogon contortus* (L.) Beauv. ex Roem. & Schult.
Digitaria adscendens Kunth Henrard	*Imperata cylindrica* (L.) P.Beauv.
Digitaria granularis (Trin.) Henrard	*Iseilema laxum* Hack.
Digitaria Pennata	*Kedrostis rostrata*
Dinebra retroflexa Panz.	*Lablab purpureus* (L.) Sweet
Dipsacus mitis	*Echinochloa colonum* Beetle
Acrachne racemosa Ohwi	*Canavalia ensiformis* (L.) DC
Ailanthus excelsa Roxb.	*Capillipedium hugelii* Stapf
Alloteropsis cimicina (L.) Stapf.	*Capillipedium parviflorum* Stapf.
Alysicarpus vaginalis Wall	*Cardiocrinum giganteum* Makino
Andropogon pumilus Roxb.	*Cassia rotundifolia* Pers.
Apluda mutica L.	*Ceiba pentandra* (L.) Gaertn.
Aristida adscensionis L.	*Celosia argentea* L.
Arthraxon prionodes (Steud.) Dandy	*Cenchrus* biflorus
Atriplex hortensis L.	*Cenchrus ciliaris* L.
Atylosia platycarpa Benth	*Cenchrus prieurii*
Atylosia scarabaeoides (L.) Benth.	*Cenchrus setigerus* Vahl
Avena fatua L.	*Chloris barbata* (L.) Nash
Avena sativa L.	*Chloris dolichostachya* Lag.
Boerhavia diffusa L.	*Chloris gayana* Kunth
Bothriochloa pertusa (L.) A.Camus	*Chrysanthemum morifolium* Ramat.
Brachiaria ramosa (L.) Stapf	*Chrysopogon fulvus (Spreng.)* Chiov.
Brachiaria setigera (Retz.) C.E.Hubb.	*Cichorium intybus* L.

Table 6. Registered germplasm in Forage species

Crop name	Collection Number	National Identity	Unique Traits
Panicum maximum	IG3/29/2-3(1)	IC567677 INGR09039	Triploid cytotype
	IG 04-164	IC567678 INGR09040	High production progenitor of ploidy series
	IG3/29/2-5(1)	IC567679 INGR09041	Pentaploid cytotype
	IG3/29/2	IC567680 INGR09042	Hexaploid cytotype
	IG3/29/2-8(1)	IC567681 INGR09043	Octoploid cytotype
	IG3/29/2-9(1)	IC567682 INGR09044	Nonoploid cytotype
Pennisetum glaucum	TetraA4; IG 08-03	IC567684 INGR09046	Tetraploid male sterile line with A4 cytotype
	TetraA1; IG 99-748	IC568548 INGR09047	Maintainer of Tetra A4 MS line
Pennisetum pedicellatum	Agros-4 INGR06018	IC546954 Octoploid cytotype 2n=72	
Pennisetum squamulatum	Apomictic cytotype INGR06017	IC546955 Apomictic cytotype 2n=56	
Sesbania aculeata	CSD 137 INGR04108	IC427827 High foliage and better sodicity tolerance	
	CSD 123 INGR06016	IC546953 Very early (120 days) and better tolerance to sodic soils	
Sesbania rostrata	TSR-1	IC296793 INGR01014	Photoperiod insensitive mutant, with long vegetative growth
Trifolium alexandrinum	PBL-123 INGR05017	IC524012 Purple Leaf and flower mutant	
Trifolium alexandrinum	Penta-1	IC567683 INGR09045	Pentafoliate mutant

out new useful forage genetic resources management alternatives.

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Heterosis and Combining Ability Studies for Oil and Protein Content in Soybean [*Glycine max* (L.) Merrill]

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Soybean [*Glycine max* (L.) Merrill] is energy rich oil seed crop in India. Heterosis and combining ability studies were carried out in F_1, F_2, and F_3 generations of 45 crosses derived from crossing of 15 soybean lines with 3 testers. Based on various estimates viz., mean performance, heterosis and combining ability the best soybean parents and crosses for quality traits were identified. For both seed oil and protein content, high heterosis and positive Specific Combining Ability (SCA) effects were recorded in crosses Pusa 40 x NRC 12, JS 79-81 x MACS 58, JS 80-21 x MACS 58 and PK 564 x PK 472 and could be further exploited. These crosses involved geographically diverse parents and at least on parent of high General Combining Ability (GCA) effects in combination of high x high, high x average and high x low. Therefore, these crosses could throw transgressive segregants in still advance generations. Future, the results of present study suggested that heterosis coupled with high SCA effects might be considered as a criteria for selecting crosses for further improvement with respect to quality traits.

Key Words: Heterosis, Combining Ability, *Glycine max* (L.) Merrill, Line x Tester

Introduction

Soybean regarded as "Wonder crop" is the richest, cheapest and easiest source of best quality proteins and fats. It contains 40-44 per cent protein with high biological value and 20-22 per cent oil and shares about 10-11 per cent of the domestic edible oil need of the country. The protein component is rich in essential amino acid lysine and used to supplement other cereals foods. It can play a vital role in meeting the acute problem of malnutrition in developing countries. Natural soybean oil is highly unsaturated and contains 7 per cent of omega 3 (alfa linolenic) fatty acid which is beneficial in the diet for the cardio-vascular health of human beings.

To develop elite and better nutritional quality varieties such cultivars a systematic approach has to be adopted. Protein and oil are polygenic characters and their improvement is basically based upon identification and selection of superior parents or lines, which can be effectively used for developing superior quality genotypes for breeding programme. Combining ability studies are regarded useful in assessing the relative nicking ability of parents, which on crossing would produce more desirable segregants and elucidate the nature and magnitude of gene action involved. The study becomes much more reliable if a good degree of correspondence is observed between various genetic estimates over filial generations.

Further, extent of heterosis will have direct effect on breeding methodology in varietal improvement programmes. Therefore, keeping aforesaid considerations in view, present study was undertaken in soybean to evaluate, identification and selection of better nutritional quality genotypes.

Materials and Methods

Experimental material consisted of F_1, F_2, and F_3 generations of 45 crosses derived from crossing of 15 soybean lines with 3 testers. The parents were selected on the basis of diverse pedigree, growth habit, geographical origin and adaptation. The experimental material including parents, F_{1S}, F_{2S} and F_{3S} were planted in randomized block design with 3 replications under rainfed conditions at the Instructional Farm, Rajasthan College of Agriculture, Udaipur during *Kharif*, 2001. One row of 3 m of parents and F_{1S} while 3 rows each of F_2 and F_3 generations were planted. Seeds were dibbled at the spacing of 45 cm x 10 cm row to row and plant to plant. Bulk seed of 10 randomly selected competitive plants of parents and F_{1S}, where as 20 plants in F_2 and F_3 generations in each replication was used for analysis of seed oil and protein content. Oil content was estimated by Soxhlet extraction while Nitrogen content in seed sample was analysed by micro–Kjeldhal's method. The average N per cent value was multiplied by the protein conversion factor 5.71 for soybean to give the per cent crude protein for each entry. Different types of heterosis viz., heterosis over mid parent, heterobeltiosis over better parent, economic heterosis over standard check (JS-335) as well as inbreeding depression

in F_2 and F_3 generations were estimated using mean values. Analysis of line x tester data for combining ability was done according to Kempthorne (1957) and Arunachalam (1974).

Results and Discussion

Analysis of variance was carried out for tester, lines and their crosses in 3 generations and that revealed highly significant differences for all the lines and crosses indicating sufficient variation in the material for both oil and protein content. However, mean squares due to testers were significant for only protein content. The study for mean and range revealed that among parents there was great variability in the lines than testers for both the characters. Among generations F_{1S} showed superiority than their parents, F_2 and F_3 generations as F_{1S} exhibited higher mean values and wide range of variation for both the characters. It was reflected that the hybrids superior in F_1 involved both or at least one parent of high *per se* performance. Almost these hybrids showed consistent performance in their subsequent generations for all the characters studied. However, a considerable decrease from F_1 to F_2 and F_2 to F_3 generations for both oil and protein content was noticed.

Among the parents JS 71-05 for both oil and protein, RAUS 97-1 for oil and MACS 58 for protein content appeared promising. Crosses JS 79-81 x MACS 58, JS 80-21 x MACS 58, PK 564 x PK 472 and JS 71-05 x PK 472 turned out to be superior for both oil and protein content over the generations. These crosses also involved one of the parents as high performer.

In heterosis studies for oil content no cross combination showed significant positive heterosis and heterobeltiosis (Table 1). However, 5 and 2 crosses were positive but insignificant for heterosis and heterobeltiosis, respectively. On the other hand, undesirable negative significant heterosis also found in 5 crosses. These findings suggested the importance of additive gene effects. Moreover, desirable economic heterosis over standard check JS 335 was reported in 13 crosses and ranged in between 4.43 to 23.33 per cent. Maximum economic heterosis was recorded for RAUS 97-1 x NRC-12 followed by JS 79-81 x MACS 58, JS 71-05 x MACS 58, JS 71-05 x PK 472 and JS 71-05 x MACS 58. Considerable inbreeding depression was expressed by 23 crosses in F_2 and 3 crosses in F_3 generation. Similar to the present study Nelson and Bernard (1984) and Chen (1987) also reported insignificant heterosis while Sabbouh *et al.* (1998) recorded significant heterobeltiosis for seed oil content.

Incase of seed protein content 4 crosses viz., JS 79-81 x MACS 58, RAUS 97-1 x PK 472, PK 564 x PK 472 and JS 80-21 x MACS 58 showed significant positive heterosis and heterosis ranged from – 5.20 to 5.62 pre cent (Table 1). Among these crosses JS 80-21 x MACS 58 also exhibited significant economic heterosis. Gadag and Upadhyaya (1995) and Sabbouh *et al*. (1998) also observed significant positive heterosis for protein content. However, 13 crosses showed desirable positive but insignificant heterobeltiosis. Significant positive inbreeding depression was recorded in 22 crosses in F_2 and 3 crosses in F_3 generations.

Based on heterosis study, crosses JS 79-81 x MACS 58 and PK 564 x PK 472 appeared superior for both oil and protein content (Table 1). While RAUS 97-1 x NRC 12 for oil and JS 80-21 x MACS 58 and RAUS 97-1 x PK 472 superior for protein content.

In autogamous crops like soybean, combining ability provides required information about the nature and magnitude of genetic variation along with nicking ability of genotypes. Over and above, the study become much more precise and reliable if the relative combining ability is analyzed in F_1, F_2, and F_3 generations so as to obtained a good degree of correspondence between these estimates which will help in identifying superior parents and crosses that could be effectively utilized in breeding progamme. Such study may also reflect the possibility of obtaining rare favourable combinations of characters in segregating generations.

Analysis of variance for combining ability for both the quality traits indicated that variance due to crosses, lines and line x tester interaction were significant for seed oil and protein content in all the 3 generations. While variance due to testers was significant for oil content in F_3 and protein content in F_1 and F_2 generations. Significance of lines and testers indicated higher contribution towards general combining ability, while for lines x tester interaction towards specific combining ability for both the characters. Predominance of estimated component of Specific Combining Ability (SCA) variance over General Combining Ability (GCA) indicated importance of non-additive genetic effects for seed protein and oil content. Contribution of lines was higher for oil content in F_1 and F_3 and for protein content in F_1 generation. Whereas higher contribution due to interaction between line and tester was for oil content in F_2 and for protein content in F_2 and F_3 generations.

Among the parents lines JS 71-05, PK 564 and JS 79-81 recorded positive significant GCA effects in all

Table 1. Estimation of heterosis (MP), heterobeltiosis (BP), economic heterosis (EP) and inbreeding depression for seed oil and protein content in soybean

S.No.	Cross	Seed oil content (%)					Seed protein content (%)				
		MP	BP	EP	IDF_2	IDF_3	MP	BP	EP	IDF_2	IDF_3
1.	Bragg x PK 472	–1.50	–	4.96	9.29	0.62	–2.03	–	–	2.98	2.14
2.	JS 79–81 x PK 472	0.74	0.00	18.02	–0.65	0.05	2.41	–	–	3.68	1.33
3.	RAUS 97–1 x PK 472	–3.37	–	17.84*	5.41	1.48	4.36*	2.58	1.31	10.43**	–0.72
4.	Pusa 24 x PK 472	–1.69	–	12.92	9.14	0.98	0.55	0.46	–	3.58*	0.92
5.	PK 416 x PK 472	–2.14	–	16.07	6.36	–0.24	0.29	0.23	–	2.85	–0.73
6.	PK 564 x PK 472	6.26	2.35	20.79*	3.62	–2.13	3.48*	2.56	3.13	2.27*	0.05
7.	JS 71–05 x PK 472	1.35	–	22.33*	5.84	–2.46	2.77	1.47	2.82	2.48**	–0.63
8.	Pusa 20 x PK 472	–1.15	–	11.87	11.83	1.14	0.96	–	–	1.58	3.54
9.	MACS 57 x PK 472	–7.84	–	7.21	–1.60	18.98*	0.38	–	–	2.28	–0.29
10.	Monetta x PK 472	–3.85	–	8.45	9.69	–1.33	1.34	0.61	–	1.95	0.10
11.	JS 80–21 x PK 472	–3.89	–	8.09	15.57*	–19.09	0.43	–	0.23	2.52*	0.21
12.	Pusa 40 x PK 472	–12.44*	–	6.20	9.51	5.29	3.72	0.33	–	3.05	1.81
13.	PK 471 x PK 472	5.19	–	13.70	12.00*	–2.07	2.22	1.43	1.74	–0.32	1.63
14.	Pusa 16 x PK 472	0.13	–	16.95*	6.52	15.45*	1.70	0.08	–	3.65	–0.87
15.	NRC 2 x PK 472	–4.69	–	14.71	10.92*	0.75	–3.97**	–	–	2.66*	–0.06
16.	Bragg x MACS 58	4.09	–	10.45	12.03	2.25	1.00	–	1.84	–0.05	1.98
17.	JS 79–81 x MACS 58	5.27	4.89	22.86*	7.21**	–2.23	5.62**	1.41	3.33	2.83**	0.70
18.	RAUS 97–1 MACS 58	–3.21	–	17.60*	5.98	13.84	–0.66	–	–	5.69*	–1.72
19.	Pusa 24 MACS 58	–2.79	–	11.22	10.62**	–0.06	0.21	–	0.45	2.53*	6.58**
20.	PK 416 x MACS 58	–7.82*	–	8.92	8.35*	0.71	0.21	–	0.61	1.53*	–0.46
21.	PK 564 x MACS 58	3.03	–	16.66*	2.73*	1.98	–0.41	–	0.81	2.15	–0.69
22.	JS 71–05 x MACS 58	0.88	–	21.32*	8.47**	–3.09*	–1.03	–	0.56	1.26	0.03
23.	Pusa 20 x MACS 58	1.55	–	14.47	11.76*	–2.63	0.12	–	–	–0.98	0.03
24.	MACS 57 x MACS 58	0.31	–	16.24	17.78**	–14.22*	–0.10	–	0.63	1.65	6.24**
25.	Monetta x MACS 58	3.10	–	15.83	21.98**	1.31	0.73	–	0.35	8.87**	–2.34
26.	JS 80–21 x MACS 58	–2.45	–	9.27	–6.11	0.31	2.49*	1.95	3.88*	2.52	6.62*
27.	Pusa 40 x MACS 58	–11.00**	–	7.56	14.83*	–1.48	–5.12*	–	–	2.22	0.70
28.	PK 471 x MACS 58	–2.33	–	5.14	–0.45	–0.56	0.04	–	1.13	11.84**	–12.70*
29.	Pusa 16 x MACS 58	–2.54	–	13.41	9.43*	2.53	0.22	–	–	3.13	–0.42
30.	NRC 2 x MACS 58	–12.91**	–	4.43	7.69	0.86	2.14	–	–	2.13	–0.41
31.	Bragg x NRC 12	4.67	–	10.87	12.68	–13.97	1.24	0.18	–	1.51	–0.51
32.	JS 79–81 x NRC 12	–0.44	–	16.01	7.84**	0.17	–3.33	–	–	5.94**	–4.84**
33.	RAUS 97–1 x NRC 12	1.66	–	23.33*	21.41**	1.28	–0.20	–	–	5.31*	–7.85*
34.	Pusa 24 x NRC 12	–5.11*	–	8.39	10.03	–16.23	0.13	–	–	3.23**	–0.48
35.	PK 416 x NRC 12	–0.47	–	17.42*	3.67	1.98	0.64	0.03	–	4.05**	1.75
36.	PK 564 x NRC 12	2.15	–	15.48	9.00**	–3.43	0.28	–	–	1.88*	–0.80
37.	JS 71–05 x NRC 12	–2.94	–	16.54*	1.57	–3.96*	0.16	–	–	2.61*	–0.26
38.	Pusa 20 x NRC 12	1.82	–	14.59	11.13**	–3.48	–0.18	–	–	4.60*	1.97
39.	MACS 57 x NRC 12	–0.09	–	15.59	10.22**	–3.45	0.55	–	–	2.75	2.30
40.	Monetta x NRC 12	2.85	–	15.36	9.47**	–1.41	–1.10	–	–	3.84	–6.88**
41.	JS 80–21 x NRC 12	1.62	–	13.64	11.69**	–1.41	0.72	–	–	11.37**	–1.99
42.	Pusa 40 x NRC 12	–1.61	–	18.72*	4.98	14.82**	0.33	–	–	–4.79*	–0.76
43.	PK 471 x NRC 12	4.32	–	12.11	9.54*	–2.80	0.31	–	–	3.76	0.69
44.	Pusa 16 x NRC 12	–0.40	–	15.71	9.90**	–1.36	0.44	–	–	–1.09	–0.98
45.	NRC 2 x NRC 12	–1.72	–	17.66*	4.67*	–1.19	0.48	–	–	9.68**	–5.40**
	Range	–12.44	2.35	4.43	–611	–19.09	–5.12	0.03	0.23	–4.79	–12.70
		–	–	–	–	–	–	–	–	–	–
		12.91	4.89	23.33	21.98	18.98	5.62	2.58	3.88	11.84	6.62
	Check JS 335	–	–	16.93	–	–	–	–	39.67	–	–

*, ** Significant at 5 % and 1% levels, respectively.

the 3 generations for seed oil content. While for seed protein content PK 564 and JS 71-05 could be considered superior as these exhibited high GCA effects in all the 3 generations (Table 2). The *per se* performance of most of the parent was moderate to high for seed oil content and seed protein content.

Among the hybrids, positive significant SCA effects for seed oil content were exhibited by JS 80-21 x MACS 58 and Pusa 40 x NRC 12 in F_2 and RAUS 97-1 x PK 472 and MACS 57 x MACS 58 in F3 generation. On the other hand for seed protein content many crosses showed significantly high SCA effects. JS 79-81 x MACS 58 showed desirable SCA effects in all the 3 generations. While Pusa 40 x NRC 12 and NRC 2 x MACS 58 depicted high SCA effects in F_2 and F_3 generations (Table 3). Among these hybrids most of them had high *per se* and involving good general combiner parents, hence, could be used effectively in quality improvement of soybean.

Therefore on the basis of combining ability effects, crosses Pusa 40 x NRC 12 and JS 80-21 x MACS 58 appeared promising for both seed oil and protein content. While RAUS 97-1 x PK 472 and JS 79-81 x MACS 58 were good specific combiner for oil and protein content, respectively.

Similar to present findings Mc Kendry *et al*. (1985) and Gadag *et al.* (1999) also reported importance of non-additive gene effects for protein content. On the contrary, Zhu *et al.* (1994) and Sabbouh *et al*. (1998) noted significant GCA and additive effects for protein content in soybean.

In case of oil content, as per present study Sharma *et al.* (1997) and Sabbouh *et al.* (1998) recorded partial dominance and non-additive gene action and Raut *et al.* (2000) reported dominance gene effects in 2 crosses for seed oil content in soybean. Contrary to this, significant additive gene action was reported by Zhu *et al*. (1994) for oil content.

To conclude, combining ability mean squares estimated over each generation reveled that both the quality traits displayed preponderance of non-additive gene effects. Further, a high degree of correspondence between combining ability (GCA and SCA) from F_1 to F_3 generation for both the characters was noticed, which

Table 2. General Combining Ability (GCA) effects for quality characters in F_1, F_2 and F_3 generations in soybean

S.No.	Genotype	Seed oil content (%)			Seed protein content (%)		
		F_1	F_2	F_3	F_1	F_2	F_3
1.	PK 472	–0.10	0.11	–0.17	0.13	0.22	–0.06
2.	MACS 58	–0.15	–0.21	–0.26	0.42**	0.45**	0.23
3.	NRC 12	0.25	0.10	0.43*	–0.55**	–0.67**	–0.17
4.	Bragg	–0.88**	–1.32**	–0.75*	0.29	1.00**	0.47
5.	JS 79–81	0.85**	1.53**	1.62**	–0.31	–0.62	–0.39
6.	RAUS 97–1	0.96**	0.36	–0.71	–0.16	–1.68**	–0.50
7.	Pusa 24	–0.52	–0.74*	0.06	0.15	0.21	–0.77*
8.	PK 416	0.03	0.51	0.32	0.24	0.42	0.29
9.	PK 564	0.63*	1.26**	1.44**	0.86**	1.30**	1.42**
10.	JS 71–05	1.04**	1.60**	2.17**	0.82**	1.26**	1.31**
11.	Pusa 20	–0.05	–0.63	–0.38	–0.86**	–0.23	–0.98**
12.	MACS 57	–0.16	–0.25	–0.48	0.33	0.74*	–0.40
13.	Monetta	–0.12	–1.12**	–1.07**	–0.09	–0.72*	0.32
14.	JS 80–21	–0.61*	–0.29	0.72	0.96**	0.06	–0.68*
15.	Pusa 40	–0.53	–0.68	–1.87**	–1.36**	–0.14	–0.42
16.	PK 471	–0.61*	–0.31	–0.04	0.71*	–0.04	1.08**
17.	Pusa 16	0.24	0.21	–0.85*	–0.26	0.28	0.51
18.	NRC 2	–0.28	–0.11	–0.16	–1.32**	–1.86**	–1.25**
	Standard Error						
	GCA_{Ti}	0.15	0.19	0.19	0.14	0.16	0.16
	GCA_{Lj}	0.30	0.37	0.38	0.28	0.32	0.31
	$GCA_{Ti–j}$	0.18	0.23	0.23	0.17	0.20	0.19
	$GCA_{Li–j}$	0.41	0.51	0.52	0.38	0.44	0.43
	$GCA_{Ti–Lj}$	0.32	0.39	0.40	0.30	0.34	0.33

*, ** Significant at 5 % and 1% levels, respectively.

Table 3. Specific Combining Ability (SPA) effects for yield characters in F_1, F_2 and F_3 generations in soybean

S.No.	Cross	Seed oil content (%)			Seed protein content (%)		
		F_1	F_2	F_3	F_1	F_2	F_3
1.	Bragg x PK 472	-0.54	-0.31	-0.73	-1.10	-1.76**	-1.81**
2.	JS 79-81 x PK 472	-0.06	0.83	0.97	0.04	0.10	-0.41
3.	RAUS 97-1 x PK 472	-0.20	0.76	1.79*	0.96	-0.51	-1.21
4.	Pusa 24 x PK 472	0.45	0.36	-0.37	-0.17	-0.44	0.40
5.	PK 416 x PK 472	0.43	0.14	0.62	-0.30	-0.41	0.22
6.	PK 564 x PK 472	0.63	0.70	1.18	0.67	0.49	0.57
7.	JS 71-05 x PK 472	0.48	0.15	0.30	0.58	0.33	0.75
8.	Pusa 20 x PK 472	-0.20	-0.42	-0.62	-0.02	-0.06	-0.43
9.	MACS 57 x PK 472	-0.88	0.94	-2.09**	-0.23	-0.34	1.13
10.	Monetta x PK 472	-0.71	-0.05	0.36	0.12	1.19	0.32
11.	JS 80-21 x PK 472	-0.28	-2.01**	0.17	-0.58	0.51	1.39*
12.	Pusa 40 x PK 472	-0.68	-0.80	-0.22	1.29*	0.06	-0.13
13.	PK 471 x PK 472	0.67	-0.50	-0.18	0.27	2.34**	0.78
14.	Pusa 16 x PK 472	0.37	0.55	-1.01	0.08	-0.69	-0.37
15.	NRC 2 x PK 472	0.51	-0.34	-0.18	-1.61**	-0.84	-1.21
16.	Bragg x MACS 58	0.44	0.34	-0.59	0.44	1.00	0.89
17.	JS 79-81 x MACS 58	0.81	0.34	0.69	1.64**	2.04**	1.68**
18.	RAUS 97-1 MACS 58	-0.18	0.93	-0.58	-0.64	-0.07	-0.47
19.	Pusa 24 MACS 58	0.22	0.14	-0.64	0.04	0.22	-1.20
20.	PK 416 x MACS 58	-0.73	-1.04	-0.96	0.00	0.47	0.93
21.	PK 564 x MACS 58	-0.01	0.52	-0.03	-0.54	-0.59	-0.28
22.	JS 71-05 x MACS 58	0.37	-0.23	-0.21	-0.60	-0.29	-0.19
23.	Pusa 20 x MACS 58	0.29	0.30	0.51	0.00	1.00	1.90**
24.	MACS 57 x MACS 58	0.70	-1.01	1.54*	-0.08	0.11	-1.05
25.	Monetta x MACS 58	0.60	-1.01	-1.25	0.23	-1.41*	-1.45*
26.	JS 80-21 x MACS 58	-0.03	2.48**	1.43	0.58	1.69**	-0.07
27.	Pusa 40 x MACS 58	-0.40	-1.24	0.19	-1.76**	-2.53**	-2.35**
28.	PK 471 x MACS 58	-0.72	0.76	0.60	-0.25	-3.00**	0.52
29.	Pusa 16 x MACS 58	-0.18	-0.25	0.38	-0.15	-0.67	-0.58
30.	NRC 2 x MACS 58	-1.17	-1.01	-1.08	1.06	2.01**	1.72**
31.	Bragg x NRC 12	0.10	-0.03	1.32	0.66	0.75	0.92
32.	JS 79-81 x NRC 12	-0.75	-1.17	-1.66*	-1.68**	-2.14**	-1.27*
33.	RAUS 97-1 x NRC 12	0.38	-1.69*	-1.21	-0.32	0.58	1.67**
34.	Pusa 24 x NRC 12	-0.67	-0.49	1.01	0.13	0.22	0.81
35.	PK 416 x NRC 12	0.30	0.90	0.34	0.30	-0.06	-1.16
36.	PK 564 x NRC 12	-0.62	-1.21	-1.15	-0.13	0.09	-0.28
37.	JS 71-05 x NRC 12	-0.85	0.08	-0.09	0.01	-0.05	-0.56
38.	Pusa 20 x NRC 12	-0.09	0.13	0.11	0.02	-0.95	-1.47*
39.	MACS 57 x NRC 12	0.18	0.07	0.55	0.31	0.23	-0.08
40.	Monetta x NRC 12	0.11	1.06	0.89	-0.35	0.22	1.14
41.	JS 80-21 x NRC 12	0.31	-0.47	-1.60*	-0.00	-2.21**	-1.33*
42.	Pusa 40 x NRC 12	1.08	2.04**	0.03	0.47	2.47**	2.48**
43.	PK 471 x NRC 12	0.05	-0.26	-0.42	-0.02	0.66	-1.29*
44.	Pusa 16 x NRC 12	-0.19	-0.30	0.63	0.07	1.35*	0.94
45.	NRC 2 x NRC 12	0.66	1.35	1.26	0.55	-1.18	-0.50
	Standard Error:						
	SCA_{ij}	0.60	0.74	0.76	0.56	0.64	0.62
	SCA_{Ti-Tj}	0.74	0.91	0.93	0.69	0.78	0.76
	SCA_{iL-jL}	0.82	1.02	1.04	0.77	0.87	0.85
	SCA_{ij-kl}	0.84	1.04	1.07	0.79	0.90	0.87

*,**Significantat5%and1%levels,respectively

reflected the reliability and consistency of results obtained with respect to nature of inheritance.

Often the unfavorable association between protein and yield generally met with are due to tight linkages, which could be broken by raising a large population. In the present study JS 79-81 x MACS 58 revealed superiority for yield as well as protein content might be considered a new favorable combination resulted due to breaking of tight linkages. Simultaneous improvement of protein content and grain yield has been achieved in wheat (Sears *et al*., 1991) and rice (Loffier *et al*., 1993). Through the use of recurrent selection suggested that such negative relationship may be caused by linkage and improvements can be made for such traits by enforcing simultaneous selection in large segregation population.

Based on various estimates viz., mean performance, heterosis and combining ability the best soybean parents and crosses for quality traits were identified (Table 4). For both seed oil content and protein content, high heterosis and positive SCA effects were recorded in crosses Pusa 40 x NRC 12, JS 79-81 x MACS 58, JS 80-21 x MACS 58 and PK 564 x PK 472 and could be further exploited. These crosses involved geographically diverse parents and at least on parent of high GCA effects in combination of high x high, high x average and high x low.

Majority of soybean breeding work is based on pedigree method, which exploits the fixable additive type of gene effects. However, this alone may be inadequate in view of the large non-additive component for both quality traits. Further, high heterosis for oil and protein

Table 4. Best parents and crosses selected on the basis of their per se performance, GCA effects, SCA effects and heterotic response for seed oil and protein content in soybean

Characters		Seed oil content	Seed protein content
Best parents *per se*		RAUS 97-1, Pusa 40, JS 71-05, NRC 2, PK 416	MACS 58, JS 71-05, JS 80-21, PK 564, PK 471
Best crosses *per se*	F_1	RAUS 97-1 x NRC 12, JS 79-81 x MACS 58, JS 71-05 x PK 472, JS 71-05 x MACS 58, PK 564 x PK 472	JS 80-21 x MACS 58, JS 79-81 x MACS 58, PK 564 x PK 472, JS 71-05 x PK 472, Bragg x MACS 58
	F_2	JS 79-81 x PK 472, PK 564 x PK 472, JS 80-21 x MACS 58, JS 71-05 x PK 472, JS 79-81 x MACS 58	PK 471 x PK 472, Bragg x MACS 58, JS 80-21 x MACS 58, PK 564 x PK 472, JS 79-81 x MACS 58
	F_3	JS 71-05 x NRC 12, PK 564 x PK 472, JS 79-81 x PK 472, JS 71-05 x PK 472, JS 79-81 x MACS 58	JS 71-05 x PK 472, PK 564 x PK 472, Pusa 40 x NRC 12, PK 471 x MACS 58, PK 471 x PK 472
Best heterotic Crosses		RAUS 97-1 x NRC 12, JS 79-81 x MACS 58, JS 71-05 x PK 472, JS 71-05 x MACS 58, PK 564 x PK 472	JS 80-21 x MACS 58, JS 79-81 x MACS 58, RAUS 97-1 x PK 472, PK 564 x PK 472, JS 71-05 x PK 472
Best GCA parents ($F_1/F_2/F_3$)		JS 71-05, PK 564, JS 79-81, RAUS 97-1, NRC 12	PK 564, JS 71-05, PK 471, MACS 58, JS 80-21
	F_1	Pusa 40 x NRC 12, JS 79-81 x MACS 58, MACS 57 x MACS 58, PK 471 x PK 472,	JS 79-81 x MACS 58, Pusa 40 x PK 472,
Best SCA Crosses		NRC 2 x NRC 12	RAUS 97-1 x PK 472, PK 564 x PK 472, Bragg x NRC 12
	F_2	JS 80-21 x MACS 58, Pusa 40 x NRC 12, NRC 2 x NRC 12, Monetta x NRC 12, MACS 57 x PK 472	Pusa 40 x NRC 12, PK 471 x PK 472, JS 79-81 x MACS 58, NRC 2 x MACS 58, JS 80-21 x MACS 58
	F_3	RAUS 97-1 x PK 472, MACS 57 x MACS 58, JS 80-21 x MACS 58, Bragg x NRC 12, NRC 2 x NRC 12	Pusa 40 x NRC 12, Pusa 20 x MACS 58, NRC 2 x MACS 58, JS 79-81 x MACS 58, RAUS 97-1 x NRC 12
Common crosses in SCA and heterosis with high cross *per se*	F_1	JS 79-81 x MACS 58	JS 79-81 x MACS 58, PK 564 x PK 472
	F_2	--	JS 80-21 x MACS 58 JS 79-81 x MACS 58
	F_3	---	---

along with positive SCA effects was observed in these crosses, which might be due to dominance or epistasis. Although heterosis breeding makes maximal use of the non-additive genetic effects appears to be difficult for improving soybean in view of the non availability of mass pollination systems needed for hybrid seed production. Accordingly, the feasible alternative is to consider simultaneous exploitation of both additive and non-additive gene action by adopting recurrent selection procedures. Under similar situation Harer and Deshmukh (1991) recommended biparental mating in soybean followed by recurrent selection. Since crossing is tedious in soybean, genetic male sterility and single seed or single pod descent method could be employed to facilitate recurrent selection schemes (Wilcox, 1998). Therefore, these crosses could throw transgressive segregants in still advance generations. Further, the results of present study suggested that heterosis coupled with high SCA effects might be considered as criteria for selecting cross for further improvement with respect to quality traits.

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Genetic Diversity and Phylogenetic Relationship Among Soybean [*Glycine max* (L.) Merrill] Varieties Based on Protein, Evolutionary and Morphological Markers

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Preliminary biochemical study was carried out to identify 14 soybean [*Glycine max* (L.) Merrill] varieties on the basis of electrophoregrams of soluble seed proteins by Discontinuous Polyacrylamide Slab Gel Electrophoresis method. Genetic diversity among soybean varieties was determined on the basis of their evolutionary, morphological and biochemical markers. Relationship was also established between varietal characters based on aforesaid parameters. In the electrophoretic study clear band patterns were observed for all 14 varieties. All type of protein band intensity i.e. low, medium and high were observed in various soybean varieties. However, in some varieties the quantitatively similar number of total protein bands were noted, but differences in presence and/or absence of particular band at particular position and their Rm values as well as different protein band intensity for common bands showed diverse nature of these varieties to each other. Results revealed that 12 varieties could easily be identified from each other as they showed their own specific characters. The variety PK 327 and JS 79-81 showed genetic diversity for their evolutionary and morphological markers, but at biochemical level they depicted identical protein banding patterns having variation only in band intensity. Such a set of varieties could possibly be discriminated by performing Slab Gel Electrophoresis under denaturing conditions or by PCR-based DNA fingerprinting. These findings could open a scope for further research in the specific area of "Varietal identification". Therefore it is concluded that all 14 soybean varieties studied were genetically diverse and could be used in breeding programme. Hence, the DPAGE technique can be effectively used for varietal identification which is found to be quick, reliable, economical, avoiding field studies.

Key Words: Variety identification, Electrophoresis, Markers, Soybean

Introduction

Variety identification with respect to its genetic purity is important in national and international seed and breeding programmes. Different cultivars are commonly identified on the basis of taxonomic differences of seed, seedling and mature plants. Distinguishing varieties on the basis of morphological characters of plants in field and seed morphology is not always possible, though it is undoubtedly, one of the most commonly used criterion. Further, parameters are highly susceptible to environmental, physiological and ecological conditions. Therefore, precise characterization of varieties should be done at both levels, viz. morphological as well as biochemical levels (McDonald, 1997). Proteins being the direct gene products, reflect the genomic composition of varieties accurately and therefore, are ideal for genotypic distinctness. Biochemical approaches like gel electrophoresis of proteins and isoenzymes are powerful tools to distinguish varieties. Seed proteins are known to controlled by multigene families (Lumen, 1990). Deletion or mutation in these structural genes or their regulatory loci results in the inhibition of transcription or translation of polypeptides and may lead to failure of protein expression (Brown *et al.*, 1981). Expression of these proteins is governed monogenically, presence being completely dominant over absence. Polypeptides varying for presence or absence could be used as markers (Naik, 1998). In the present investigation genetic diversity among soybean varieties was determined on the basis of their evolutionary, morphological and protein markers. Attempts were also made to establish the relationship between varietal characters on the basis of morphological characters and biochemical profile analysed through Discontinuous Polyacrylamide Slab Gel Electrophoresis (DPAGE) method by Davis (1964).

Materials and Methods

Healthy seeds of 14 soybean varieties namely JS 335, MACS 57, Monetta, NRC12, PK 416, PK 564, Pusa 20, Pusa 24, PK 327, JS 79-81, RAUS 97-1, Pusa 22, Pusa 20 and PK 471 were procured from soybean breeder and field experiment was conducted at Instructional Farm,

Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur. Each variety was planted in one row of 3 m length in 3 replications and seeds were dibbled at the spacing of 45 cm x 10 cm row to row and plant to plant. Observations for quantitative characters were recorded on 10 randomly selected competitive plants. Seed protein content was estimated as per standard micro–Kjeldhal method.

The experiment for identification of soybean varieties on the basis of electrophoregrams of soluble seed protein was carried out at Biochemistry and Plant Physiology Laboratory, Seed Technology Research, Rajasthan Agricultural University, Agricultural Research Station, Durgapura, Jaipur. Seeds of each variety were crushed and powdered using pestle and mortar. Seed powder (0.5 g) was vigorously mixed in ethylacetate (5 ml) for 20 minutes with the simultaneous addition of sodium sulphite (1 mg) and sodium metabisulphite (1 mg) and centrifuged at 5000 RPM for 10 minutes. The ethylacetate is decanted off and residue was treated with CMA solution (Chloroform : Methanol: Acetone, 2:1:1, v/v/v, respectively) for 20 minutes with vortexing and then solution was decanted off. The treatment was repeated one more time as above and centrifuged at 5000 RPM for 10 minutes. The final residue was kept in suitable volume (1 ml) of extraction buffer (0.1 M Tris-HCl buffer pH 7.5) for 18 hours in cold. Contents were then centrifuged at 10,000 RPM for 15 minutes. The clear supernatant was used as protein sample for electrophoretic analysis. During protein extraction, treatments with ethylacetate and CMA solution removed most of the lipids, as presence of lipids interferes during isolation of proteins (Stegemann and Pietsch, 1983). To prevent auto-oxidation of phenols, sodium sulphite and sodium metabisulphite were added. The loss of proteins by above treatment was negligible. Discontinuous Polyacrylamide Slab Gel Elctrophoresis (DPAGE) was carried out according to standard method (Davis, 1964) using 12% acrylamide separating gel (0.5 M Tris-HCl buffer pH 8.8) with a top layer of 6% acrylamide stacking gel (0.5 M Tris-HCl buffer pH 6.8). The standardized volume of protein sample (40 µl) was loded on slab gel wells. Electrophoresis was conducted at a constant current of 36 mA for 45 minutes and then raised to 58 mA until the tracking dye (bromophenol blue) migrated to the anode end of the slab gel. The staining was done for 2 hours in coomassie brilliant blue R-250 (CBBR) solution (0.5 g CBBR dye was dissolved in 250 ml methanol, 10 ml acetic acid and 240 ml water). The gels were destained by repeated washing with methanol : acetic acid : water (50:70:880, v/v/v, respectively). The protein bands were numbered from cathode end and their relative mobilities (Rm) were calculated.

Results and Discussion

Analysis of seed proteins using electrophoresis (PAGE) has been employed for identification of varieties and elucidation of evaluation and phylogenetic relationship in soybean viz. Hilty and Schmitthenner (1966), Larson (1967), Wagner and McDonald (1982), Cardy and Bevers darg (1984), Kumar and Ram (1989), McDonald (1982), Goyal and Sharma (1988) and Anonymous (2003).

The protein banding pattern of all 14 soybean varieties were compared and are shown in Figure 1 and 2 and

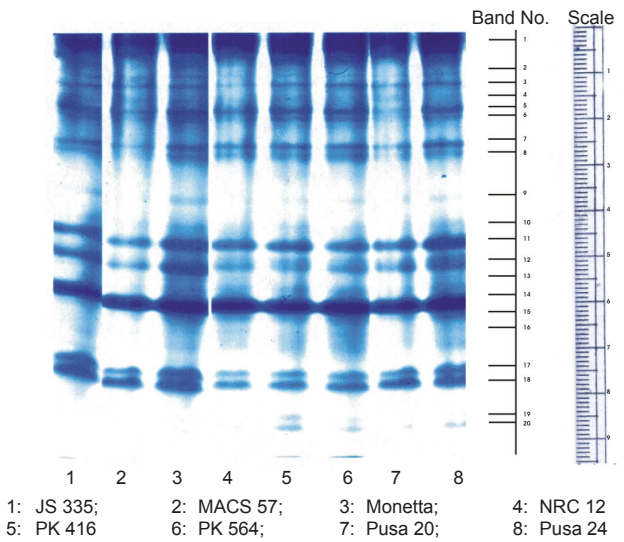

Fig. 1: Protein banding patterns of soybean varieties

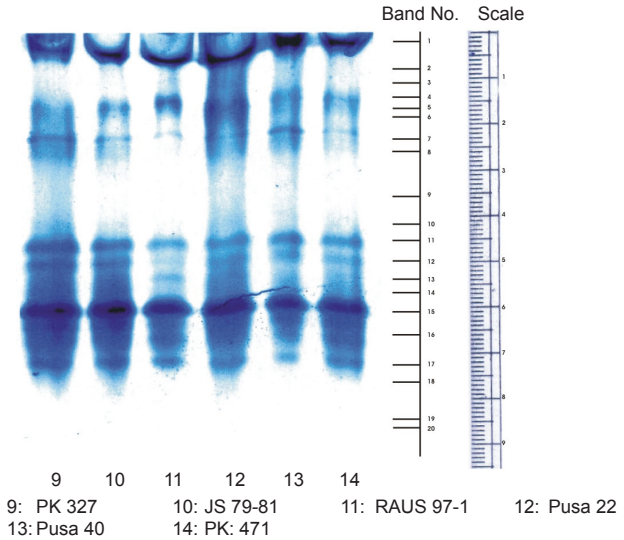

Fig. 2: Protein banding patterns of soybean varieties

results are presented in Table 1 and 2. The inter-varietal differences were clearly expressed in these patterns. Rm values ranged from 0.021 to 0.920 and indicated different mobility pattern thereby suggesting wider range of variability in protein band expression. In all 20 protein bands of different Rm values were identified on the basis of electrophoretic mobility among 14 soybean varieties being maximum (17) in PK 416 and minimum (7) in PK 327 and JS 79-81 (Table 2). Sampat (1981) also reported 18-25 protein bands in different Vigna species, while total 15 protein bands in 8 soybean [*Glycine max* (L.) Merril] varieties were also observed by Goyal and Sharma (1998). The similarity in certain protein bands among varieties as observed from the Table 2 were noted and this might be due to genetic relationship among them as also reported by Goyal *et al.* (1998) in cotton (*Gossypium herbaceum*), Singh *et al.* (2002) in *Catharanthus rosesus* and Goyal and Sharma (2003) in cluster bean. On the basis of protein electrophoregram pattern, it was observed that protein band No. 2, 3, 4, 5, 6, 8, 9, 10, 13, 14, 15 and 18 were useful for discriminating varieties as they showed variation in their expression. This indicated distinct variations among the soybean varieties at biochemical level used in the study, further substantiated the evolutionary and morphological diversity (Table 1). The presence and absence of these bands could help in determination of inter-varietal differences as reported by Chand and Kole (2002) in mungbean (*Vigna radiata*).

On the other hand protein band No. 16 was distinctly present in only 2 varieties, namely, RAUS 97-1 and PK 471, while band No. 10 was found in Monetta, PK 416 and Pusa 24 (Table 2). The specific presence of these 2 bands in aforesaid varieties showed their specific identity which also reflected from their evolutionary as well as morphological markers (Table 1). It was noticed that protein band No.1, 7, 11, 12 and 17 were observed to be universally present in all 14 varieties studied indicated the genes controlling the expression of these protein bands appeared to behave a single block as also revealed by Padmavathi *et al*. (1999) in rice (*Oryza sativa*) . The protein band No. 19 and 20 were only present in 3 varieties, viz., PK 416, PK 564 and Pusa 24. For PK 416 and PK 564 this might be because of their common geographical origin and over and above on account of 2 common parents in their pedigree. However, the protein band intensity of these 2 bands was categorized as low and these bands were missing in rest all 11 varieties. Possibly, the genes controlling the expression of these bands might be linked. This assumption could, however, be verified through linkage analysis using segregating populations as also reported by Padmavathi *et al.* (1999) in rice (*Oryza sativa*).

Multigene inheritance of seed protein expression could be identified from electrophoregram. Multigene inheritance of seed protein expression is well established in other crops (Lumen, 1990). Seed protein expression is known to be under monogenic control with co-dominance of alleles of diverse molecular weight variants and dominance of the presence over absence. The association of protein bands with agrobotanic characteristics has previously been reported. Whereas Larson (1967) observed genotypes with a particular banding pattern to have linkage with hilum colour in soybean.

Polyacrylamide gel electrophoresis in different soybean varieties belonging to same geographical origin revealed variation in number, width, relative mobility and intensity of bands. In general, geographical origin does not influence genotype specific seed protein content and its polymorphism as also reported in grass pea (*Lathyrus sativus*) by Roy *et al*. (2001). The study by and large demonstrated genotype – specific protein polymorphism which is not always influenced by geographical origin.

All type of protein band intensity i.e. low, medium and high were observed in various soybean varieties. Most of the soybean varieties expressed their own specific characteristics which differentiate them from other varieties. However, in some varieties the quantitatively similar number of total protein bands were noted, but differences in presence and/or absence of particular band at particular position and their Rm values, as well as different protein band intensity for common bands showed diverse nature of these varieties to each other. Table 2 revealed total 12 protein bands in electrophoregram of variety JS 335 and NRC 12, but band position was found variable. The band No.6 was characteristically present in JS 335 while missing in NRC 12. Similarly band No. 13 was present in NRC 12 and missing in JS 335. Besides this, JS 335 and NRC 12 could be differentiated to each other considerably based on their geographical origin, evolutionary pedigree and morphological traits particularly with respect to growth habit, type, leaf intensity of green colour, seed shape, seed hilum colour and other quantitative characters studied (Table 1).

Electrophoregrams of variety MACS 57, Pusa 22 and PK 471 (Table 2) showed quantitatively equal 11

Table 1. Genetic diversity for evolutionary and morphological markers in different varieties of soybean

Characters	JS 335	MACS 57	Monetta	NRC 12	PK 416	PK 564	Pusa 20	Pusa 24	PK 327	JS7 9-81	RAUS 97-1	Pusa 22	Pusa 40	PK 471
(A) Evolutionary Markers														
Year/ Notification year	1994	1992	1985	1997	1986	1991	1988	1987	1982	1990	1989	1983	1981	1988
Geographical origin	Jabalpur (JNKVV)	Pune (MACS)	Selection from exotic culture	Indore (NRCS)	Pantnagar (GBPUAT)	Pantnagar (GBPUAT)	New Delhi (IARI)	New Delhi (IARI)	Pantnagar (GBPUAT)	Jabalpur (JNKVV)	Kota (ARS,RAU)	New Delhi (IARI)	New Delhi (IARI)	Pantnagar (GBPUAT)
Evolutionary pedigree	JS78-77 x JS 71-05	JS2 x Improved/ Pelicon	PL71608 from Nanking, China	Mutant of Bragg	UPSM 534 x S 38	(UPSM 534 x S-38) x Bragg	Bragg x Lee	Shelby x Bragg	UPSM 82 x Sammens	Bragg x Hara Soya	Punjab 1 x Monetta	Punjab Clark 63	S3 x Lee	Hardee x Punjab 1
Area of adaptation	Central Zone	Maharashtra	Central and Southern Zone	Central Zone	Northern Plain and Hill Zone	Northern Plain Zone	Northern Hill Zone	Northern Plain and Central Zone	Northern Plain and Hill Zone	Central Zone	Central Zone	Northern Plain and Central Hill Zone	Southern Zone	Southern Zone
(B) MORPHOLOGICAL MARKERS														
(I) **Qualitative Characters**														
Growth habit	Semi-determinate	Semi-determinate	Determinate	Determinate	Determinate	Determinate	Semi-determinate	Semi-determinate	Determinate	Determinate	Determinate	Determinate	Determinate	Determinate
Growth type	Semi-erect	Semi-erect	Erect	Erect	Erect	Semi-erect	Semi-erect	Semi-erect	Semi-erect	Erect	Erect	Erect	Erect	Erect
Flower colour	Violet	Violet	Violet	Violet	White	White	White	White	Violet	Violet	Violet	Violet	Violet	White
Leaf intensity of green colour	Dark	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Dark	Medium	Medium	Medium
Seed shape	Spherical flattened	Spherical	Spherical	Spherical	Elongated	Spherical flattened	Spherical	Spherical	Spherical	Spherical	Spherical flattened	Round	Round	Spherical
Seed hilum colour	Black	Brown	Brown	Brown	Black	Brown	Brown	Black	Brown	Brown	Brown	Black	Black	Brown
(II) **Quantitative Characters**														
Days to flowering	38.33	42.00	43.33	39.67	43.67	39.33	44.67	45.33	41.00	44.00	44.33	41.33	46.67	45.33
Days to maturity	96.67	102.00	99.67	97.00	102.33	96.33	101.67	102.00	97.00	101.33	103.33	103.33	106.00	103.67
Plant height (cm)	48.98	48.17	47.67	39.35	52.10	43.85	41.74	51.03	46.25	42.85	45.70	47.10	41.18	40.15
Pod Length (cm)	3.63	3.44	3.48	3.19	3.68	3.70	3.46	3.51	3.55	3.34	3.25	3.58	3.23	3.38
Height of pod insertion (cm)	6.32	6.05	6.88	7.56	6.15	6.05	6.43	7.13	5.64	7.29	6.95	5.71	7.44	6.10
100-seed weight (g)	10.44	9.50	9.61	8.01	10.32	9.50	10.64	11.26	11.83	10.13	9.20	11.95	9.43	8.80
Protein content (%)	39.67	39.49	38.61	38.74	39.22	39.88	37.10	39.10	39.35	37.19	37.83	38.51	36.61	39.78

Table 2. Protein banding patterns of soybean varieties

Protein band No.	Rm value	Varieties (Presence/absence of protein bands and their intensity)													
		JS 335 (12)	MACS 57 (11)	Monetta (15)	NRC 12 (12)	PK 416 (17)	PK 564 (16)	Pusa 20 (13)	Pusa 24 (16)	PK 327 (7)	JS 79–81 (7)	RAUS 97–1 (9)	Pusa 22 (11)	Pusa 40 (8)	PK 471 (11)
1.	0.021	+++	+++	+++	+++	+++	+++	+++	+++	+++	++	++	+++	+++	++
2.	0.085	++	+	++	+	++	++	+	++	–	–	–	+	–	–
3.	0.122	++	++	++	+	++	++	+	++	–	–	–	+	–	–
4.	0.146	–	+	+	–	–	–	+	–	+	++	+++	+++	+	+
5.	0.175	++	++	++	++	++	++	+	++	–	–	–	++	+	+
6.	0.191	+	–	+	–	++	++	–	++	–	–	–	–	–	–
7.	0.252	++	+	++	++	++	+++	+	+++	+++	++	+	+	++	+
8.	0.284	++	–	+++	++	++	+++	+	++	–	–	–	–	–	+
9.	0.382	–	–	++	–	+	+	+	+	–	–	–	–	–	–
10.	0.452	–	–	+	–	+	–	–	+	–	–	–	–	–	–
11.	0.486	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	++	+++	+++	+++
12.	0.537	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+	+++	++	++
13.	0.582	–	–	–	+	+	+	–	–	–	–	+	+	–	+
14.	0.617	+++	+++	+++	+++	+++	+++	+++	+++	–	–	–	–	–	–
15.	0.654	–	–	–	–	–	–	–	–	+++	+++	+++	+++	+++	+++
16.	0.696	–	–	–	–	–	–	–	–	–	–	+	–	–	+
17.	0.781	++	++	++	++	++	++	++	++	+++	+++	+++	+++	+++	+++
18.	0.816	++	++	++	++	++	++	++	++	–	–	–	–	–	–
19.	0.898	–	–	–	–	+	+	–	+	–	–	–	–	–	–
20.	0.920	–	–	–	–	+	+	–	+	–	–	–	–	–	–

+++ : High, ++ : Medium and + : Low intensity. The values in parenthesis indicate the total number of protein bands

protein bands, but diverse banding pattern revealed clear-cut differences among them. For example, band No. 14 and 18 were present in MACS 57 and absent in Pusa 22, whereas band No. 13 present in Pusa 22 and missing in MACS 57. Similarly, presence of band No. 2, 3, 14 and 18 in MACS 57 and band No. 8, 13 and 16 in PK 471 made great variation between them. This genetic diversity was also mirrored in evolutionary and morphological features (Table1) of variety MACS 57 and Pusa 22 (geographical origin, evolutionary pedigree, growth habit, growth type, seed shape, seed hilum colour and protein content) as well as for MACS 57 and PK 471 (geographical origin, evolutionary pedigree, growth habit, growth type, flower colour and other quantitative traits). Total number of protein bands of PK564 were equivalent to that of Pusa 24 but difference in the presence and/or absence of band NO. 10 in Pusa 24 and 13 in PK 564 discriminated them (Table 2). However, variation in intensity of protein bands were also noted for different common bands. This might serve as a representative of evolutionary and morphological diversity in these 2 varieties viz., geographical origin, evolutionary pedigree, growth habit, seed shape, seed hilum colour and other quantitative traits (Table 1).

On the other hand, soybean varieties viz., PK 327 and JS 79-81 displayed a different kind of situation as they had identical banding pattern (Table 2) in their electrophoregrams indicating their high order of closeness in seed protein polymorphism/profile. However, differences were observed in the protein band intensity e.g., band No. 1 and 7 were more intense in PK 327, while band No. 4 was relatively less intense as compared to that of JS 79-81. Such type of close relationships and/or minor variations were also observed by Sasek *et al.* (1995) in barley (*Hordium vulgare*), Kharkwal (1999) in chick pea (*Cicer arietinum*), Roy *et al.* (2001) in grass pea (*Lathyrus sativus*) and Singh *et al.* (2002) in *Cathranthus rosesus*. However, evolutionary and morphological markers indicated great variability in these 2 varieties for geographical origin, evolutionary pedigree, area of adaptation, growth type and other quantitatively governed traits like days to flowering, days to maturity, plant height, 100-seed weight, pod length, height of pod insertion and protein content, hence considered as genetically diverse. But, for clear discrimination between PK 327 and JS 79-81 work on Slab Gel Electrophoresis under denaturing conditions or by PCR based DNA fingerprinting is needed.

These findings could open a scope for further research in the specific area of "Varietal identification". Therefore it is concluded that all 14 soybean varieties studied were genetically diverse and could be used in breeding programme. Hence, the DPAGE technique can be effectively used for varietal identification which is found to be quick, reliable, economical and avoiding the field work.

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Yucca gloriosa L. (Agavaceae) - A Potential Ornamental Plant in India

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Yucca gloriosa L. widely known for its value as ornamental and garden hedge was observed in flowering during 2001 to 2003 in the parts of Delhi and adjoining areas. This species in comparision with other species of the genera was found suitable for plantation on the roadside, road dividers (verge) and landscape in different parts of urban India. Botanical description, ecology, ornamental value and different uses of *Y. gloriosa* have been highlighted.

Key Words: *Yucca gloriosa*, Ornamental, Garden plant, Hedge plant, Botanical description

Introduction

Yucca gloriosa L. an ornamental shrub found growing in some parts of Delhi drew the attention of the authors because of its beautiful showy, greenish-white flowers. Observations of flowering and fruiting were made at different growth period from south and west parts of Delhi during 2001 to 2003. Herbarium specimens and seeds samples were collected and deposited in the National Herbarium of Cultivated Plants (NHCP), National Bureau of Plant Genetic Resources, New Delhi (HS no. 17869, Seed Sample no. 2495). In the present communication the ornamental value of the species (in comparison to other species of the genera) for planting on the roadside, road dividers (verge) and landscape areas in parts of urban India has been discussed.

Yucca species are native to hot and dry parts of Mexico, North America, Central America and the West Indies and introduced in different parts of the world for ornamental value (Ellison, 1995). The genus comprising of 40-50 species are stem-less perennial growing to the stature of small trees. Four species are recorded as having been introduced in India (Wealth of India, 1976), of which three (*Y. aloifolia* L., *Y. filamentosa* L. and *Y. gloriosa* L.) are commonly found (Babu, 1977). All three species are reported for ornamental and have potential use as medicine, fibre and detergent. Flowers and fruits of *Y. aloifolia and Y. filamentosa* are edible and rhizomes of *Y. gloriosa* is a source of Costa Rica Arrowroot starch.

All of them grow well in hot and dry conditions, in sub-tropical and semi-temperate zones. *Y. aloifolia* is common in the gardens of warm tropical regions and along road sides in Himalaya (altitude 2000m) (Hajra and Verma, 1996; Polunin and Stainton, 1985) and Bilaspur, Chhattisgarh (Khanna *et al*., 2005). *Y. filamentosa*, is an evergreen rare shrub from tropical regions of India. *Y. gloriosa* is more common that thrives well in arid to semi-arid regions and has become naturalized in parts of Himalaya and in the peninsular India. The tough rosette of evergreen leaves and showy flowers make it suitable as ornamental in different gardens of the world including India (Wealth of India, 1976).

On the basis of comparison in ecological and botanical characters, it was observed that all three species of *Yucca* have same origin and habitat. *Y. filamentosa* and *Y. gloriosa* are acaulescent shrubs with woody stems whereas *Y. aloifolia* is caulescent shrub and tallest among the three with simple stem and stiff leaves with sharp tips and denticulate margin that can easily cause painful punctures. *Y. filamentosa* having filamentous, blue green strappy leaves spread by short side growth. *Y. gloriosa* is a medium high plant with leaves crowned at the ground or at summit of the trunk. Flowers of *Y. aloifolia* and *Y. filamentosa* are creamy white whereas in *Y. gloriosa* flowers are greenish-white, reddish or purplish-tinged. Panicle of *Y. aloifolia* is shortest as compared to *Y. filamentosa* and *Y. gloriosa*. In comparison to others, *Y. gloriosa* has restricted growth and does not spread as a weed. It is propagated by seed, cuttings or suckers. The plant is a perennial with characteristic secondary growth that makes it a tough hedge plant. Observations pertaining to origin, distribution, habitat, botanical characters and economic uses have been recorded in Tables 1 and 2.

Botanical description of *Y. gloriosa* L. (http://en.wikipedia.org/wiki/Yucca)

***Yucca gloriosa* L.** (Maheshwari, 1963): A short-trunked, perennial, branched or unbranched small tree up to 3.4 m tall with several small stems arising from the base; base thickened in the adult specimens; **Leaves:** 60-75 X 5 cm, dark green to light grey-green, margins entire, smooth, stiff, forming a crown at the ground or at the summit of the trunk, apex sharp needle-pointed;

Table 1. Observations on Yucca species in India

Phyto-geographical, and botanical features	*Y. aloifolia*	*Y. filamentosa*	*Y. gloriosa*
Origin	Mexico, West Indies and USA	Mexico, West Indies and USA	Mexico, North America, Central America and West Indies
Distribution	Temperate to sub-temperate regions;	Mainly in tropical regions	Tropical to sub-tropical regions; naturalised in Indian gardens in peninsular and lower slopes
Habitat	Hot and dry parts	Hot and dry parts	Hot and dry parts
Habit	Caulescent shrub, 6.0-7.5 m tall	Acaulescent shrub, 2.5-3.0 m tall	Acaulescent shrub, 3.0-4.0 m tall
Leaf	Dagger-like, very sharp pointed apex, grey-green, up to 75 cm, finely toothed, pungent reddish-brown horn at the top	Oblong-lanceolate, long curly threads on margins, up to 75 cm long	Stiff smooth, pointed tip, forming a tough crown of secondary branches at the ground, up to 75 cm long
Flower	Panicles 0.60-0.90 m long, creamy-white flowers, often tinged with purple colour	Panicles 1.0-3.6 m long, yellow-white flowers	Panicle 1.0-1.8 m or longer, greenish-white, reddish or purplish-tinged
Fruit	Black purple, baccate	Dry capsule	Dry, drooping capsule
Seed	Black compressed	Black compressed	Black, shiny, irregularly compressed
Flowering and fruiting	June-August	July-August	June-August

Inflorescence: paniculate with alternate branches, 1.0-1.8 m, partially inferior to the leaves; **Flowers:** campanulate to elongate, numerous, pendulus, greenish-white, reddish or purplish-tinged, closely packed in a narrowly conical, solitary, drooping, bell-shaped, hermaphrodite; perianth lobes waxy; **Stamens:** six, embracing the ovary; styles connate forming a central canal; stigmas three, bilobed and forming a stigmatic chamber below; **Scape:** solitary central, woody, 2 m or even more in height; **Fruits:** a dry, drooping, green capsule, brownish on ripening, indehiscent, 5-8 X 2.5 cm, obovate; **Seeds:** black, shiny, irregularly compressed, thickened, roundish; **Flowering and fruiting**: June to late August.

Distribution, ecology and uses

Y. gloriosa grows on sand dunes along the coast and barrier islands of the southeastern USA, along with other species (*Y. filamentosa, Y. recurvifolia* and *Opuntia* species). This species has been successfully planted over a wide range of habitat and soil conditions. Generally it thrives well in arid to semi-arid conditions and adapted to diverse climatic and ecological habitats from rocky deserts, grassland, in mountainous regions, and even in sub-tropical and semi-temperate regions. It has been reported from Bilaspur (Chhattisgarh) (Khanna *et al*., 2005), and Tamil Nadu (Henry *et al*., 1989). Some of the significant uses for which this species has been introduced in India are given below:

Ornamental value: Like many other *Yucca* species, *Y. gloriosa* is also valued as ornamental for gardens, as hedge plant and also in pots (Maheshwari and Singh, 1965; Wiersema and Loen, 1999). Plant is very handsome with creamy-white pendulous attractive flowers. This species is observed growing on the roadsides, especially on the flyovers and on road divider and public gardens. Bold sword like foliage provides it a handsome appearance suitable for landscape. The plant flowers during end of summer and autumn when blooming in most other ornamentals is over.

Fibre value: Rough fibre obtained from leaves is used in same way as that of sisal (*Agave sisalana* Perr.), jute (*Corchorus olitorius* L.) and hemp (*Cannabis sativus* L.) and used for making carpets and mats, ropes, cords, paper-making, etc. (Gamble, 1957; Wealth of India, 1976). The fibre extracted from leaves is wiry, round, moderately flexible and strong but harsh with good dyeing capacity. It is more water-resistant than hemp.

Medicinal value: The fruit is reported to be purgative (Hussain *et al*., 1992; Kirtikar and Basu 1975). The Santal tribals use the plant for rheumatism, sores and ulcers, and also for dysentery, bronchitis, asthma, leprosy, hemorrhagic septicemia, etc. (Singh *et al*., 1965).

Starch and detergent: The rhizome is a source of Costa Rica Arrowroot (Ambasta *et al*., 1986; Tanaka, 1976). The underground parts possess detergent property used as an ingredient in soap manufacturing. Extract is employed to produce foam in beverages (Singh *et al*., 1965; Watt, 1972).

Other uses: Some of the other potential uses include planting as windbreaks, dried plant parts as fuel (lowest ignition temperature), a trunk used as stockade and leaves for thatching and thin stem as tool handles.

Table 2. Uses of *Yucca* species for various purposes

Uses	Plant part	Plant species	References
Ornamental	Whole plant	*Y. aloifolia, Y. filamentosa, Y. gloriosa*	Maheshwari (1963), Maheshwari & Singh (1965), Singh *et al*. (1965), Wealth of India (1976), Wiersema & Loen (1999)
Edible	Flowers, fruits *and rhizomes*	*Y. aloifolia, Y. filamentosa, Y. gloriosa*	Ambasta *et al*. (1986), Kirtikar & Basu (1975), Singh *et al*. (1965), Tanaka (1976)
Fibre	Leaves	*Y. aloifolia, Y. filamentosa, Y. gloriosa*	Ambasta *et al*. (1986), Gamble (1957), Singh *et al*. (1965), Wealth of India (1976), Watt (1972)
Medicinal	Fruits	*Y. aloifolia, Y. filamentosa, Y. gloriosa*	Ambasta *et al*. (1986), Hussain *et al*. (1992), Kirtikar & Basu (1975), Singh *et al*. (1965), Wealth of India (1976)
Detergent	Rhizomes	*Y. aloifolia, Y. filamentosa, Y. gloriosa*	Ambasta *et al*. (1986), Kirtikar & Basu (1975), Singh *et al*. (1965), Watt (1972)

Conclusions

All the three species of *Yucca* in India have ornamental value both for foliage and flowers and have many potential uses. *Y. gloriosa* is found suitable to semi-arid urban areas as hardy and good performer under low water input conditions and has low maintenance requirements (of pruning/ cutting, etc.) than many other species used for similar purpose. This species can be successfully planted on roadsides, on road dividers and flyovers, in parking lots, front or backyards of the houses where intense heat and light prohibits many other plants to grow. It can be used as a good barrier or hedge plant because of sharp leaves and tips/ margins and tough growth. Beside its value as ornamental it can be promoted on commercial scale for quality of fibre for cottage industry. Thus, this plant can be grown more extensively for different uses in various parts of India.

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Standardization of Callus Induction and Shoot Regeneration in Twelve Species of *Dioscorea*

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Protocol was standardised for callus induction and shoot regeneration from leaf/stem/petiole/bulbil or root explants in 12 species of *Dioscorea* namely *Dioscorea bulbifera, D. pentaphylla, D. hispida, D. oppositifolia, D. belophylla, D. wightii*, *D. spicata, D. intermedia, D. hamiltonii* and *D. pubera*. While in 2 species no callus could be induced. Type of explants as well as the type, concentrations and combinations of hormones used influenced callus induction and regeneration. The most proliferative callus was obtained from leaf on MS + 2,4-D (1-3 mg/l) in all the species. In *D. intermedia*, leaf explants cultured in MS medium with NAA (8 mg/l) and BA (2 mg/l) resulted in high callusing. 2,4-D in conjunction with BA in *D. spicata* and Kinetin in *D. intermedia* induced callus. Distinct variation in colour and texture of callus was noticed. White friable/powdery callus was produced in medium containing 2,4-D alone or in combination with BA. In *D. wightii* and *D. belophylla*, leaf explant in 2,4-D (3 mg/l) produced brownish highly regenerative compact callus. 2,4-D derived callus gave the maximum callus regeneration. In *D. bulbifera* and *D. pentaphylla*, callus regeneration occurred in MS basal medium itself, while, addition of Kn (2 mg/l) was essential for shoot induction (1-3 shoots/callus) in five species. In *D. belophylla* 4 shoot buds regenerated in BA (4 mg/l). In *D. hamiltonii* TDZ (1 mg/l) gave a maximum of 22 shoots. Synergistic effect of BA (2 mg/l) and Kn (1 mg/l) induced 6 shoots in *D. bulbifera,* 4 in *D. hispida* and 5 in *D. wightii*. Single shoot was regenerated in *D. belophylla* in combination with BA and IBA, while Kn with IBA produced 2 shoots in *D. pentaphylla* and 4 in *D. hispida*. A combination of BA and Kn along with NAA also resulted in shoot regeneration in *D. pentaphylla* (2 shoots/callus), D. *oppositifolia* (2 shoots/callus) and *D. intermedia* (2-3 shoots/callus).

Key Words: *Dioscorea*, **Callus induction, Callus regeneration, Caulogenesis**

Introduction

Dioscorea containing 620 species, producing tubers, bulbils or rhizomes of considerable economic importance (Ammirato, 1984; Purseglove, 1972), constitute the staple carbohydrate food having high protein and minerals for millions in tropical and subtropical countries (Onwueme, 1978; Ayensu and Coursey, 1972). Many wild species have medicinal and pharmacological value (Coursey, 1967), being source of steroidal sapogenin diosgenin, the precursor of sex hormone and corticosteroids. The present experiment was aimed to standardize protocols for the rapid clonal multiplication of the species of *Dioscorea* through indirect organogenesis.

Callus regeneration and indirect organogenesis have been reported in *D. alata* (Belarmino, *et al*., 1991; Acedo, 1994; Paneque *et al*., 1995; Nair and Chandrababu, 1996; Amoroso, 1999), *D. esculenta* (Belarmino *et al*., 1991), *D. rotundata* (Esenowo, 1986; Belarmino *et al*., 1991; Nwachukwu *et al*., 1996), *D. cayenensis* (Viana and Mantell, 1989), *D. floribunda* (Sengupta *et al*., 1984), *D. composita* (Rao, 1982; Viana and Mantell, 1989) and *D. deltoidea* (Mascarenhas *et al*., 1976; Singh, 1978; Chaturvedi and Chowdury, 1980).

In the present experiment, callus induction and shoot regeneration was achieved from leaf explants in ten species of *Dioscorea,* namely *Dioscorea bulbifera* (IC202349), *D. pentaphylla* (IC202367), *D. hispida* (IC202370), *D. oppositifolia* (IC202386), *D. belophylla* (IC248181), *D. wightii* (IC214855), *D. spicata* (IC202383), *D. intermedia* (IC202384), *D. hamiltonii* (IC202328) and *D. pubera* (IC202382). *D. wallichii* and *D. tomentosa* failed to initiate callus in any of the hormonal combinations tried.

Materials and Methods

One accession each from the 12 species of *Dioscorea* having distribution in Southern Western Ghats, procured from NBPGR Regional Station, Thrissur and grown in the green house of the Department of Botany, University of Kerala, Thiruvananthapuram, served as the explant source. Leaf, stem, petiole, root and bulbil segments from vines of healthy and disease free 4-month-old plants were used. The explants were initially washed in running tap water for 30-60 minutes, then in aqueous 10% Labolene for 15-20 minutes and again in tap water and in sterile distilled water to remove the adhering surface contaminants. They were then sterilized inside the laminar airflow chamber using

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aqueous 0.1% $HgCl_2$ for 5-20 minutes and then rinsed in sterile double distilled water 4-5 times. The explants were then trimmed to appropriate sizes by removing off the cut ends after blotting in sterile filter paper before inoculation.

For the induction of callus, single explant each of leaf and bulbil segments (0.5 cm^2), stem, petiole and root explants (0.5-1.0 cm) were inoculated onto MS basal medium (Murashige and Skoog, 1962) augmented with varying concentrations and combinations of hormones, *viz.,* 2,4-D, NAA, IAA and IBA (0.5-10 mg/l) alone or in combination with cytokinins BA/Kn/2-iP (0.5-5 mg/l). The cultures were then kept in the culture room maintained under 12 h photoperiod at a light intensity of 3000 at 25±1^{o}C and at 70-80% RH. The callusing responses were recorded after every two weeks. The primary calluses after 30-45 days of inoculation were subcultured to fresh media containing similar or varied hormonal combination for further proliferation, maintenance and organogenesis. The growth of the calluses was evaluated by measuring the callus proliferated per unit area of the samples.

For callus regeneration, the initiated and proliferated calli were transferred to basal MS or to the regeneration media, containing BA/Kn/TDZ/2-iP (0.5-4 mg/l) alone or in combination with 2,4-D, IAA, IBA or NAA (0.5-4 mg/l).

Results

Callus Induction

Various explants like leaf, stem, petiole, root and bulbil segments from species of *Dioscorea* were tested for callus induction from species of *Dioscorea* on MS medium supplemented with different concentrations and combinations of phytohormones. Surface sterilization for 8-10 min. for leaf and petiole and 12-15 min in case of stem, root and bulbil explants was adequate to establish 85-90% contaminant free cultures. Callus induction was achieved in these explants in MS medium containing auxins *viz*. 2,4-D, IAA, IBA and NAA (0.5-10 mg/l) either alone or in combination with BA/Kn (0.5-3 mg/l). Explants inoculated on to 2,4-D resulted in induction of callus in 7-10 days of culture. Initial responses like curling of the leaf explants and inflation of the petiole segment tip started from the 4th day itself. The type and concentration of hormones used exhibited significant influence on callogenesis. In most of the cases white or cream friable callus was formed. Of the various auxins used for callus induction, 2,4-D gave the best callus initiation and proliferation followed by NAA, IAA and IBA in all the species. Likewise callus morphology also varied with explant. Young explants showed better response giving high callus proliferation. Mature explants showed mild response in callusing, which was arrested after 15-25 days and dried off. Among the different explants used, leaf segments gave the most proliferative callus followed by petiole, stem and bulbil segments. Due to high phenolic exudation in species like *D. pentaphylla* and *D. hispida*, browning of the calli and death of the explant was observed in some cultures upon ageing. In order to overcome this, frequent subculturing of such calli was done to maintain their regenerative capacity.

In *D. bulbifera*, of the various explants tried, leaf explants responded early and produced white callus from cut ends within 7 days in 2,4-D (1 mg/l) (Fig. 1). The callus is yellowish and nodular at 2-3 mg/l of 2,4-D (Fig. 2). From stem explants, white powdery callus was developed in 2-3 mg/l while petiole, irrespective of the concentration of 2,4-D tried (0.5-3 mg/l), produced powdery white callus (Table 1). Bulbil explants, at higher concentrations of 2,4-D (5 mg/l), produced powdery white callus (Fig. 3), while, at 3 mg/l black callus was formed (Table 1).

In *D. pentaphylla*, leaf explants in 3 mg/l 2,4-D induced callus. At 5 mg/l, black glutinous callus was produced. When medium was augmented with BA (3 mg/l) + Kn (1 mg/l) + NAA (1 mg/l), cream, compact organogenetic callus was produced (Table 2). Petiole explants in 2,4-D (5 mg/l) alone or in combinations of cytokinins and auxins, *viz*., BA (3 mg/l), Kn (1 mg/l) and NAA (1 mg/l), initiated brown powdery callus from cut ends (Fig. 4). Bulbil segments in 2,4-D (5 mg/l) initiated black callus

Table 1. Effect of 2,4-D on callus induction in *Dioscorea bulbifera*

Explant	Conc. (mg/l)	Callus morphology	Roots	Rate of callusing*
Leaf	1.0	White	–	+++
	2.0	Yellow	–	+
	3.0	Yellow nodular, compact	–	++
Stem	1.0	White	–	+
	2.0	White powdery	+	++
	3.0	White powdery	–	++
Petiole	0.5	White powdery	–	+
	1.0	White powdery	–	+
	2.0	White powdery	–	+
	3.0	White powdery	–	++
Bulbil	1.0	White powdery	–	+
	2.0	White powdery	–	+
	3.0	Black	–	+
	5.0	White powdery	–	++

* Rate of callusing, n = callus proliferated per unit area of the samples

Fig. 1 – 20: Callus induction in species of *Dioscorea*

Table 2. Effect of phytohormones on callus induction in *D. pentaphylla* and *D. hispida*

Species	Explant	Hormones conc. (mg/l)				Callus morphology	Rate of callusing*
		2,4–D	BA	Kin	NAA		
D. pentaphylla	Leaf	1	–	–	–	Brown powdery	++
		3	–	–	–	Nodular compact	+++
		5	–	–	–	Black glutinous	+
		–	3	1	1	Cream compact organogenetic	++
	Petiole	1	–	–	–	Brown powdery	+
		3	–	–	–	Brown powdery	+
		5	–	–	–	Brown powdery	++
		–	3	1	1	Brown powdery	++
	Bulbil	1	–	–	–	Brown	+
		3	–	–	–	Brown	+
		5	–	–	–	Black	++
D. hispida	Leaf	0.5	–	–	–	Black glutinous	+
		1	–	–	–	Black glutinous	+
		3	–	–	–	Compact proliferative	++
		5	–	–	–	Compact	+

* Rate of callusing, n= callus proliferated per unit area of the samples

(Fig. 5). In *D. hispida*, black glutinous callus was formed from leaf explants in medium containing 2,4-D (0.5-1 mg/l). At 3 mg/l 2,4-D, compact proliferative callus was induced (Table 2).

In *D. oppositifolia*, powdery white callus was initiated from cut ends of leaf segments in 2,4-D at 3 mg/l, while, at higher concentrations (5 mg/l), meager white powdery non regenerative callus was formed from the whole surface (Fig. 6). At still higher concentrations (> 5 mg/l), rhizogenesis alone was noticed (Table 3). Petiole in 2,4-D (3 mg/l) produced white compact callus (Fig. 7). Powdery white callus obtained in 2,4-D (3 mg/l) on transfer to medium containing 2,4-D (4 mg/l) and Kn (2 mg/l) produced compact light brown non-regenerative callus.

In *D. belophylla*, explants responded very well in cultures containing 2,4-D (0.5-3 mg/l) (Table 3). Leaf explants produced highly regenerative compact brown callus at 3 mg/l (Fig. 8), while, petiole explants produced creamy glutinous callus in 2,4-D (0.5 mg/l). Stem explants did not produce any callus. In *D. wightii*, leaf segments produced brown compact callus in 2,4-D (3 mg/l) (Fig. 9), which became regenerative on transfer to TDZ (2 mg/l) enriched medium. Callus was also induced from cut ends of leaf segments in medium containing Kn (3 mg/l) and 2,4-D (0.5 mg/l).

In *D. spicata*, root explants produced shiny globular callus in 2,4-D (3 mg/l), while, stem explants produced shiny glutinous callus (Fig. 10). In presence of BA (0.5-2 mg/l) and 2,4-D (0.5-1 mg/l), root explants produced powdery non-regenerative callus (Table 4). Petiole, in medium containing BA (2 mg/l) and 2,4-D (6 mg/l) produced creamy compact callus (Fig. 11). Root explants planted in 2,4-D (0.5 mg/l) also showed similar results on transfer to TDZ (3 mg/l). Mature leaf explants in 2,4-D (0.5-2 mg/l) gave rise to dull green callus, which also showed rhizogenesis (Table 4). At 3 mg/l 2,4-D, greenish powdery compact callus showing rhizogenesis was obtained (Fig. 12). Young explants in 2,4-D at 3 mg/l induced white nodular regenerative callus, which became brown lateron (Fig. 13).

In *D. intermedia*, leaf and petiole explants responded similarly in cultures. At 2,4-D (1 mg/l), maximum callusing was noticed (Table 5). The callus was proliferative and powdery white at 1 and 3 mg/l, while, at 2 mg/l, nodular callus was formed. At higher concentrations of 2,4-D (5 mg/l), brown nodular callus (Fig. 14) and at 10 mg/l, white friable callus was produced (Fig. 15). Young petiole explant produced shiny glutinous callus from the cut ends in 2,4-D (3 mg/l) (Fig. 16).

Apart from 2,4-D, the other auxins also induced callus in leaf explants of *D. intermedia* (Table 5). Leaf segments in IAA, IBA and NAA produced white compact callus at low concentrations (0.5-1 mg/l). At higher levels (5 mg/l), callusing along with rhizogenesis was noticed. NAA derived callus on transfer to TDZ (0.5 mg/l) produced proliferative nodular compact callus. Friable white callus was produced in a combination of 2,4-D (4 mg/l) and Kn (2 mg/l) (Fig. 17), while, creamy compact proliferative callus was produced in NAA (8 mg/l) and BA (2 mg/l) (Fig. 18). Lower concentration of NAA (0.5 mg/l) along with BA (4 mg/l) initiated nodular organogenetic callus (Table 5).

The most regenerative callus was obtained in *D. hamiltonii* where the leaf explants in 2,4-D (1 mg/l) developed compact regenerative callus (Fig. 19), while petiole explant yielded black and glutinous callus. In *D. pubera,* bulbil explant in 2,4-D (3 mg/l) induced white compact callus (Fig. 20). Explants from two other species namely, *D. wallichii* and *D. tomentosa* failed to initiate callus in any of the hormonal combinations tried.

Callus Regeneration

Organogenetic/morphogenetic calluses induced from leaf, stem, petiole, root and bulbil segments were subcultured on to basal MS or to lower concentrations of the initiation medium or to different regeneration media containing BA/Kn/2-iP alone or in combination with NAA/IAA/IBA/2,4-D, in order to get regeneration from the calli.

In *D. bulbifera*, yellowish nodular regenerative leaf callus initiated in 2,4-D (3 mg/l), on subculturing to a medium containing BA/Kn (2 mg/l) produced two shoots (Fig. 21), while, combination of BA (2 mg/l) and Kn (1 mg/l) in the regeneration medium resulted in the formation of 4 shoots (Fig. 22). The same callus on transfer to BA (2 mg/l) and then to BA (2 mg/l) and Kn (1 mg/l) developed 1-2 shoots. The same callus upon subculture to Kn (2 mg/l) instead of BA and then to BA (2 mg/l) and Kn (1 mg/l), developed 6 shoots (Fig. 23; Table 6).

Similarly, the yellowish nodular regenerative petiole callus raised in 2,4-D (3 mg/l) upon transfer to BA (2 mg/l) or BA (2 mg/l) and Kn (1 mg/l) also developed 2-3 shoots. 2,4-D (5 mg/l) raised callus in BA (2 mg/l) developed single shoot with 3 branches and roots, while, in medium containing Kn (2 mg/l) or a combination of BA (2 mg/l) and Kn (1 mg/l) developed 2 more shoots with 8 branches and roots (Fig. 24).

Table 3. Effect of 2,4–D on callus induction in (*D. oppositifolia, D. belophylla, D. hamiltonii, D. wightii* and *D. pubera)*

Explant		MS+ 2,4–D (mg/l)	Callus morphology	Roots	Rate of callusing*
D. oppositifolia	Leaf	1	White	–	+
		3	White powdery	–	+++
		5	White powdery non regenerative	–	+
		10	No callus formation	+	–
	Petiole	1	White	+	+
		3	White compact	+	+
		5	White	++	+
D. belophylla	Leaf	0.5	Brown	–	+
		1	Brown compact	–	++
		3	Brown compact highly regenerative	–	+++
		5	Black	–	+
	Petiole	0.5	Creamy glutinous	–	++
		1	White	–	+
		3	White nodular	–	+
		5	Brown powdery	–	+
D. hamiltonii	Leaf	1	Nodular compact regenerative	–	+++
		3	Compact	–	++
		5	Powdery	–	+
	Petiole	1	Black glutinous	–	++
		3	Black	–	+
		5	Black	–	+
D. wightii	Leaf	1	Brown	–	+
		3.0	Brown compact	–	+++
		5	Brown	–	+
D. pubera	Bulbil	1	White powdery	–	+
		3	White compact	–	++
		5	Brown powdery	–	+

Table 4. Effect of phytohormones on callus induction in *Dioscorea spicata*

Explant	Conc. (mg/l) 2,4–D	BA	Callus morphology	Roots	Rate of callusing*
	0.5	–	Chlorophyllous	+	+
	1	–	Chlorophyllous	+	+
	3	–	White nodular regenerative	–	+++
Leaf	5	–	Greenish powdery compact	–	++
	1	–	Powdery non– regenerative	+	+
	3	–	Powdery non regenerative	+	+
	5	–	No callus formation	+	–
Petiole	6	2	Creamy compact	–	+++
	1	–	Shiny	–	+
	3	–	Shiny glutinous	–	+++
Stem	5	–	Shiny	–	+
	1	–	Shiny	–	+
	3	–	Shiny glutinous globular	–	+
	5	–	Powdery	–	+
	0.5	0.5	Powdery non– regenerative	–	+
	0.5	1	Powdery non–regenerative	–	+
	1	1	Powdery non– regenerative	–	+
	0.5	2	Powdery non– regenerative	–	+
Root	1	2	Powdery non– regenerative	–	+

* Rate of callusing, n= callus proliferated per unit area of the samples

Table 5. Effect of phytohormones on callus induction in *D. intermedia*

Explant	Hormones conc. (mg/l)						Callus morphology	Roots	Rate of callusing*
	2,4–D	BA	Kin	IAA	IBA	NAA			
	1	–	–	–	–	–	Powdery white proliferative	–	++++
	2	–	–	–	–	–	Nodular	–	++
	3	–	–	–	–	–	White powdery proliferative	–	++
	5	–	–	–	–	–	Brown nodular	–	++
	10	–	–	–	–	–	White friable	–	+
	4	–	2	–	–	–	White friable	–	+
	–	2	–	–	–	8	Creamy compact	–	+++
	–	4	–	–	–	0.5	Nodular organogenetic	–	+++
	–	–	–	0.5	–	–	White compact	–	++
	–	–	–	1	–	–	White compact	–	++
	–	–	–	3	–	–	White	+	+
	–	–	–	5	–	–	White	+	+
	–	–	–	10	–	–	No callus	+	–
Leaf	–	–	–	–	0.5	–	White compact	–	++
	–	–	–	–	1	–	White compact	–	++
	–	–	–	–	3	–	White	+	+
	–	–	–	–	5	–	White	+	+
	–	–	–	–	10	–	No callus	++	–
	–	–	–	–	–	0.5	White compact	–	++
	–	–	–	–	–	1	White compact	–	++
	–	–	–	–	–	3	White	+	+
	–	–	–	–	–	5	White	+	+
	–	–	–	–	–	10	No callus	+++	–
	1	–	–	–	–	–	White compact	–	++
	2	–	–	–	–	–	White compact	–	++
Petiole	3	–	–	–	–	–	Shiny glutinous	–	++
	5	–	–	–	–	–	Crystalline	–	+
	10	–	–	–	–	–	White	+	+

* *Rate of callusing, n*= callus proliferated per unit area of the samples

Table 6. Effect of cytokinins (mg/l) alone or in combination on callus regeneration

Explant	Hormones conc. (mg/l)				Number of shoots induced									
	BA	Kin	2–iP	TDZ	1	2	3	4	5	6	7	8	9	10
Leaf	2	–	–	–	2	–	–	–	–	–	–	–	–	–
	–	2	–	–	2	–	–	–	–	–	–	–	–	–
	2	1	–	–	6	–	–	–	–	–	–	–	–	–
Petiole	2	–	–	–	2	–	–	–	–	–	–	–	–	–
	2	1	–	–	3	–	–	–	–	–	–	–	–	–
	2	–	–	–	1		–	–	–	–	–	–	–	–
Bulbil	–	2	–	–	3	–	–	–	–	–	–	–	–	–
	2	1	–	–	3	–	–	–	–	–	–	–	–	–
	–	–	2	–	4	–	–	–	–	–	–	–	–	–
	–	3	–	–	–	2	–	–	–	–	–	–	–	–
	4	2	–	–	–	2	–	–	–	–	–	–	–	–
	–	–	–	0.5	–	1	–	–	–	–	–	–	–	–
	2	1	–	–	–	–	4	–	–	–	–	–	–	–
	2	–	–	–	–	–	–	1	–	–	–	–	–	–
Leaf	3	–	–	–	–	–	–	1	–	–	–	–	–	–
	4	–	–	–	–	–	–	–	4	–	–	–	–	–
	–	–	2	–	–	–	–	–	1	–	–	–	–	–
	2	–	–	–	–	–	–	–	–	3	–	–	–	–
	2	1	–	–	–	–	–	–	–	5	–	–	–	–
Petiole	–	2	–	–	–	–	–	–	–	–	1	–	–	–
	2	1	–	–	–	–	–	–	–	–	1	–	–	–
Leaf	–	–	–	1	–	–	–	–	–	–	–	–	22	–
Petiole	–	–	–	1	–	–	–	–	–	–	–	–	6	–
Bulbil	–	3	–	–	–	–	–	–	–	–	–	–	–	1

1. *D. bulbifera,* 2. *D. pentaphylla,* 3. *D. hispida,* 4. *D. oppositifolia,* 5. *D. belophylla,*
6. *D. wightii,* 7. *D. spicata,* 8. *D. intermedia,* 9. *D. hamiltonii,* 10. *D. pubera*

Bulbil callus raised from 2,4-D (5 mg/l), on transfer to Kn (2 mg/l) or a combination of BA (2 mg/l) and Kn (1 mg/l) developed 3 shoots (Table 6). Later on it produced 4-8 branches from each shoot and bulbils from each axils (Fig. 25). The same callus on transfer to BA (2 mg/l) and NAA (0.5 mg/l) or 2-iP (2 mg/l) developed 4 shoots with 3-5 branches each (Table 7). Black callus produced from bulbils in medium with 2,4-D (3 mg/l) on subculture to lower concentrations of 2,4-D (1 mg/l) and BA (0.5 mg/l) formed vitrified shoots (Fig. 26). Moreover, the basal callus formed in BA (2 mg/l) and NAA (0.5 mg/l) produced single shoot with 6 branches and bulbils from each axil on transfer to basal MS medium (Fig. 27).

Leaf, petiole and bulbil callus was regenerative in *D. pentaphylla* and *D. hispida*. The callus got blackened in these due to high phenol exudation and hence frequent subculturing was necessary to retain the regenerative capacity of the callus. In *D. pentaphylla*, brown compact BA (2 mg/l) and NAA (2 mg/l) derived callus from leaf developed 2 shoot buds in BA (4 mg/l) and Kn (2 mg/l) containing medium (Fig. 28; Table 6). Leaf callus in 2,4-D (3 mg/l) on transfer to Kn (3 mg/l) developed 2 shoots. Nodular, compact 2,4-D (3 mg/l) raised callus on transfer to TDZ (0.5 mg/l) developed a single shoot, while, in BA (2 mg/l) and NAA (0.5 mg/l), developed 2 shoots with branches (Fig. 29). Cream compact organogenetic leaf callus cultured in medium containing BA (3 mg/l), Kn (1 mg/l) and NAA (1 mg/l) gave 2 shoot buds (Table 7). Petiole derived glutinous callus developed in the same medium upon transfer basal MS, regenerated 2 shoot buds.

In *D. hispida*, black glutinous leaf callus obtained in 2,4-D (0.5 mg/l) gave rise to 4 shoots in medium containing BA (2 mg/l) and Kn (1 mg/l). Compact callus derived from 2,4-D (3 mg/l) on on transfer to medium with Kn (2 mg/l) and IBA (0.5 mg/l) resulted in the formation of 3-4 healthy shoots (Fig. 30; Table 7).

In *D. oppositifolia,* the 2,4-D derived leaf callus when subcultured to regeneration medium with BA (2-3 mg/l) produced a single shoot with roots. In presence of BA (3 mg/l) + Kn (1 mg/l) + NAA (1 mg/l), leaf callus from 2,4-D (3 mg/l) developed 2 shoots (Fig. 31).

In D. *belophylla*, brown compact organogenetic callus derived from leaf explants in 2,4-D (3 mg/l) on subculture to BA (4 mg/l) developed 4 - 8 shoots (Table 6). These shoots elongated and produced branches on transfer to basal MS medium (Fig. 32). Meanwhile, the black compact regenerative leaf callus derived in 2,4-D (0.5 mg/l) on transfer to BA (2 mg/l) and IBA (0.5 mg/l) developed a single shoot along with rhizogenesis (Fig. 33; Table 7). In 2-iP (2 mg/l) also a single shoot got differentiated. Petiole callus derived in 2,4-D (0.5 mg/l), upon transfer to medium containing Kn (2 mg/l) developed suppressed shoots with underdeveloped roots (Fig.34).

In *D. wightii*, the organogenetic leaf callus derived from 2,4-D (3 mg/l) produced 2-3 shoots in regeneration medium supplemented with BA (2 mg/l). When regeneration medium was complemented with Kn (1 mg/l) along with BA (2 mg/l), an increase in the number of shoots to 3 – 5 was noticed (Fig. 35; Table 6).

The cream compact nodular petiole callus of *D. spicata* induced in medium containing 2,4-D (6 mg/l) and BA (2 mg/l) on transfer to Kn (2 mg/l) or BA (2 mg/l) and Kn (1 mg/l) developed a single shoot (Fig. 36; Table 6). The powdery leaf callus derived in 2,4-D (3 mg/l) showed only rhizogenesis in BA (2 mg/l).

In *D. intermedia*, 2,4-D (5 mg/l) leaf callus on transfer to basal MS developed a single plant with roots, while, the same callus on subculture to BA (3 mg/l) + Kn (1 mg/l) + NAA (1 mg/l) developed 2 shoots (Table 7). Nodular callus developed in BA (4 mg/l) and NAA (0.5 mg/l) showed signs of regeneration and on transfer to BA (3 mg/l) + Kn (1 mg/l) + NAA (1 mg/l) developed 3 shoots and many shoot initials (Fig. 37).

In *D. hamiltonii*, black glutinous callus developed from petiole explant in 2,4-D (1 mg/l) on subculture to TDZ (1 mg/l) developed 6 shoots (Fig. 38), while, the nodular compact leaf callus raised in the same hormonal regime upon transfer to TDZ (1 mg/l) produced 22 shoots (Fig. 39; Table 6). In *D. pubera*, bulbil callus raised in 2,4-D (3 mg/l) upon subculture to Kn (3 mg/l) or BA (2 mg/l) and Kn (1 mg/l) developed single shoot (Fig. 40; Table 6).

Discussion

Callus Induction

The type, concentrations and combinations of hormones as well as the type of explants influenced callus induction in *Dioscorea* species. In the present study, a significant difference was recorded in the rate of callusing of the different explants. This difference in callusing potential may be due to the species variation, physiological status of the explant source, culture conditions and sterilization procedures (Dodds and Roberts, 1995). Among the different explants used *viz*., leaf, stem, petiole, root and bulbil, most proliferative callus was obtained from leaf.

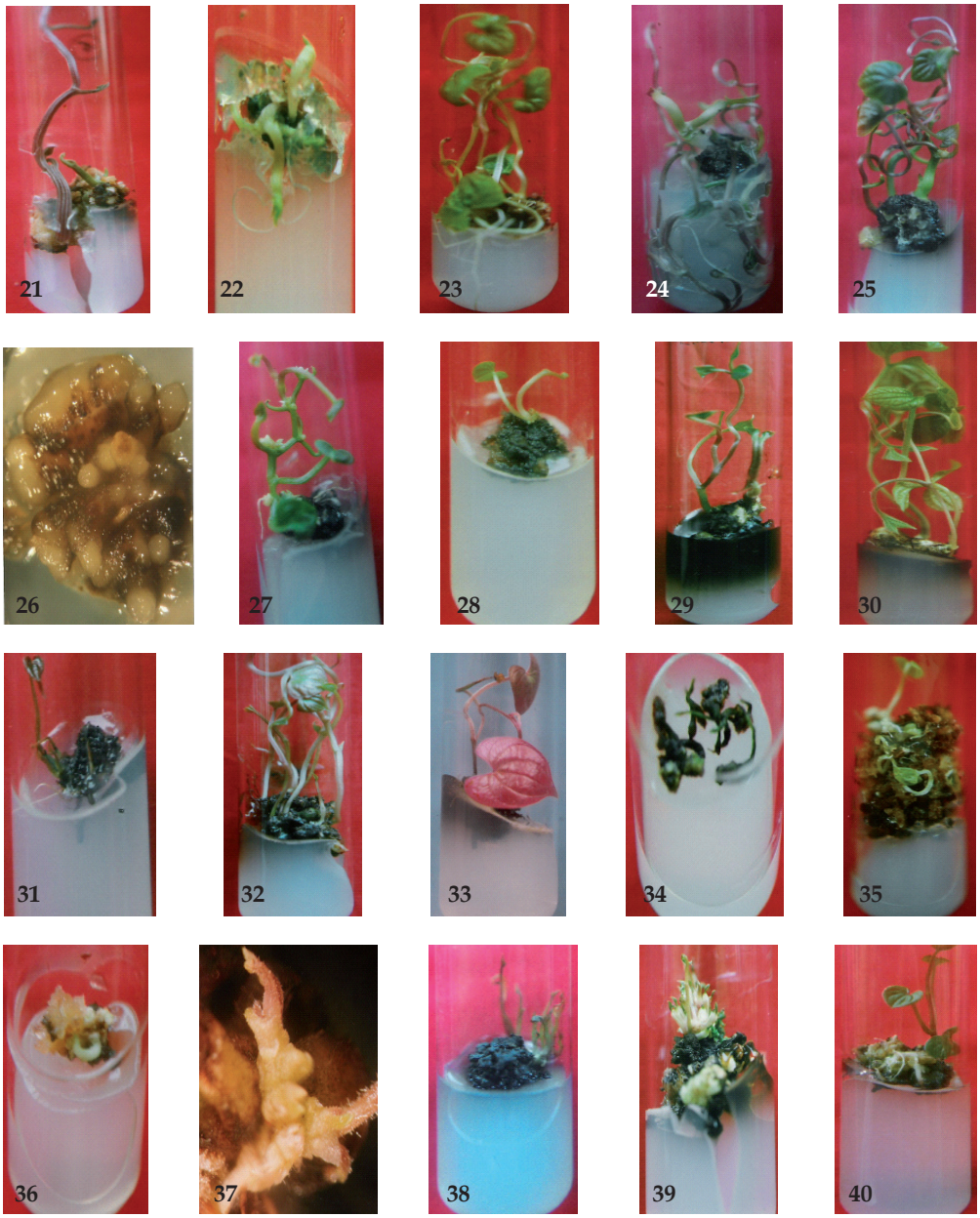

Fig. 21-40: Callus regeneration in *Dioscorea* species

Table 7. Effect of auxins in combination with cytokinins on callus regeneration

Explant	Hormones conc. (mg/l)				Number of shoots induced									
	BA	Kin	NAA	IBA	1	2	3	4	5	6	7	8	9	10
Bulbil	2	–	0.5	–	4									
Stem	2	–	0.5	–	1	–	–	–	–	–	–	–	–	–
	2	–	0.5	–	–	2	–	–	–	–	–	–	–	–
	3	1	1	–	–	2	–	–	–	–	–	–	–	–
	–	2	–	0.5	–	–	4	–	–	–	–	–	–	–
Leaf	3	1	1	–	–	–	–	2	–	–	–	–	–	–
	2	–	–	0.5	–	–	–	–	1	–	–	–	–	–
	3	1	1	–	–	–	–	–	–	–	–	2	–	–

1. D. bulbifera, 2. D. pentaphylla, 3. D. hispida, 4. D. oppositifolia, 5. D. belophylla
6. D. wightii, 7. D. spicata, 8. D. intermedia, 9. D. hamiltonii, 10. D. pubera

Wernicke and Park (1993) reported leaf explants as the best source for callus induction in *D. bulbifera*.

In the present study, of the various auxins tried alone, 2,4-D was the best for callus induction and proliferation in *Dioscorea* species. According to George (1993), the most frequently employed auxin to initiate callus is 2,4-D. Similar results of 2,4-D as efficient for induction of callus were reported in *D. bulbifera* (Wernicke and Park, 1993), *D. alata* (Acedo, 1994; Paneque, *et al*., 1995) and D. *cayenesnsis* (Viana and Mantell, 1989). Moreover, amongst the various concentrations of 2,4-D tried, leaf explant in 1 mg/l is the best giving maximum proliferation. Effectiveness of 2,4-D (1 mg/l) in inducing highest amount of callus was reported in *D. alata* by Acedo, *et al*. (1994). Higher concentrations of 2,4-D (above 5 mg/l), inhibited callus formation. This may be due to the toxic effect of the hormone beyond an optimum level.

The other auxins NAA/IAA/IBA in lower concentrations (0.5-1.0 mg/l) resulted in callus formation whereas in higher concentration (3.0-10.0 mg/l) rhizogenesis was observed.

2,4-D in conjunction with BA in *D. spicata* and Kn in *D. intermedia* induced callus. Efficiency of 2,4-D along with BA/Kn in inducing callus was reported by Sengupta *et al*. (1984) in *D. floribunda*.

Addition of cytokinins BA/Kn along with auxins resulted in callus induction in some species. In *D. intermedia*, leaf explants cultured in medium with NAA (8 mg/l) in combination with BA (2 mg/l) resulted in high rate of callusing. Similar reports of profuse callus formation in NAA and BA containing medium was reported in *D. alata* (Acedo *et al*., 1994; Amoroso, 1999) and *D. praehensilis* (Malaurie *et al*., 1995).

The synergistic effect of auxin NAA along with cytokinins BA and Kn also evoked good results in *D. intermedia*. This observation is concomitant with that in *Salvia officinalis* (Bolta *et al*., 2000), where, a combination of NAA, BA and Kn produced compact callus.

Based on the hormonal type and concentrations used, calluses raised in cultures showed variation in morphology, texture, colour and quality in *Dioscorea* spp. Development of callus with varying morphology with respect to hormones was reported in *Azhadirachta indica* (Ramesh and Padhya, 1990). Macek (1989) observed difference in texture ranging from compact to friable texture with a range of colours in calluses induced simultaneously under the same hormonal conditions in *Solanum* species. White friable/powdery callus was produced in all in medium containing 2,4-D alone or in combination with BA. Similar results of white friable callus formation in presence of 2,4-D alone or in conjunction with BA/Kn was reported in *Solanum nigrum* (Shahzad and Hassan, 1999).

In *D. wightii* and *D. belophylla,* medium containing 2,4-D at 3 mg/l induced brownish highly regenerative compact callus from leaf explants. The report on brown friable callus formation in presence of 2,4-D in *Hypericum brasilience* (Cardosa and de Oliveira, 1996) supports the present result. BA (3 mg/l), Kn (1 mg/l) and NAA (1 mg/l) produced compact organogenetic callus from leaf and petiole explants of *D. pentaphylla*. Nodular compact regenerative callus was formed in all in presence of 2,4-D (1-3 mg/l). The influence of 2,4-D in inducing nodular compact callus was reported in species such as *Sorghum bicolor* (Syamala and Devi, 2003).

Callus Regeneration

Callus regeneration was obtained by transferring the callus to basal MS medium or regeneration medium containing varying concentrations and combinations of cytokinins and auxins. Callus mediated adventitious shoot regeneration has the advantage of generating somaclonal variations having desirable qualities which can be selected and propagated.

In almost all the cases of callus regeneration, 2,4-D derived callus gave the maximum callus regeneration on transfer to basal MS medium or to the regeneration medium containing cytokinins (BA/Kn/TDZ/2-iP) alone or their combination or in combination with auxins (NAA/IBA). In *D. bulbifera* and *D. pentaphylla*, callus regeneration occurred in MS basal medium itself. Nair and Chandrababu (1996) obtained regeneration from callus cultures of *D. alata* and *D. esculenta* on MS medium.

Of the various cytokinins tried alone, Kn (2 mg/l) was found to be a potent cytokinin for shoot induction (1-3) from callus in all the species studied. The potentiality of Kn in inducing shoot bud formation from callus was reported in *Asparagus racemosus* (Daniel *et al*., 1999).

Considering the number of shoots regenerated from the callus, BA was found to be better than other cytokinins. In *D. belophylla* 4 shoot buds developed from callus in BA at 4 mg/l. Positive effect of BA on organogenesis from callus was also reported in a wide range of genera like Niger (Ahmed and Pandey, 1988), *Ocimum* spp.(Patnaik and Chand, 1996) and *Piper nigrum* (Bhat *et al*., 1995).

However, in *D. hamiltonii* TDZ when used alone at 1 mg/l gave a maximum of 22 shoots from the callus. TDZ has been shown to have high cytokinin activity by influencing endogenous cytokinin biosynthesis (Hutteman and Preece, 1993).

Regeneration medium containing a combination of cytokinins (BA+Kn) gave better results in all. Synergistic effect of the two (BA at 2 mg/l + Kn at 1 mg/l) produced 6 shoots in *D. bulbifera,* 4 in *D. hispida* and 5 in *D. wightii*. Synergistic effect of cytokinins in callus regeneration was reported by Mascarenhas *et al*. (1976) in *D. deltoidea.*

Synergistic effect of BA/Kn with NAA/IBA favoured shoot regeneration from callus in all. Promotion of shoot bud regeneration by BA in combination with NAA has been reported in species of *Dioscorea* such as *D. composita* (Datta *et al*., 1982), *D. floribunda* (Sengupta *et al*., 1984), *D. rotundata* (Belarmino *et al*., 1991; Nwachukwu *et al*., 1996), *D. alata* (Belarmino *et al*., 1991; Nair and Chandrababu, 1996; Amoroso, 1999) and *D. esculenta* (Belarmino *et al*., 1991; Nair and Chandrababu, 1996).

Synergistic effect of BA and IBA resulted in caulogenesis (single shoot) in *D. belophylla*, and Kn with IBA produced 2 and 4 shoots in *D. pentaphylla* and *D. hispida*. Moreover, the cytokinins BA and Kn along with NAA also resulted in shoot regeneration in *D. pentaphylla* (2 shoots), *D. oppositifolia* (2 shoots) and *D. intermedia* (2-3 shoots). Similar results of cytokinin-auxin combination inducing shoot regeneration were reported in *Plumbago zeylanica* (Rout *et al*., 1999) and *Catalpa ovata* (Lisowska and Wysokinska, 2000).

The present study results on callus induction and regeneration in wild species of *Dioscorea* from various explants achieved in MS medium under varied hormonal concentrations and combinations will be of much importance in large-scale multiplication of quality plants and effective management of the wild germplasm of Dioscoreas.

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Plant Germplasm Registration Notice

The Plant Germplasm Registration Committee of ICAR in its XIXth meeting held on March 13, 2009 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 69 germplasm lines out of 129 proposal considered.

1. ARC 15831 (IC567515; INGR09001), a Rice (*Oryza sativa*) Germplasm with Resistance to Rice Gall Midge Biotype 1, 2, 3, 4 and 4 M

Directorate of Rice Research, Hyderabad

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2. INRC 3021 (IC567516; INGR09002)), a Rice (*Oryza sativa*) Germplasm with Resistance to Rice Gall Midge Biotype 1, 2, 3, 4 and 4 M

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3. INRC 202 (IC567517; INGR09003), a Rice (*Oryza sativa*) Germplasm with Resistance to Rice Gall Midge Biotype 1, 2, 3, 4 and 4 M

Directorate of Rice Research, Hyderabad

The rice variety INRC 202 is derived from a land race from Chhattisgarh, conferring resistance against the Asian rice gall midge (*Orceolia oryzae*). It has been systematically evaluated against all the prevailing gall midge biotypes under the All India Coordinated Improvement Programme (AICRIP); DRR. It showed resistance against biotypes 1, 2, 3, 4 and 4 M (Kalode *et al.*, 1983; Vijaya Lakshmi *et al.*, 2006).

4. Aganni (IC567518; INGR09004)), a Rice (*Oryza sativa*) Germplasm with Resistance to Rice Gall Midge Biotype 1, 2, 3, 4 and 4 M

Directorate of Rice Research, Hyderabad

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References

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5. HS-492 (IC566223; INGR09005), a Wheat (*Triticum aestivum)* Germplasm Resistant Against all the Pathotypes of Leaf Rust

Sanjay Kumar, Dharam Pal, DK Bhatnagar and Rashmi Bhatnagar
Indian Agricultural Research Institute, RS, Shimla

HS-492 has been registered as a source of resistance against all the pathotypes of brown leaf rust (*Puccinia triticina*). It has been derived from HPW42/CPAN2032/ /UNATH KS.

6. PHSL-5 (IC566633; INGR09006), a Wheat (*Triticum aestivum)* Germplasm with Bold Seed

SK Singh, NVPR Ganga Rao, Jag Shoran, Ravish Chatrath, BS Tyagi, Gyanendra Singh and B Mishra
Directorate of Wheat Research, Karnal

PHSL-5 has been registered as a unique source of very bold seed (67.9 g TGW). The genotype also has high protein content, long spikes and more grains per spike as compared to the best checks. This is a cross of Chinese wheat germplasm Long 94 444 and released wheat variety WH542.

7. PHSL-10 (IC566634; INGR09007), a Wheat (*Triticum aestivum)* Germplasm with High 1000– Grain Weight

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9. PHR-1011 (IC566636; INGR09009), a Wheat (*Triticum aestivum)* Germplasm with High Protein Content

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10. LBRL-11 (IC566637; INGR09010), a Wheat (*Triticum aestivum)* Germplasm with Resistance to Leaf Blight

Gyanendra Singh, Ravish Chatrath, Jag Shoran, DP Singh, BS Tyagi, SK Singh and B Mishra
Directorate of Wheat Research, Karnal

LBRL-11 has been registered as a source of resistance to leaf blight (*Bipolaris sorokiniana*). The genotype along with parents and a susceptible check (Sonalika) was evaluated for *Helminthosporium* Leaf Blight (HLB) reaction under artificial epiphytotic conditions for three years (2005-2008) at Karnal and also at 15 locations across the agro-climatic zones for one year (2007-08). The genotype has true resistance aganist HLB, both at seedling as well as adult plant stage and therefore can be used as an ideal source of resistance for managing leaf blight in wheat through host resistance.

11. LBRL-13 (IC566638; INGR09011), a Wheat (*Triticum aestivum)* Germplasm with Resistance to Leaf Blight

Gyanendra Singh, Ravish Chatrath, Jag Shoran, DP Singh, BS Tyagi, SK Singh and B Mishra
Directorate of Wheat Research, Karnal

LBRL-13 has been registered as a source of resistance to leaf blight (*Bipolaris sorokiniana*). The genotype along with parents and a susceptible check (Sonalika) was evaluated for *Helminthosporium* Leaf Blight (HLB) reaction under artificial epiphytotic conditions for three years (2005-2008) at Karnal and also at 15 locations across the agro-climatic zones for one year (2007-08). The genotype has true resistance aganist HLB, both at seedling as well as adult plant stage and therefore can be used as an ideal source of resistance for managing leaf blight in wheat through host resistance.

12. VQL 3 (IC568701; INGR09012), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

Maize is a globally important crop and a preferred staple food for more than one billion people in Sub-Saharan Africa, Latin America and Asia. In normal maize, all the proteins fractions except zeins are balanced for the amino acid content and are rich in lysine as well as tryptophan content. Normal maize protein is known to have a biological value of 40% of that of milk. The essential amino acids like lysine, tryptophan and threonine are in reduced quantities in maize, lysine being the most limiting followed by tryptophan. In contrast, Quality Protein Maize (QPM) has nearly twice the amount of lysine and tryptophan, which make the protein of QPM equivalent to 90% of the milk protein. This has so far been done by the deployment of mutants through conventional breeding but it can now be accomplished more precisely and rapidly by applying molecular breeding tools (Babu *et al.*, 2005; Gupta *et al.*, 2009). VQL 3 is the QPM version of CM 145 developed through 'Marker Assisted Selection' (MAS).

Morpho-agronomic Characteristics

VQL 3 is an extra early short duration QPM inbred developed by converting CM 145 by using MAS. CM 145 is one of the parents of the elite maize hybrid, Vivek Maize Hybrid 9. VQL 3 is similar to CM 145 except thet VWL 3 has the following traits, *viz*., wide leaf angle between blade and stem; anthocynin pigment present at the brace root and base of glumes; kernels being orange flint; kernel opaqueness present; and small kernel weight with high tryptophan content. It was developed by crossing CM 145 x CML 170. It has 10.29% protein and 0.85% tryptophan (of protein) where as the protein content of CM 145 is 9.5% and the tryptophan content is 0.52%. Both the protein content and the quality got improved in VQL 3 over CM 145, the increase of tryptophan over CM 145 being 63.5% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the

10. LBRL-11 (IC566637; INGR09010), a Wheat (*Triticum aestivum)* Germplasm with Resistance to Leaf Blight

Gyanendra Singh, Ravish Chatrath, Jag Shoran, DP Singh, BS Tyagi, SK Singh and B Mishra
Directorate of Wheat Research, Karnal

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11. LBRL-13 (IC566638; INGR09011), a Wheat (*Triticum aestivum)* Germplasm with Resistance to Leaf Blight

Gyanendra Singh, Ravish Chatrath, Jag Shoran, DP Singh, BS Tyagi, SK Singh and B Mishra
Directorate of Wheat Research, Karnal

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HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

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Morpho-agronomic Characteristics

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12. VQL 3 (IC568701; INGR09012), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

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Morpho-agronomic Characteristics

VQL 3 is an extra early short duration QPM inbred developed by converting CM 145 by using MAS. CM 145 is one of the parents of the elite maize hybrid, Vivek Maize Hybrid 9. VQL 3 is similar to CM 145 except thet VWL 3 has the following traits, *viz*., wide leaf angle between blade and stem; anthocynin pigment present at the brace root and base of glumes; kernels being orange flint; kernel opaqueness present; and small kernel weight with high tryptophan content. It was developed by crossing CM 145 x CML 170. It has 10.29% protein and 0.85% tryptophan (of protein) where as the protein content of CM 145 is 9.5% and the tryptophan content is 0.52%. Both the protein content and the quality got improved in VQL 3 over CM 145, the increase of tryptophan over CM 145 being 63.5% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the

morphological traits like anthocynin pigmentation of glumes and silk, time of silk emergence, ear placement, number rows of grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 3 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is recommended for children, adults, women and monogastric animals. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system.

13. VQL 8 (IC568703; INGR09013), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 8 is an extra early short duration QPM inbred developed by converting CM 145 by using MAS. CM 145 is one of the parents of the elite maize hybrid, Vivek Maize Hybrid 9. VQL 8 is similar to CM 145 except that it has the following traits, *viz*., wide leaf angle between blade and stem, straight blade attitude, anthocynin pigment present at the brace root and base of glumes, kernels orange flint, kernel opaqueness present, and medium kernel weight with high tryptophan content. It was developed by crossing CM 145 x CML 173. It has 8.84% protein and 0.94% tryptophan (of protein) where as the protein content of CM 145 is 9.5% and the tryptophan content is 0.52%. Both the protein content and the quality got improved in VQL 3 over CM 145, the increase of tryptophan over CM 145 being 80.1% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the morphological traits like anthocynin pigmentation of glumes and silk, time of silk emergence, ear placement, number rows of grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 8 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is recommended for children, adults, women and monogastric animals. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2.5 tonnes per hectare.

14. VQL 12 (IC568706; INGR09014), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 12 is an extra early short duration QPM inbred developed by converting V 25 using MAS. V 25 is an elite maize inbred suitable for the North-western Himalayan states of India. VQL 12 is similar to V 25 except that VQL 12 has small leaf angle between blade and stem, anthocynin pigment present at the brace root and base of glumes, kernels orange flint, kernel opaqueness present, conico-cylindrical ear shape and medium kernel weight with high tryptophan content. It was developed by crossing CM 145 x CML 184. It has 8.42% protein and 0.75% tryptophan (of protein) where as the protein content of V 25 is 9.6% and the tryptophan content is 0.45%. Both the protein content and the quality got improved in VQL 12 over V 25, the increase of tryptophan over V 25 being 66.7% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the

morphological traits like anthocynin pigmentation of glumes and silk, time of silk emergence, ear placement, number rows of grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 3 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is recommended for children, adults, women and monogastric animals. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system.

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Associated Characters and Cultivated Practices

VQL 8 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is recommended for children, adults, women and monogastric animals. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2.5 tonnes per hectare.

14. VQL 12 (IC568706; INGR09014), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 12 is an extra early short duration QPM inbred developed by converting V 25 using MAS. V 25 is an elite maize inbred suitable for the North-western Himalayan states of India. VQL 12 is similar to V 25 except that VQL 12 has small leaf angle between blade and stem, anthocynin pigment present at the brace root and base of glumes, kernels orange flint, kernel opaqueness present, conico-cylindrical ear shape and medium kernel weight with high tryptophan content. It was developed by crossing CM 145 x CML 184. It has 8.42% protein and 0.75% tryptophan (of protein) where as the protein content of V 25 is 9.6% and the tryptophan content is 0.45%. Both the protein content and the quality got improved in VQL 12 over V 25, the increase of tryptophan over V 25 being 66.7% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the

morphological traits like anthocynin pigmentation of glumes and silk, time of silk emergence, ear placement, number rows of grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 3 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is recommended for children, adults, women and monogastric animals. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system.

13. VQL 8 (IC568703; INGR09013), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

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Associated Characters and Cultivated Practices

VQL 8 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is recommended for children, adults, women and monogastric animals. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2.5 tonnes per hectare.

14. VQL 12 (IC568706; INGR09014), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 12 is an extra early short duration QPM inbred developed by converting V 25 using MAS. V 25 is an elite maize inbred suitable for the North-western Himalayan states of India. VQL 12 is similar to V 25 except that VQL 12 has small leaf angle between blade and stem, anthocynin pigment present at the brace root and base of glumes, kernels orange flint, kernel opaqueness present, conico-cylindrical ear shape and medium kernel weight with high tryptophan content. It was developed by crossing CM 145 x CML 184. It has 8.42% protein and 0.75% tryptophan (of protein) where as the protein content of V 25 is 9.6% and the tryptophan content is 0.45%. Both the protein content and the quality got improved in VQL 12 over V 25, the increase of tryptophan over V 25 being 66.7% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the

morphological traits like anthocynin pigmentation of anthers, glumes and silk, time of silk emergence, ear length, type of grains, number of rows of grains, colour of the grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 12 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2.5 tonnes per hectare. It is recommended for children, adults, women and monogastric animals for food and nutritional security.

15. VQL 16 (IC569174; INGR09015), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 16 is an extra early short duration QPM inbred developed by converting V 340 by using MAS. V 340 is one of the parents of the elite maize inbred suitable for the north western Himalayan states of India. VQL 16 is similar to V 340 except that VQL 16 has wide leaf angle between blade and the stem, anthocynin pigment absent at the brace root and present at the base of glumes, kernels yellow flint, kernel opaqueness present, cylindrical ear shape and medium kernel weight with high tryptophan content. It was developed by crossing V 340 x CML 173. It has 8.30% protein and 0.73% tryptophan (of protein) where as the protein content of V 340 is 8.73% and the tryptophan content is 0.43%. Both the protein content and the quality got improved in VQL 16 over V 340, the increase of tryptophan over V 340 being 69.8% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the morphological traits like, anthocynin pigmentation of anthers, glumes, sheath and silk, time of silk emergence, ear length, type of grains, number of rows of grains, density of grains, kernel 1000-grain weight, colour of the grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the non-QPM and QPM inbreds.

Associated Characters and Cultivated Practices

VQL 16 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2 tonnes per hectare. It is recommended for children, adults, women and monogastric animals as food for the nutritional security.

morphological traits like anthocynin pigmentation of anthers, glumes and silk, time of silk emergence, ear length, type of grains, number of rows of grains, colour of the grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 12 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2.5 tonnes per hectare. It is recommended for children, adults, women and monogastric animals for food and nutritional security.

15. VQL 16 (IC569174; INGR09015), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 16 is an extra early short duration QPM inbred developed by converting V 340 by using MAS. V 340 is one of the parents of the elite maize inbred suitable for the north western Himalayan states of India. VQL 16 is similar to V 340 except that VQL 16 has wide leaf angle between blade and the stem, anthocynin pigment absent at the brace root and present at the base of glumes, kernels yellow flint, kernel opaqueness present, cylindrical ear shape and medium kernel weight with high tryptophan content. It was developed by crossing V 340 x CML 173. It has 8.30% protein and 0.73% tryptophan (of protein) where as the protein content of V 340 is 8.73% and the tryptophan content is 0.43%. Both the protein content and the quality got improved in VQL 16 over V 340, the increase of tryptophan over V 340 being 69.8% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the morphological traits like, anthocynin pigmentation of anthers, glumes, sheath and silk, time of silk emergence, ear length, type of grains, number of rows of grains, density of grains, kernel 1000-grain weight, colour of the grains, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the non-QPM and QPM inbreds.

Associated Characters and Cultivated Practices

VQL 16 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2 tonnes per hectare. It is recommended for children, adults, women and monogastric animals as food for the nutritional security.

16. VQL 30 (IC569176; INGR09016), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 30 is an extra early short duration QPM inbred developed by converting V 360 by using MAS. V 360 is an elite maize inbred suitable for the North-western Himalayan states of India. VQL 30 is similar to V 360 except that VQL 30 has anthocynin pigment absent at the brace root and at base of glumes, kernels orange flint with cap, kernel opaqueness present, cylindrical ear shape, and medium kernel weight with high tryptophan content. It was developed by crossing V 360 x CML 189. It has 8.07% protein and 0.71% tryptophan (of protein) content where as the protein content of V 360 is 8.75% and the tryptophan content is 0.48%. Both the protein content and the quality got improved in VQL 30 over V 360, the increase of tryptophan over V 360 being 47.9% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the morphological traits like the angle between blade and stem, anthocynin colouration of brace root, anthocynin pigmentation of anthers, glumes and silk, time of silk emergence, ear length, type of grains, number of rows of grains, colour of the grains, density of spikelets, time of silk emergence, shape and diameter of ear, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 30 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for the hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2.5 tonnes per hectare. It is recommended for children, adults, women and monogastric animals as food and feed for the nutritional security.

References

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Gupta HS, PK Agrawal, V Mahajan, VP Mani, GS Bisht, A Kumar, P Verma and R Babu (2009) Quality protein maize for nutritional security: Rapid development of short duration hybrids through molecular marker assisted breeding. *Current Sci*. **96**: 230-237.

17. SPV 1742 (IC565017; INGR09017), a Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, Good Roti and Dough Making Qualities

M Elangovan, UD Chavan, VR Bhagwat, TG Nageswararao, B Venkatesh Bhat and CV Ratnavathi
National Research Centre for Sorghum, Hyderabad

Sorghum variety SPV 1742 (INGR09017) with superior roti and dough quality was identified at National Research Centre for Sorghum (NRCS), Hyderabad. The variety was developed through selection from the exotic collection EC515837 imported from Sri Lanka. It was analysed for roti and dough quality parameters at All India Coordinated Sorghum Improvement Project centres during 2007-08. It was identified as superior genotype in eight out of ten roti quality parameters and six out of seven dough quality parameters. The evaluation of roti quality was done on a hedonic scale 1 to 9 ranging from like extremely excellent (1) to dislike extremely (9). The quality parameters of SPV 1742 and check are presented in Table 1.

16. VQL 30 (IC569176; INGR09016), a Maize (*Zea maize* L.) Germplasm, a High Tryptophan Coupled with Reasonably High Protein Content

HS Gupta, PK Agrawal, B Kalyana Babu, Vinay Mahajan, S Saha, GS Bisht and MC Pant
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

VQL 30 is an extra early short duration QPM inbred developed by converting V 360 by using MAS. V 360 is an elite maize inbred suitable for the North-western Himalayan states of India. VQL 30 is similar to V 360 except that VQL 30 has anthocynin pigment absent at the brace root and at base of glumes, kernels orange flint with cap, kernel opaqueness present, cylindrical ear shape, and medium kernel weight with high tryptophan content. It was developed by crossing V 360 x CML 189. It has 8.07% protein and 0.71% tryptophan (of protein) content where as the protein content of V 360 is 8.75% and the tryptophan content is 0.48%. Both the protein content and the quality got improved in VQL 30 over V 360, the increase of tryptophan over V 360 being 47.9% (Agrawal *et al.*, 2008; Babu *et al.*, 2009). Both these lines are resistant to turcicum blight and both have hard grains. The duration of both the inbreds range from 85-90 days. Besides, the morphological traits like the angle between blade and stem, anthocynin colouration of brace root, anthocynin pigmentation of anthers, glumes and silk, time of silk emergence, ear length, type of grains, number of rows of grains, colour of the grains, density of spikelets, time of silk emergence, shape and diameter of ear, kernel waxiness, kernel poppyness, sweetness (absent) are similar between both the inbreds.

Associated Characters and Cultivated Practices

VQL 30 being QPM is a better replacement of normal maize for better nutrition. It will improve the nutritional status of food and feed. It is also resistant to turcicum blight which is a major disease of maize. Being a short duration crop, it is suitable for the hills, peninsular India and those parts of plains where a short duration maize crop will fit to the prevalent cropping system. It is highly responsive to fertilizer application. Under good agronomic conditions, the inbred seed production goes up to 2.5 tonnes per hectare. It is recommended for children, adults, women and monogastric animals as food and feed for the nutritional security.

References

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17. SPV 1742 (IC565017; INGR09017), a Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, Good Roti and Dough Making Qualities

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Table 1. Roti and dough quality analysis at AICSIP trials

Parameters	Dharwad check	SPV 1742
Dough quality		
Water absorption capacity (%)	186.60	172.67
Soluble proteins (%)	1.29	1.26
Crude protein (%)	10.25	9.38
Starch (%)	69.75	70.58
Total soluble sugars (%)	2.19	2.11
Hecto litre weight of the grain (kg/hl)	81.70	81.38
Roti quality		
Water required for dough (ml/ 100 g flour)	125.00	104.44
Colour and appearance	1.67	2.27
Flavour/ aroma	2.00	2.50
Texture	2.03	2.67
Taste 2.17	2.90	
Overall acceptability	1.67	2.47
Kneading quality of dough	1.00	1.00
Storage study of roti (4 h) and 8 h	1.65, 2.47	1.67, 2.47

Source: AICSIP (2008)

The variety is medium in height, semi-compact and elliptical panicle shape. Its seeds are bold and pearly white in colour. It recorded 27 q/ ha and 14 t/ ha of grain yield and fodder yield, respectively with recommended dose of fertilizer. Apart from the roti quality and grain yield, it is also resistant to grain mold and anthracnose in Zone I; resistant to shoot fly in Zone II; resistant to spotted stem borer in Zone I and III; midge resistant in Zone II and III; and resistant to head bug in Zone II.

As sorghum grains are very nutritious and traditional food for the millions of farmers living in the semi-arid tropics of the country. It is consumed as unleavened bread (*bhakri*). The variety also can be used in these regions.

Reference

AICSIP (2008) Report on the AICSIP coordinating team. AICSIP Tech. Pub. Number – 1/2008 (Book 1 of 3 – AGM 08, pre-meet).

18. MS Line 126A and B (IC567687 and IC567688; INGR09018), Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, a Source of Male Sterility

S Audilakshmi, C Aruna and N Seetharama
National Research Centre for Sorghum, Hyderabad

MS line 126A and B is a new sweet sorghum MS line with sweet and grey yellow grain colour. The male sterile line 126A and B was developed from a cross between 2219B x SPV 126 during 1990 by pedigree breeding. The F_2 population was raised during the year 1992, and 20 agronomic superior derivatives were advanced. Based on agronomic superiority the selections were reduced down to six in F_2. The superior cross derivatives in F_4 were test crossed for identification of line with maintainer gene and the steriles were advanced further to BC_5. One argonomically superior male sterile line having good combining ability was developed as 126B male sterile line.

Table 1. Roti and dough quality analysis at AICSIP trials

Parameters	Dharwad check	SPV 1742
Dough quality		
Water absorption capacity (%)	186.60	172.67
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As sorghum grains are very nutritious and traditional food for the millions of farmers living in the semi-arid tropics of the country. It is consumed as unleavened bread (*bhakri*). The variety also can be used in these regions.

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18. MS Line 126A and B (IC567687 and IC567688; INGR09018), Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, a Source of Male Sterility

S Audilakshmi, C Aruna and N Seetharama
National Research Centre for Sorghum, Hyderabad

MS line 126A and B is a new sweet sorghum MS line with sweet and grey yellow grain colour. The male sterile line 126A and B was developed from a cross between 2219B x SPV 126 during 1990 by pedigree breeding. The F_2 population was raised during the year 1992, and 20 agronomic superior derivatives were advanced. Based on agronomic superiority the selections were reduced down to six in F_2. The superior cross derivatives in F_4 were test crossed for identification of line with maintainer gene and the steriles were advanced further to BC_5. One argonomically superior male sterile line having good combining ability was developed as 126B male sterile line.

19. MS Line 91A and B (IC567689 and IC567690; INGR09019), Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, a Source of Male Sterility

S Audilakshmi, C Aruna and N Seetharama
National Research Centre for Sorghum, Hyderabad

MS line 91A and B is new medium dwarf sweet sorghum male sterile line with yellow grain color, source of male sterility. The male sterile line 91A and B was developed from a cross between 2219B x SPV 221 during 1994. The F_2 population was raised during the year 1996, and 25 agronomically superior derivatives were advanced. The selections were reduced down to six in F_4. The superior cross derivatives in F_4 were test crossed for identification of lines with maintainer gene and the steriles were advanced further to BC_5. One argonomically superior male sterile line having good combining ability was developed as 91B male sterile line.

20. MS Line 356A and B (IC567691 and IC567692; INGR09020), Sorghum [*Sorghum bicolor* (L) Moench] Germplasm, a Source of Male Sterility

S Audilakshmi, C Aruna and N Seetharama
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MS line 356A and B is new medium dwarf tall sweet sorghum male sterile line with high cane yield, source of male sterility. The male sterile line 356A and B was developed from multiple cross among 2219B (female parent of CSH 6), IS 3691 (a germplasm line) and M 35-1 (Indian local) during 1994. The F_2 population was raised during the year 1996, and 22 agronomically superior derivatives were advanced. The selections were reduced down to six in F_4. The superior cross derivatives in F_4 were test crossed for identification of lines with maintainer gene and the steriles were advanced further to BC_5. One argonomically superior male sterile line having good combining ability was developed as 356B male sterile line.

21. MS Line 288A and B (IC567693 and IC567694; INGR09021), Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, a Source of Male Sterility

S Audilakshmi, C Aruna and N Seetharama
National Research Centre for Sorghum, Hyderabad

MS line 288A and B is new tall and very bold sweet sorghum male sterile line with, source of male sterility. The male sterile line 288A and B was developed from crossing two elite MS lines; one Kharif MS line and 422B and one rabi MS line during 1996. Selection was made according to pedigree method in F_2. The F_2 population was raised during 1998, and 20 agronomically superior derivatives were advanced. The selections were reduced down to six in F_4. The superior cross derivatives in F_4 were test crossed for identification of lines with maintainer gene and the steriles were advanced further to BC_5. One argonomically superior male sterile line having good combining ability was developed as 288B male sterile line.

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22. MS Line 45A and B (IC567695 and IC567696; INGR09022), Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, a Source of Male Sterility

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MS line 45A and B is new medium tall and bold grain sweet sorghum male sterile line with, source of male sterility. The male sterile line MS line 45A and B was developed from crossing two elite MS lines 296B with Indian local M 35-1 during 1992. The F_2 population was raised during 1994, and 25 agronomically superior derivatives were advanced. The selections were reduced down to six in F_4. The superior cross derivatives in F_4 were test crossed for identification of lines with maintainer gene and the steriles were advanced further to BC_5. One argonomically superior male sterile line having good combining ability was developed as 45B male sterile line.

23. Kagazi madira (B 29) (IC568707; INGR09023), a Barnyard millet (*Echinochloa frumentacea*) Germplasm, Easy De-hulling Type

Arun Gupta, Vinay Mahajan, HS Gupta, KP Singh and GS Bisht
Vivekanand Parvatiya Krishi Anusandhan Sansthan, ICAR, Almora

One of the major hurdles in popularizing small millet except finger millet is the need for de-hulling and pearling before use it for cooking. This process is time consuming and causes drudgery to women as the grains are firmly encased inside the lemma. Identifying varieties which have loose lemma covering and easy to remove is a very important character to utilize in crop improvement programme. B 29 an easy dehulling accession identified from barnyard millet germplasm. The validity test was conducted by rubbing 100 seeds, 100 times on palm. About 48 to 62% seeds of B 29 were dehulled as compared to 5-7% in VL Madira 172.

24. GT-289 (IC565832; INGR09024), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-289A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and SKNP 289 as non-recurrent and recurrent parent, respectively. It has determinate growth with early maturity. Red flowers with unique open petals, purple red stem and red bold seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Associated Characters

GT-289A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	DT
2	Pod bearing habit	Bunch
3	Days of flower	95
4	Maturity days	141
5	Plant height (cm)	75
6	Average number of branches/plant	4.7
7	Average number 0of pods/plant	87
8	Average pod length (cm)	4.7
9.	Average number of seeds/pod	4.0
10	100-seed weight (g)	10.6
11	Seed colour	Red
12	Flower colour	Red
13	Stem colour	Red
14	Average yield/plant (g)	29

22. MS Line 45A and B (IC567695 and IC567696; INGR09022), Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm, a Source of Male Sterility

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Associated Characters

GT-289A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

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13	Stem colour	Red
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24. GT-289 (IC565832; INGR09024), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

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Associated Characters

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10	100-seed weight (g)	10.6
11	Seed colour	Red
12	Flower colour	Red
13	Stem colour	Red
14	Average yield/plant (g)	29

25. GT-308A (IC565833; INGR09025), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-308A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and ICPL 87051 as non-recurrent and recurrent parent, respectively. It has determinate growth with green stem, early maturity, red flowers and creamy white medium seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	101
4	Maturity days	148
5	Plant height (cm)	132
6	Average number of branches/plant	10.0
7	Average number of pods/plant	187
8	Average pod length (cm)	4.2
9	Average number of seeds/pod	3.8
10	100-seed weight (g)	9.3
11	Seed colour	Creamy white
12	Flower colour	Red
13	Stem colour	Green
14	Average yield/plant (g)	44

Associated Characters

GT-308A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

26. GT-310A (IC565834; INGR09026), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-310A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and BDN 31 as non-recurrent and recurrent parent, respectively. It has determinate growth with green stem, early maturity, yellow flowers and creamy white medium seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	DT
2	Pod bearing habit	Spreading
3	Days of flower	96
4	Maturity days	143
5	Plant height (cm)	89
6	Average number of branches/plant	14.0
7	Average number of pods/plant	148
8	Average pod length (cm)	4.6
9	Average number of seeds/pod	3.6
10	100-seed weight (g)	9.4
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	34

Associated Characters

GT-310A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

25. GT-308A (IC565833; INGR09025), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-308A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and ICPL 87051 as non-recurrent and recurrent parent, respectively. It has determinate growth with green stem, early maturity, red flowers and creamy white medium seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	101
4	Maturity days	148
5	Plant height (cm)	132
6	Average number of branches/plant	10.0
7	Average number of pods/plant	187
8	Average pod length (cm)	4.2
9	Average number of seeds/pod	3.8
10	100-seed weight (g)	9.3
11	Seed colour	Creamy white
12	Flower colour	Red
13	Stem colour	Green
14	Average yield/plant (g)	44

Associated Characters

GT-308A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

26. GT-310A (IC565834; INGR09026), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-310A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and BDN 31 as non-recurrent and recurrent parent, respectively. It has determinate growth with green stem, early maturity, yellow flowers and creamy white medium seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	DT
2	Pod bearing habit	Spreading
3	Days of flower	96
4	Maturity days	143
5	Plant height (cm)	89
6	Average number of branches/plant	14.0
7	Average number of pods/plant	148
8	Average pod length (cm)	4.6
9	Average number of seeds/pod	3.6
10	100-seed weight (g)	9.4
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	34

Associated Characters

GT-310A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

27. GT-501A (IC565835; INGR09027), a Pigeon pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-501A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and ICPL 7622 as non-recurrent and recurrent parent, respectively. It is a medium maturity line with non-determinate growth habit, green stem, yellow flowers and creamy white bold seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	108
4	Maturity days	160
5	Plant height (cm)	152
6	Average number of branches/ plant	6.4
7	Average number of pods/ plant	129
8	Average pod length (cm)	3.5
9	Average number of seeds/ pod	3.3
10	100-seed weight (g)	10.0
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	35

Associated Characters

GT-501A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

28. GT-505A (IC565836; INGR09028), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-505A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and AGS 55 as non-recurrent and recurrent parent, respectively. It is a medium maturity line with non-determinate growth habit, green stem, yellow flowers and creamy white medium seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	110
4	Maturity days	157
5	Plant height (cm)	164
6	Average number of branches/ plant	7.4
7	Average number of pods/ plant	146
8	Average pod length (cm)	3.9
9	Average number of seeds/ pod	3.8
10	100-seed weight (g)	9.1
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	40

Associated Characters

GT-505A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

27. GT-501A (IC565835; INGR09027), a Pigeon pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-501A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and ICPL 7622 as non-recurrent and recurrent parent, respectively. It is a medium maturity line with non-determinate growth habit, green stem, yellow flowers and creamy white bold seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	108
4	Maturity days	160
5	Plant height (cm)	152
6	Average number of branches/ plant	6.4
7	Average number of pods/ plant	129
8	Average pod length (cm)	3.5
9	Average number of seeds/ pod	3.3
10	100-seed weight (g)	10.0
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	35

Associated Characters

GT-501A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

28. GT-505A (IC565836; INGR09028), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] CGMS Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GT-505A is an unique stable cytoplasmic-genic male sterile line developed at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar through back crossing method using GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) and AGS 55 as non-recurrent and recurrent parent, respectively. It is a medium maturity line with non-determinate growth habit, green stem, yellow flowers and creamy white medium seeds. The genetic stock is a *sui-generis* new cytoplasmic genetic male sterile line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	110
4	Maturity days	157
5	Plant height (cm)	164
6	Average number of branches/ plant	7.4
7	Average number of pods/ plant	146
8	Average pod length (cm)	3.9
9	Average number of seeds/ pod	3.8
10	100-seed weight (g)	9.1
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	40

Associated Characters

GT-505A is a potent male sterile line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

29. GTR-7 (IC565837; INGR09029), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-7 was selected from stable line ICPL 8976 having fertility restoration properties of *scarabaeoides* background cytoplasm sterile line GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It was developed through selection from ICP 8976, medium duration material. It has determinate growth habit with late maturity, green stem, yellow flowers and creamy white medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	130
4	Maturity days	210
5	Plant height (cm)	185
6	Average number of branches/ plant	8.4
7	Average number of pods/ plant	136
8	Average pod length (cm)	4.0
9	Average number of seeds/ pod	3.5
10	100-seed weight (g)	9.4
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green

Associated Characters

GTR-7 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

30. GTR-35 (IC565838; INGR09030), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-35 was F_5 derivative of SKNPCH 10-1-2-1-2, where SKNPCH 10 (CMS GT 288A x GTR 11) having fertility restoration properties developed through pedigree selection at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has determinate growth habit with early maturity, green stem, yellow flowers and red medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	DT
2	Pod bearing habit	Bunch
3	Days of flower	98
4	Maturity days	142
5	Plant height (cm)	84
6	Average number of branches/ plant	5.0
7	Average number of pods/ plant	95
8	Average pod length (cm)	5.2
9	Average number of seeds/ pod	4.2
10	100-seed weight (g)	9.0
11	Seed colour	Red
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	

Associated Characters

GTR-35 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

29. GTR-7 (IC565837; INGR09029), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-7 was selected from stable line ICPL 8976 having fertility restoration properties of *scarabaeoides* background cytoplasm sterile line GT 288A (first stable cytoplasmic-genic male sterile line developed by using *Cajanus scarabaeoides* as female and *Cajanus cajan* as male) at the Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It was developed through selection from ICP 8976, medium duration material. It has determinate growth habit with late maturity, green stem, yellow flowers and creamy white medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	130
4	Maturity days	210
5	Plant height (cm)	185
6	Average number of branches/ plant	8.4
7	Average number of pods/ plant	136
8	Average pod length (cm)	4.0
9	Average number of seeds/ pod	3.5
10	100-seed weight (g)	9.4
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green

Associated Characters

GTR-7 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

30. GTR-35 (IC565838; INGR09030), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-35 was F_5 derivative of SKNPCH 10-1-2-1-2, where SKNPCH 10 (CMS GT 288A x GTR 11) having fertility restoration properties developed through pedigree selection at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has determinate growth habit with early maturity, green stem, yellow flowers and red medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	DT
2	Pod bearing habit	Bunch
3	Days of flower	98
4	Maturity days	142
5	Plant height (cm)	84
6	Average number of branches/ plant	5.0
7	Average number of pods/ plant	95
8	Average pod length (cm)	5.2
9	Average number of seeds/ pod	4.2
10	100-seed weight (g)	9.0
11	Seed colour	Red
12	Flower colour	Yellow
13	Stem colour	Green
14	Average yield/plant (g)	

Associated Characters

GTR-35 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

31. GTR-42 (IC565839; INGR09031), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-42 was F_4 derivative of SKNPCH 8-1-1-5, where SKNPCH 8 (CMS 288A x GTR-8) having fertility restoration properties developed through pedigree selection at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has non-determinate growth habit with medium maturity, green stem, yellow flowers and creamy white small seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	102
4	Maturity days	151
5	Plant height (cm)	152
6	Average number of branches/ plant	7.0
7	Average number of pods/ plant	97
8	Average pod length (cm)	4.1
9	Average number of seeds/ pod	4.0
10	100-seed weight (g)	7.25
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green

Associated Characters

GTR-42 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

32. GTR-43 (IC565840; INGR09032), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-43 was F_4 derivative of SKNPCH 6-3-1-3, where SKNPCH 6 (CMS 288A x GTR-6) having fertility restoration properties developed through pedigree selection method at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has non-determinate growth habit with medium maturity, green stem, yellow flowers and red medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	120
4	Maturity days	172
5	Plant height (cm)	164
6	Average number of branches/ plant	5.0
7	Average number of pods/ plant	125
8	Average pod length (cm)	4.2
9	Average number of seeds/ pod	4.0
10	100-seed weight (g)	8.25
11	Seed colour	Red
12	Flower colour	Yellow
13	Stem colour	Green

Associated Characters

GTR-43 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea.

31. GTR-42 (IC565839; INGR09031), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-42 was F_4 derivative of SKNPCH 8-1-1-5, where SKNPCH 8 (CMS 288A x GTR-8) having fertility restoration properties developed through pedigree selection at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has non-determinate growth habit with medium maturity, green stem, yellow flowers and creamy white small seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	102
4	Maturity days	151
5	Plant height (cm)	152
6	Average number of branches/ plant	7.0
7	Average number of pods/ plant	97
8	Average pod length (cm)	4.1
9	Average number of seeds/ pod	4.0
10	100-seed weight (g)	7.25
11	Seed colour	Creamy white
12	Flower colour	Yellow
13	Stem colour	Green

Associated Characters

GTR-42 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

32. GTR-43 (IC565840; INGR09032), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Fertility Restorer Line

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-43 was F_4 derivative of SKNPCH 6-3-1-3, where SKNPCH 6 (CMS 288A x GTR-6) having fertility restoration properties developed through pedigree selection method at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has non-determinate growth habit with medium maturity, green stem, yellow flowers and red medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Table 1. Morpho-agronomic characteristics

S.N	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	120
4	Maturity days	172
5	Plant height (cm)	164
6	Average number of branches/ plant	5.0
7	Average number of pods/ plant	125
8	Average pod length (cm)	4.2
9	Average number of seeds/ pod	4.0
10	100-seed weight (g)	8.25
11	Seed colour	Red
12	Flower colour	Yellow
13	Stem colour	Green

Associated Characters

GTR-43 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea.

33. GTR-55 (IC565841; INGR09033), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Germplasm, a Fertility Restorer

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-55 was F_4 derivative of SKNPCH 9-2-2-1, where SKNPCH 9 (CMS 288A x GTR-9) having fertility restoration properties developed by adopting pedigree selection method at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has non-determinate growth habit with early maturity, green stem, yellow flowers and red medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Associated Characters

GTR-55 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	98
4	Maturity days	142
5	Plant height (cm)	118
6	Average number of branches/plant	7.0
7	Average number of pods/plant	132
8	Average pod length (cm)	4.2
9	Average number of seeds/pod	4.0
10	100-seed weight (g)	8.16
11	Seed colour	Red
12	Flower colour	Yellow
13	Stem colour	Green

Reference

Acharya S, JB Patel, PT Patel and SBS Tikka (2005) Characterization of stable and diversified CGMS (A) and restorer (R line) of Pigeonpea. *GAU Res. J.* **30(1-2)**: 1-7.

34. MUB-4 (IC557433; INGR09034), a Black Gram (*Vigna mungo* L. Hepper) Mutant with Shining Yellow Seeds

AK Sharma
Sardar Ballavbhai Patel University and Technology, Meerut

Urdbean (Black gram) is well known for its black rough seeds and black colour and almost all the varieties of blackgram are generally of rough black seed with black pods. The present mutant MUB 4 has brown colour pods, yellow shining seeds, tall and high yielding with higher 100 seed weight (4.84 g). Four hundred pure, uniform, healthy and dry (9.5 % moisture) seeds of cultivar Pant Urd-30 were treated with ^{60}Co gamma rays (100, 200, 300 and 400 Gy doses), EMS (0.2, 0.4, 0.6 and 0.8%) and combination of gamma doses, *viz.*, 100, 200, 300 and 400 Gy with 0.2 % EMS during Summer, 2001 at Research Farm, Institute of Ag. Sciences, BHU, Varanasi. In M_2 generation, eight double mutations for seed and pod colour were observed in different frequencies in various treatments of EMS, gamma rays and combination of both. A brown colour pods with yellow rough seed mutant was identified and selected in the 300Gy+0.2% combination dose of gamma rays and EMS. This mutant was evaluated during two consecutive years in the field conditions alongwith parent.

The data were recorded on 10 randomly selected plants from each replication for different yield and yield attributing traits, *viz.*, plant height, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and grain yield per plant whereas days to flowering and days to maturity were observed on the plot basis in M_4 generation during Kharif, 2002. Such seed and pod colour mutants accompanied higher grain yield (7.1 g) may be used as a variety or breeding line directly and indirectly for the improvement of blackgram crop. Such mutations for different seed colour were also reported in other pulse crops, *viz.*, buff and black colour mutants in arhar (Ali Khan and Veeraswamy, 1974), yellow colour mutations in soybean (Takagi and Hiraiwa, 1980) and dull green to shining green and golden yellow tester mutant in mungbean (Singh *et al*., 1982). A single gene but the simultaneous variations for yields and other morphological characters indicate a gross change or perhaps very closely related linked group of genes are controlling this trait (Saini *et al*., 1974). Such pod and

33. GTR-55 (IC565841; INGR09033), a Pigeon Pea [*Cajanu cajan* (L.) Millsp] Germplasm, a Fertility Restorer

S Acharya, JB Patel and SBS Tikka
SD Agricultural University, Sardarkrushinagar, Gujarat

GTR-55 was F_4 derivative of SKNPCH 9-2-2-1, where SKNPCH 9 (CMS 288A x GTR-9) having fertility restoration properties developed by adopting pedigree selection method at Main Pulses Research Station, SD Agricultural University, Sardarkrushinagar. It has non-determinate growth habit with early maturity, green stem, yellow flowers and red medium seeds. The genetic stock is a *sui-generis* restorer line. The line was identified as a genetically diverse material by SDAU Germplasm Identification Committee vide its meeting held on August 31, 2007.

Associated Characters

GTR-55 is a good restore line which can be further utilized in development of CGMS based hybrids in pigeonpea (Table 1).

Table 1. Morpho-agronomic characteristics

S.N.	Description of character	
1	Growth habit	NDT
2	Pod bearing habit	Spreading
3	Days of flower	98
4	Maturity days	142
5	Plant height (cm)	118
6	Average number of branches/plant	7.0
7	Average number of pods/plant	132
8	Average pod length (cm)	4.2
9	Average number of seeds/pod	4.0
10	100-seed weight (g)	8.16
11	Seed colour	Red
12	Flower colour	Yellow
13	Stem colour	Green

Reference

Acharya S, JB Patel, PT Patel and SBS Tikka (2005) Characterization of stable and diversified CGMS (A) and restorer (R line) of Pigeonpea. *GAU Res. J.* **30(1-2)**: 1-7.

34. MUB-4 (IC557433; INGR09034), a Black Gram (*Vigna mungo* L. Hepper) Mutant with Shining Yellow Seeds

AK Sharma
Sardar Ballavbhai Patel University and Technology, Meerut

Urdbean (Black gram) is well known for its black rough seeds and black colour and almost all the varieties of blackgram are generally of rough black seed with black pods. The present mutant MUB 4 has brown colour pods, yellow shining seeds, tall and high yielding with higher 100 seed weight (4.84 g). Four hundred pure, uniform, healthy and dry (9.5 % moisture) seeds of cultivar Pant Urd-30 were treated with ^{60}Co gamma rays (100, 200, 300 and 400 Gy doses), EMS (0.2, 0.4, 0.6 and 0.8%) and combination of gamma doses, *viz.*, 100, 200, 300 and 400 Gy with 0.2 % EMS during Summer, 2001 at Research Farm, Institute of Ag. Sciences, BHU, Varanasi. In M_2 generation, eight double mutations for seed and pod colour were observed in different frequencies in various treatments of EMS, gamma rays and combination of both. A brown colour pods with yellow rough seed mutant was identified and selected in the 300Gy+0.2% combination dose of gamma rays and EMS. This mutant was evaluated during two consecutive years in the field conditions alongwith parent.

The data were recorded on 10 randomly selected plants from each replication for different yield and yield attributing traits, *viz.*, plant height, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and grain yield per plant whereas days to flowering and days to maturity were observed on the plot basis in M_4 generation during Kharif, 2002. Such seed and pod colour mutants accompanied higher grain yield (7.1 g) may be used as a variety or breeding line directly and indirectly for the improvement of blackgram crop. Such mutations for different seed colour were also reported in other pulse crops, *viz.*, buff and black colour mutants in arhar (Ali Khan and Veeraswamy, 1974), yellow colour mutations in soybean (Takagi and Hiraiwa, 1980) and dull green to shining green and golden yellow tester mutant in mungbean (Singh *et al*., 1982). A single gene but the simultaneous variations for yields and other morphological characters indicate a gross change or perhaps very closely related linked group of genes are controlling this trait (Saini *et al*., 1974). Such pod and

Table 1. Mean values of yield and yield attributing traits of different seed colour mutants in M_4 generation

Mutant line	Days to flowering	Days to maturity	Plant height (cm)	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100-seed weight (g)	Grain yield plant^{-1}(g)
MUB 4	40.0	86.5	38.7	34.6	4.9	4.8	4.8	7.1
Parent (PU-30)	46.0	100.0	41.9	26.8	3.85	4.71	3.92	4.85
LSD (5%)	0.50	0.81	2.34	0.70	0.72	0.31	0.78	1.24

Fig. 1: Yellow shining seed with brown colour pods

seed colour mutations will increase the demand and market value of the blackgram among the consumer and also help in genetic and molecular study of the traits in future.

References

Ali Khan WM and R Veeraswamy (1974) Mutations induced in redgram (*Cajanus cajan* L.) by gamma radiation and EMS. *Rad. Bot.* **14**: 237-242.

Grover IS and SK Tejpaul (1979) Induced mutation in green gram. *Genet. Pol*. **20**: 529-540.

Saini, RG, JL Minocha and A Singh (1974) Sterile mutant of *Phaseolus aureus. Sci. Cul.* **40(1)**: 37-38.

Singh VP, RDS Yadav, BD Singh, RM Singh and RB Singh (1982). Note on a golden seed coat colour mutant of mungbean (*Vigna radiata* L.) induced by gamma radiation. *Legume Res.* **5(2)**: 111-114.

Takagi Y and S Hiraiwa (1980) Seed coat colour mutant in soyabean (*Glycine max* L.). *Agril. Bull. Saga. Uni.* **48**: 87-92.

35. RG 2787 (IC374319; INGR09035), a Castor (*Ricinus communis* L.) Germplasm, a Source of Multiple Resistance

K Anjani and MA Raoof
Directorate of Oilseeds, Rajendranagar, Hyderabad-500 030

Fusarium wilt, *Macrophomina* root rot and *Botrytis* grey rot are the major yield losing disease in castor. In addition to these, presence of nematodes further aggravates wilt incidence in the wilt infested castor fields. A common resistance source for all the major biotic stress is a boom to plant breeder to work with in multiple disease resistance breeding programme aimed at development of cultivar resistant all these biotic stress.

RG 2787 is a unique accession exhibiting stable multiple resistance to *Botrytis* grey rot, *Fusarium* wilt, *Macrophimina* root rot and nematodes. It is the first source of resistance reported to be resistance to the most devastating *Botrytis* grey rot disease in castor. It is a selection from germplasm accession KA37/01 collected from Tamil Nadu (Ashoka Vardhana Reddy *et al.*, 2002).

RG 2787 was screened against *Botrytis* grey rot (*Botryrits ricini*) under heavy disease pressure created under artificial inoculation condition in the field from 2003-04 to 2007-08. It showed resistant reaction consistently in all years of screening where the disease incidence in the susceptible check VP-I was from 82.5 to 100% (Table 1).

T able 1. Resistant reaction of RG 2787 against *botrytis* grey rot under artificial inoculation conditions

Year of screening	*Botrytis* incidence (%)*	
	RG2787	Susceptible check VP-1
2003-04	0.0	82.5
2004-05	6.22	89.5
2006-07	2.9	100.0
2007-08	0.0	–

*<10% disease is rated resistant

RG 2787 was screening against wilt (*Fusarium ozysporum* f.sp. *ricini*), in three wilt sick plots from 2003-04 to 2007-08 in AICRP (Castor) disease screening trails. It consistently exhibited resistant reaction (0-17.6%) at both locations in all the years of screening (Table 2).

Table 1. Mean values of yield and yield attributing traits of different seed colour mutants in M_4 generation

Mutant line	Days to flowering	Days to maturity	Plant height (cm)	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100-seed weight (g)	Grain yield plant^{-1}(g)
MUB 4	40.0	86.5	38.7	34.6	4.9	4.8	4.8	7.1
Parent (PU-30)	46.0	100.0	41.9	26.8	3.85	4.71	3.92	4.85
LSD (5%)	0.50	0.81	2.34	0.70	0.72	0.31	0.78	1.24

Fig. 1: Yellow shining seed with brown colour pods

seed colour mutations will increase the demand and market value of the blackgram among the consumer and also help in genetic and molecular study of the traits in future.

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2004-05	6.22	89.5
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2007-08	0.0	–

*<10% disease is rated resistant

RG 2787 was screening against wilt (*Fusarium ozysporum* f.sp. *ricini*), in three wilt sick plots from 2003-04 to 2007-08 in AICRP (Castor) disease screening trails. It consistently exhibited resistant reaction (0-17.6%) at both locations in all the years of screening (Table 2).

Table 2. Resistant reaction of RG2787 against wilt in wilt sick plots

Year of	Wilt resistance (%)*			
	DOR, Hyderabad		S.K. Nagar	
	RG2787	SC	RG2787	SC
2003-04	14.3	VP-1 (SC): 88.5	0.0	GAUCH-1 (SC): 98.5
2005-06	5.8	VP-1 (SC): 93.8	0.0	JI-35 (SC): 100
2006-07	17.6	VP-1 (SC): 100	0.0	JI-35 (SC): 100
2007-08	15.3	JI-35 (SC): 100	10.0	JI-35 (SC): 100

*<20% wilt incidence is rated as resistant; SC: Susceptible check

RG 2787 was screened against root rot (*Macrophomina phaseolina*) in root rot sick plot from 2003-04 to 2007-08 under AICRP (Castor) disease screening trials. It exhibited high resistance reaction (0-5.8%) against root rot consistently in all the years of screening (Table 3).

Table 3. Resistant reaction of RG2787 against root rot sick plot

Year of screening	Root rot incidence (%)*	
	RG 2787	Susceptible check (SC)
2003-04	0.0	GCH-4 (SC): 72.08
2004-05	0.0	GCH-4 (SC): 85.5
2005-06	0.0	JI-259 (SC): 89.33GCH-4 (SC): 87.2
2006-07	5.8	GCH-4 (SC): 84.5
2007-08	0.0	GCH-4 (SC): 84.63

*<20% root rot incidence is rated as resistant

RG2787 was screening against nematode (*Rotylenchulus renifirmis*) in pots under artificial inoculation from 2004-05 to 2005-06. It consistently showed resistant reaction against nematode in both years of screening (Table 4).

Table 4. Resistant reaction of RG2787 against nematode

Year of screening	No. of embedded females/plant*
2004-05	1.3
2005-06	0.0

*Resistant: 1-2 females/plant

Reference

Ashoka Vardhana Reddy P, K Anjani and M Manikyam (2002) Collecting castor (*Ricinus communis* L.) landrace from Tamil Nadu, India. *Plant Genet. Resour. Newsletter*, **132:** 60-62.

36. FC and RI-HC 32 (IC566227; INGR09036), a Jatropha (*Jatropha curcas*) Germplasm, a Brownish Purple Colour Fruit

KT Parthiban, M Govinda Rao, K Krishaveni, N Natarajan, P Thiyagarajan, R Senthil Kumar and V Subbulakshmi
Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam-641 301

Intensive hybridization programme was initiated through interspecific hybridization. The cultivated species *J. curcas* was used as female parent and eight wild species were used as pollen donor. Among the crosses attempted, the cross between *J. curcas* and *J. integerrima* produced successful hybrids. But the F_1 plants produced only small sized seeds. Hence back was with MTP1 *J. curcas* clone and the BC_1 progenies exhibited significantly different results interms of fruit characteristics.

Unique Fruit Characters

Among 34 variable back crossed derivatives, (FC and RI-HC32) expressed significantly distinct fruit colour, *viz*, brownish purple colour fruit compared to the yellow colour check variety. This hybrid clone expressed early superiority in terms of flowering and fruiting and recorded a yield of 150 g/plant within 6 months after plantation.

Method of Propagation

The new Jatropha hybrid clone can be multiplied vegetatively through cuttings. Cuttings from individual ramets could be collected once in every 60 to 90 days and successful rooting can be achieved in a simple polythene container with the mixture of soil, sand and farmyard manure (3:1:1). Rooting of cutting starts from third week after planting and 90 to 120 days old rooted cuttings (ramets) could be used for planting.

Table 2. Resistant reaction of RG2787 against wilt in wilt sick plots

Year of	Wilt resistance (%)*			
	DOR, Hyderabad		S.K. Nagar	
	RG2787	SC	RG2787	SC
2003-04	14.3	VP-1 (SC): 88.5	0.0	GAUCH-1 (SC): 98.5
2005-06	5.8	VP-1 (SC): 93.8	0.0	JI-35 (SC): 100
2006-07	17.6	VP-1 (SC): 100	0.0	JI-35 (SC): 100
2007-08	15.3	JI-35 (SC): 100	10.0	JI-35 (SC): 100

*<20% wilt incidence is rated as resistant; SC: Susceptible check

RG 2787 was screened against root rot (*Macrophomina phaseolina*) in root rot sick plot from 2003-04 to 2007-08 under AICRP (Castor) disease screening trials. It exhibited high resistance reaction (0-5.8%) against root rot consistently in all the years of screening (Table 3).

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2005-06	0.0	JI-259 (SC): 89.33GCH-4 (SC): 87.2
2006-07	5.8	GCH-4 (SC): 84.5
2007-08	0.0	GCH-4 (SC): 84.63

*<20% root rot incidence is rated as resistant

RG2787 was screening against nematode (*Rotylenchulus renifirmis*) in pots under artificial inoculation from 2004-05 to 2005-06. It consistently showed resistant reaction against nematode in both years of screening (Table 4).

Table 4. Resistant reaction of RG2787 against nematode

Year of screening	No. of embedded females/plant*
2004-05	1.3
2005-06	0.0

*Resistant: 1-2 females/plant

Reference

Ashoka Vardhana Reddy P, K Anjani and M Manikyam (2002) Collecting castor (*Ricinus communis* L.) landrace from Tamil Nadu, India. *Plant Genet. Resour. Newsletter*, **132:** 60-62.

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Method of Propagation

The new Jatropha hybrid clone can be multiplied vegetatively through cuttings. Cuttings from individual ramets could be collected once in every 60 to 90 days and successful rooting can be achieved in a simple polythene container with the mixture of soil, sand and farmyard manure (3:1:1). Rooting of cutting starts from third week after planting and 90 to 120 days old rooted cuttings (ramets) could be used for planting.

37. FC and RI-HC 21 (IC566228; INGR09037), a Jatropha (*Jatropha curcas*) Germplasm, Oblong Fruit

KT Parthiban, M Govinda Rao, K Krishaveni, N Natarajan, P Thiyagarajan, R Senthil Kumar and V Subbulakshmi
Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam-641 301

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Unique Fruit Characters

Among 34 variable back crossed derivatives, (FC and RI-HC21) expressed significantly distinct fruit shape, *viz,* oblong fruit compared to the round check variety. This hybrid clone expressed early superiority in terms of flowering and fruiting and recorded a yield of 260 g/plant within 6 months after plantation.

Method of Propagation

The new Jatropha hybrid clone can be multiplied vegetatively through cuttings. Cuttings from individual ramets could be collected once in every 60 to 90 days and successful rooting can be achieved in a simple polythene container with the mixture of soil, sand and farmyard manure (3:1:1). Rooting of cutting starts from third week after planting and 90 to 120 days old rooted cuttings (ramets) could be used for planting.

38. PKVG8 (IC570070; INGR09038), a Ground Nut (*Arachis hypogaea*) Germplasm, a Source of Tolerance to Iron Chlorosis

Subhash N Deshmukh and Manish Y Ladole
Dr. Panjbrao Deshmukh Krishi Vidyapeeth, Akola

Iron deficiency which is expressed as yellowing of leaves and known as iron-chlorosis, is of common occurrence in groundnut in calcareous and alkaline soils world wide. This Fe-deficiency chlorosis occurs as an interveinal to complete chlorosis in young and emerging groundnut leaves, which depending upon the intensity of the chlorosis may recover with crop growth stages or in extreme cases may result in death of plant causing little yield losses to complete crop failure. In groundnut the Fe-deficiency appears 10-15 days after emerging in the field and remaining throughout the cropping season, but maximum intensity was in between 30-70 days after emerging. (Singh and Choudhary 1991; 1993). The susceptibility of groundnut to iron deficiency is very sensitive to genetic control which appears to be located in the root behavior and the rate of efficiency in iron absorption from the soil. However, by growing iron chlorosis tolerant genotypes or by utilizing these genotypes in breeding programme can be a good option to ward off iron deficiency in groundnut.

The genotype PKVG-8 was developed at Oilseeds Research Init, Dr. PDKV, Akola, from a cross derivative JL 24 x NcAc 17127 by pedigree method of selection. Confirmation of it's tolerance to iron-chlorosis was done at Directorate of Groundnut Research, Junagadh and it was appeared to be tolerant. Now it can be use as donor parent. The seed of PKVG-8 is maintained at Crop Research Unit (Oilseeds), Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444 104 (MS).

37. FC and RI-HC 21 (IC566228; INGR09037), a Jatropha (*Jatropha curcas*) Germplasm, Oblong Fruit

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39. IG3/29/2-3(1) (IC567677; INGR09039), a Guinea Grass (*Panicum maximum*) Germplasm, a Triploid Cytotype

Pankaj Kaushal, DR Malaviya and AK Roy
Indian Grassland and Fodder Research Institute, Jhansi-284 003

Polyploidy is an important area in plant research, since most of the crops that cater to our needs for food, feed, fodder and fiber, are polyploids. Polyploidy research aim towards understanding the effect of genome dosage in expression of important traits. For this, synthetic polyploids and haploids are often produced. Two events, *viz,* apomeiosis (development of unreduced embryo-sac that contain unreduced egg cell) and parthenogenesis (embryo development without fertilization) that may affect the ploidy status of progeny are inherent components of apomictic from of reproduction in some angiosperms, chiefly grasses (Nogler, 1994; Koltunow and Grassniklaus, 2003; Kaushal *et al.,* 2005; VanDijk and Ozias-Akins, 2007). These components work in close functional linkage to maintain the ploidy in progeny of the apomictic crops. However, recombinational events leading to independent expression of individual components (apomeiosis and parthenogenesis) may modify the progeny and produce high frequency of triploids (3n, termed B_{III} hybrids arising from fertilization of unreduced egg cell by reduced sperm cell) and haploids (n, termed M_I plants arising by parthenigenetic development of reduced egg cell), respectively.

Guinea grass (*Panicum maximum* Jacq.) is an important fodder crop with apomixes as predominant form of reproduction. Global germplasm collection (Malaviya and Kaushal, 2005) was subjected to survey reproductive diversity and fingerprinting reproductive pathway of seed development in this crop utilization technique such as flow cytometric seed screen (Matzk *et al.,* 2000) and ovule clearing (Young *et al.,* 1979). The study resulted in identification of Germplasm lines with enhanced expression of portioned apomixis components arising because of recombinational events between apomixis components favouring a heterozygosity model (Kaushal *et al.,* 2008a).

Fact that portioned apomixis components can modify the ploidy of the progeny, we developed a method for ploidy manipulation in apomictic crop termed as Hybridization-supplemented Apomixi-components Partitioning Approach (HAPA), whereby portioned apomixis components are supplemented with appropriate breeding schemes to obtain a ploidy series (Kaushal *et al.,* 2008b). Utilizing HAPA we have generated a ploidy series in guinea grass represented by plants with 3x, 4x, 5x, 6x, 8x, and 9x ploidy level, all derived from a single 4x (2n=32) progenitor. Presently, this series is the world's largest ploidy series available in a crop plant. Fact that these plants are derived from single progenitor, adds to the advantage on study ploidy regulated gene expression whereby increments of genomes is achieved by inherent capacity of the plant itself instead of utilizing chemical (such as colchicines, anther culture media etc.).

A locally collected tetraploid (2n=4x=32 germplasm line, *viz,* IG 04-164 has been identified to produce high frequency of B_{II} hybrids, was highly aposporous and male fertile (Kaushal *et al.,* 2008a), and thus used as progenitor to develop ploidy series. 6x (2n=48) plants were obtained following self-pollination as a consequence of B_{III} hybridization from IG 04-164. Second cycle of B_{III} hybridization yielding 9x (2n=72) plants from 6x plant. Haploid parthenogenesis (M_I) from 6x plants yielded 3x (2n=24) plant. Ploidies, *viz,* 5x (2n=40) and 8x (2n=64) were obtained by sexual hybridization utilizing 6x plant (*viz,* 3/29/2) pollinated with reduced pollen from tetraploid IG 04-164 through involvement of reduced egg (3x+2x=5x) and unreduced egg represented in Table 1. Ploidied of the resultant plants were confirmed utilizing somatic cell flow cytometry as well as cytological analysis and were characterized for morphological and fertility traits (Kaushal *et al.,* 2008b).

The series offer opportunities to study not only ploidy (dosage) dependent expression studies on various morphological, cytological, physiological, biochemical and molecular traits, but also may shed light on ploidy regulation of complex traits such as stress tolerance and apomixis (Galitski *et al.,* 1999; Riddle *et al.,* 2006; Udall and Wendel, 2006). It also offers the only way to manipulate half the monoploid dosage for understanding embryo:endosperm interactions, e.g. by producing ca. 5.5x, 6x, ca. 6.5x and 7x endosperm with 4x embryo by virtue of the pseudogamous nature of endosperm development in guinea grass (Kaushal *et al.,* 2008b) when apomictic 4x line is pollinated by 3x, 4x, 5x and 6x plants.

Since the independent expression of apomixis components yields a variety of seeds (2n, 3n, n etc.), the selfed seeds may not breed true-to-type and hence vegetative propagation of these cytotypes would be preferred. These plants are perennial and respond well to vegetative multiplication through rooted slips and hence can be clonally multiplied easily.

Salient features of individual members follows:

Triploid cytotype-3/29/2-3(1): The triploid cytotype contained 2n=3x=24 chromosomes with 8_I+8_{II} configuration at Diakinesis. The cytotype has origin from parthenogenetic development from reduced egg cell (M_I plant) from the 6x cytotype viz. 3/29/2. The plant is perennial, moderately male fertile (55%) and set lesser seed owing to unbalanced gamets.

40. IG 04-164 (IC567678; INGR09040), a Guinea Grass (*Panicum maximum*) Germplasm, a High Production Progenitor of Ploidy Series

Pankaj Kaushal, DR Malaviya and AK Roy
Indian Grassland and Fodder Research Institute, Jhansi-284 003

Tetraploid cytotype-IG 04-164: It is a selection from the global guinea grass Germplasm with 2n=4x=32 Chromosomes. It is progenitor of ploidy series for it being highly aposporous (80%), highly male fertile and high production of B_{III} hybrids (40%). Average chromosome configuration at Diakinesis was 8_I+4_{IV}. It is characterized by perennial growth habit and can be easily propagated through rooted slips

41. IG3/29/2-5(1) (IC567679; INGR09041), a Guinea Grass (*Panicum maximum*) Germplasm, a High Production Progenitor of Ploidy Series

Pankaj Kaushal, DR Malaviya and AK Roy
Indian Grassland and Fodder Research Institute, Jhansi-284 003

Pentaploid cytotype-3/29/2-5(1): This plant contained 2n=5x=40 chromosomes and was 85% male fertile. It was produced by sexual hybridization between 6x and 4x cytotype (3/29/2 x IG 04-164). The plant was perennial and amenable to vegetative propagation through rooted slips.

42. IG3/29/2 (IC567680; INGR09042), a Guinea Grass (*Panicum maximum*) Germplasm, a Pentaploid Cytotype

DR Malaviya, Pankaj Kaushal and AK Roy
Indian Grassland and Fodder Research Institute, Jhansi-284 003

Hexaploid cytotype-3/29/2: The plant contained 2n=6x=48 chromosomes with $9_{II}+6_{IV}+1_{VI}$ average meiotic configuration. It was obtained in selfed pollinated seeds of tetraploid IG 04-164 following B_{III} hybridization (unreduced egg cell fertilized). It was perennial and highly male and female fertile with good seed set. It showed partitioning of both the apomixis components (apomeiosis and parthenogenesis) and produced 9x (B_{III}) and 3x (M_I) seeds in higher proportions. The plant is propagated through rooted slips. This plant was the female parent for cytotype 3x, 5x, 8x and 9x.

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43. IG3/29/2-8(1) (IC567681; INGR09043) a Guinea Grass (*Panicum maximum*) Germplasm, a Octoploid Cytotype

DR Malaviya, Pankaj Kaushal and AK Roy
Indian Grassland and Fodder Research Institute, Jhansi-284 003

Octaploid cytotype-3/29/2-8(1): The plant was perennial and highly male fertile. It was produced from 6x 3/29/2 (unreduced egg) when pollinated with 4x IG 04-164 (reduced pollen) and contained 2n=8x=64 chromosomes. This is also a novel cytotype in guinea grass never reported earlier. The plant was maintained clonally through vegetative propagation through rooted slips.

44. IG3/29/2-9(1) (IC567682; INGR09044) a Guinea Grass (*Panicum maximum*) Germplasm, a Nonoploid Cytotype

DR Malaviya, Pankaj Kaushal and AK Roy
Indian Grassland and Fodder Research Institute, Jhansi-284 003

Nanoploid cytotype-3/29/2-9 (1): This is a novel cytotype (2n=9x=72) in guinea grass produced through B_{III} hybridization from 6x cytotype 3/29/2. Average chromosome configuration was $3_I+18_{II}+3_{III}+1_{IV}+4_V$ at Diakinesis. The plant was highly male and female fertile, perennial and amenable to vegetative propagation through rooted slips.

Table 1. Formation of ploidy series utilizing HAPA

Plant identity	Ploidy	Female parent	Male parent	Reproductive pathway of embryo formation	Broader category	Male fertility
3/29/2-3(1)	2n=3x=24	6x	6x	Reduced ES + parthenogenesis	MI	55%
IG 04-164	2n=4x=32	4x	4x	Aposporous ES + parthenogenesis	Apomictic	85%
3/29/2-5(1)	2n=5x=40	6x	4x	Reduced ES + fertilization (2x sperm)	Sexual	88%
3/29/2	2n=6x=48	4x	4x	Aposporous ES + fertilization (2x sperm)	BIII	86%
3/29/2-8(1)	2n=8x=64	6x	4x	Aposporous ES + fertilization (2x sperm)	BIII	95%
3/29/2-9(1)	2n=9x=72	6x	6x	Aposporous ES + fertilization (3x sperm)	BIII	88%

ES: Embryo-sac, reduced ES contains haploid (n) egg cell while unreduced ES contains diploid (2n) egg cell.

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43. IG3/29/2-8(1) (IC567681; INGR09043) a Guinea Grass (*Panicum maximum*) Germplasm, a Octoploid Cytotype

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Octaploid cytotype-3/29/2-8(1): The plant was perennial and highly male fertile. It was produced from 6x 3/29/2 (unreduced egg) when pollinated with 4x IG 04-164 (reduced pollen) and contained 2n=8x=64 chromosomes. This is also a novel cytotype in guinea grass never reported earlier. The plant was maintained clonally through vegetative propagation through rooted slips.

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3/29/2-9(1)	2n=9x=72	6x	6x	Aposporous ES + fertilization (3x sperm)	BIII	88%

ES: Embryo-sac, reduced ES contains haploid (n) egg cell while unreduced ES contains diploid (2n) egg cell.

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45. Penta-1 (IC567683; INGR09045), a Berseem (*Trifolium alexandrinum*) Germplasm, a pentafoliate Mutant

DR Malaviya, AK Roy and Pankaj Kaushal
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A possible approach for increasing yield of Berseem could be through increasing photosynthesis area, *i.e.* leaf area. Presence of multifoliate (mf) leaves has been reported to distinctly increase in percentage of mf leaves occurred in crosses between mf plants and the trifoliate (Tf) cultivars when the mf genotype was the maternal parent white clover. Presence of multifoliate leaves in alfalfa is reported to substantially increase in photosynthetic area of the plants. The proportion of leaves in Berseem is associated with number of leaves per plant, with number and size of leaflets on the leaf. Cultivars of Berseem clover possess trifoliate leaves however, occasional occurrence of multifoliate plants in observed sporadically in natural population. Its frequency in the natural population is only 0.004% and that too the expression of multifoliate leaves in one plants is 1 to 2% only. Multifoliate Berseem cultivars, with 4 or more leaflets per leaf instead of 3, can be useful for forage production and could used as a new variety serving for greater nutritive value and intake potential than standard trifoliate cultivars. Hence, identification of plant type with multifoliate trait will be of considerable importance. In addition to high biomadd gain, developing true breeding pentafoliate will also open up opportunities for understanding the mechanism of inheritance of this trait which is yet not known.

The process of developing multifoliate berseem started about a decade back. However, in the last few years with the help of recurrent phenotypic selection and maintenance of plants in isolation has resulted in plants type with very high percentage and expression of pentafoliate trai. Lines with above near 100% percentage and 90% expressivity of pentafoliate leaves have been developing which clearly shown significant difference in the expression of different type of leaves. The lines possess considerable importance because of high expression of pentafoliate leaves with large leaflet size which in true may exhibit high rate of photosynthesis per plant and consequently increase in the biomass yield.

46. TetraA_4; IG 08-03 (IC567684; INGR09046), a Pearl Millet (*Pennisetum glaucum*) Germplasm, Tetraploid Male Sterile Line with A_4 Cytotype

Pankaj Kaushal, AK Roy and DR Malaviya
Indian Grassland and Fodder Research Institute, Jhansi

Tetraploidy is often induced in crop plants for understanding polyploidy effects, production of cytogenetics stocks as well as to overcome incompatibility barriers in interspecific crosses arising due to ploidy level differences in parental genotypes.

Pearl millet (*Pennisetum glaucum* L.) is an important dual-purpose crop utilized both for food and fodder purposes. The genus Pennisetum consists of many wild species belonging to secondary and tertiary gene pool that harbours desirable genes, such as perenniality, fodder traits and apomixes, for pearl millet improvement (Hanna, 1987). Most of these species are polyploids and hence, show poor crossability withthe cultivated diploid pearl millet (2n=2x=14). However, upon raising the ploidy level of pearl millet, the crossability is improved thereby yielding several crosses of potential importance (Dujardin and Hanna, 1989a; Kaushal *et al.*, 2007; 2008). The efficiency of such crosases could greatly be enhanced by availability of a male sterile tetraploid line, as it further reduced the efforts to screen seeds arising from self-pollination in otherwise male fertile tetraploid lines. We therefore induced tetraploidy in a diploid male sterile as well as its maintainer line utilizing colchicines (Kaushal *et al.*, 1999; 2007; Anonymous, 2008). The induced tetraploids were characterized for their cytology (chromosome behaviour), DNA content using cytometry, stomatal characteristics and reproductive behaviour.

This is perhaps the first report of set of male-sterile and maintainer tetraploid in pearl millet in India.

This is a male sterile tetraploid pearl millet (2n=4x=28) line induced from diploid ICRISAT line 81A4 with A4 cytoplasm (CMS). The plants in C_o

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Pearl millet (*Pennisetum glaucum* L.) is an important dual-purpose crop utilized both for food and fodder purposes. The genus Pennisetum consists of many wild species belonging to secondary and tertiary gene pool that harbours desirable genes, such as perenniality, fodder traits and apomixes, for pearl millet improvement (Hanna, 1987). Most of these species are polyploids and hence, show poor crossability withthe cultivated diploid pearl millet (2n=2x=14). However, upon raising the ploidy level of pearl millet, the crossability is improved thereby yielding several crosses of potential importance (Dujardin and Hanna, 1989a; Kaushal *et al.*, 2007; 2008). The efficiency of such crosases could greatly be enhanced by availability of a male sterile tetraploid line, as it further reduced the efforts to screen seeds arising from self-pollination in otherwise male fertile tetraploid lines. We therefore induced tetraploidy in a diploid male sterile as well as its maintainer line utilizing colchicines (Kaushal *et al.*, 1999; 2007; Anonymous, 2008). The induced tetraploids were characterized for their cytology (chromosome behaviour), DNA content using cytometry, stomatal characteristics and reproductive behaviour.

This is perhaps the first report of set of male-sterile and maintainer tetraploid in pearl millet in India.

This is a male sterile tetraploid pearl millet (2n=4x=28) line induced from diploid ICRISAT line 81A4 with A4 cytoplasm (CMS). The plants in C_o

generation were weaker however, subsequently the vigour was restored in advanced generation (C_{2-4}). The plants were characterized by DNA content utilizing flow cytometry to contain double the content of the parent line 81A4. The average chromosome configuration at Diakinsis was $0.04_{I}+11.16_{II}+0.12_{III}+1.32_{IV}$. The pleat was highly male sterile (on stainable pollin) and set no seed on selfing. However, seed set is good (>80%) when pollinated with another male fertile tetraploid line IG 99-748. The male sterility is maintained by IG 99-748. Presently plants are in C_5 generation and we did not find any diploid revertent or a male-fertile contaminant.

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47. TetraA$_1$; IG 99-748 (IC568548; INGR09047), a Pearl Millet (*Pennisetum glaucum*) Germplasm, Maintainer of TetraA$_4$ MS Line

Pankaj Kaushal, AK Roy and DR Malaviya
Indian Grassland and Fodder Research Institute, Jhansi

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This is perhaps the first report of set of male-sterile and maintainer tetraploid in pearl millet in India.

This is an induced tetraploid line from diploid ICRISAT line 81B. IG 99-748 is able to maintain the male sterility of IG 08-03, since its progernitor 81B is a maintainer of 81A4. The line IG 08-03 is highly male fertile (>95%) pollen stainability)and set good seed (>80%) upon selfing (Kaushal *et al.,* 2007), which is contrary to previously reported male fertile pearl millet lunes which are poor pollen shedders and poor seed setters (Patil, *et al.,* 1961, Dujardin and Hanna, 1989b). Average chromosome configuration was $0.2_{I}+11.17_{II}+0.13_{III}+1.26_{IV}$ at Diakinesis. This line is crossable with some of the wild species such as *P. squamulatum* and *P. orientale* hybrids (Kaushal *et al.,* 2007; 2008; Anonymous, 2008). The plants are now in C_{12} generation, able to maintain their fertility and tetraploid status.

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48. Agnisikha (IC565675; INGR09048), a Canna ('Keli') (*Canna generalis*) Germplasm, a Unique New Flower Colour, Flowers in Cluster Form

Rup Kumar Roy

National Botanical Research Institute, RP Marg, Lucknow

Canna is a popular ornamental plant in India grown for its magnificent flowers with wide array of colours. Nevertheless, some cultivars have stunning foliage which is equally attractive as flowers. Cannas are mainly used for bedding purpose in gardens and parks (Roy and Sachan, 1993; Roy and Banerji, 2006). Considering its ornamental importance, a collection of 50 cultivars has been built up which are used for breeding work for the development of new varieties. Mutation breeding and hybridization techniques are successful methods for developing new cultivars (Khoshoo, 1972; Khoshoo and Guha, 1975).

The new cultivar *Canna generalis* 'Agnisikha' is a mutant of *Canna generalis* 'Lucifer'. Rhizomes were treated with different doses of gamma rays (Cobalt 60) and planted in the beds. Mutated plant was identified by change of flower colour, isolated, multiplied vegetatively, evaluated in the successive generations and found distinct, uniform and stable mutant (Roy, 2004). This breeding work including irradiation of the rhizomes, field trials were carried out in the Botanic Garden, National Botanical Research Institute, Lucknow.

Morpho-agronomic Characteristics

Morphological Characters

A. VEGETATIVE

Stature – Medium (0.90–1.20 m).

Stem – Stout, 2.5–3.5 cm in diameter with moderate suckering habit.

Leaves – Light green, tip cute, margin entire, surface smooth, 40-48 x 12-15 cm in size.

Rhizome – Creamy-white in colour; 2.0-2.5 cm in dia.; fresh weight varies from 10-15 g per 2.5 cm length, internode length-1.5-2.5 cm; no scales; roots 0.3-0.6 cm in dia., sparsely present.

B. FLORAL

Inflorescence – Simple, 25-30 cm long; contains 12-16 flowers.

Flower – 8.0 to 10.0 cm in dia., 9.5-10.0 cm in length; bi-coloured, canary yellow (2) along the margin like an irregular band having 2.0-4.0 mm width covering 15% of the individual petal; rest of the petal (85%) is geranium lake – 20 (a shade of red) like flame of fire; margin slightly frilled (Roy, 2007).

Fig. 1: Canna generalis *'Agnisikha'*

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Fig. 1: Canna generalis *'Agnisikha'*

Associated Characters and Cultural Practices

The colour combination of the flowers is like flame of fire, a combination of yellow and red, very attractive and distinct (Fig. 1). It's a medium height variety, suitable for bedding purpose, free flowering type, peak flowering season is February to October. The cultivar also performs well when grown in pots and suitable for growing in tropical /sub-tropical conditions.

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49. IIHRRs-1 (IC567489; INGR09049), a Rose (*Rosa indica*) Germplasm, an Ideal Rootstock Resistant to Powdery Mildew

Tejaswini, Dhananjaya MV and N Ramachandra
Indian Institute of Horticultural Research, Hessaraghatta, Bangalore

IIHRRs-1 is an Ideal rootstock resistant to powdery mildew (*Podosphera pannosa*). It has tall plant with moderately spreading plant habit with dark glossy leaves. The genotypes IIHRRs-1 was scored at higher threshold disease occurrence along with 416 other genotypes. The accessions were scored in 1-4 scale, with 1 being highly resistant and 4 as highly susceptible based on severity of incidence. IIHRRs-1 along with IIHRRs-2 was scored as highly resistant with the score of 1. These two highly resistant lines were further evaluated along with a highly susceptible line under higher threshold of disease occurrence for final confirmation. Experimental evaluation was conducted in a Randomised complete block design with seven replications. For maximization of disease threshold, highly susceptible line IIHRRs-1 was planted all around the experimental plot to ensure adequate inoculum for heavy disease incidence. Percentage of disease incidence was recorded for three years during maximum period of infestation. Based on stable resistant reaction of the genotype to disease incidence over the years, IIHRRs-1 was identified as a highly resistant.

50. IIHRRs-2 (IC567490; INGR09050), a Rose (*Rosa multiflora*) Germplasm, a Ideal Rootstock Resistant to Powdery Mildew

Dhananjaya MV, Tejaswini and N Ramachandra
Indian Institute of Horticultural Research, Hessaraghatta, Bangalore

IIHRRs-2 is an **i**deal rootstock resistant to powdery mildew (*podosphera pannosa*). Stems are thornless. Leaves are green in colour. Leaves are less pubescent. The genotypes IIHRRs-1 was scored at higher threshold disease occurrence along with 416 other genotypes. The accessions were scored in 1-4 scale, with 1 being highly resistant and 4 as highly susceptible based on severity of incidence. IIHRRs-2 along with IIHRRs-1 was scored as highly resistant with the score of 1. These two highly resistant lines were further evaluated along with a highly susceptible line under higher threshold of disease occurrence for final confirmation. Experimental evaluation was conducted in a Randomised complete block design with seven replications. For maximization of disease threshold, highly susceptible line IIHRRs-1 was planted all around the experimental plot to ensure adequate inoculum for heavy disease incidence. Percentage of disease incidence was recorded for three years during maximum period of infestation. Based on stable resistant reaction of the genotype to disease incidence, IIHRRs-2 was identified as a highly resistant.

Associated Characters and Cultural Practices

The colour combination of the flowers is like flame of fire, a combination of yellow and red, very attractive and distinct (Fig. 1). It's a medium height variety, suitable for bedding purpose, free flowering type, peak flowering season is February to October. The cultivar also performs well when grown in pots and suitable for growing in tropical /sub-tropical conditions.

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Associated Characters and Cultural Practices

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51. IC210421/VU/97-82 (IC210421; INGR09051), a *Alpinia calcarata* Germplasm, a Source of High 1,8-Cineole Content and α-fenchyl Acetate Content in Rhizome Essential Oil

Archana P Raina, Z Abraham and SK Mishra
National Bureau of Plant Genetic Resources, New Delhi

Alpinia calcarata Rosc. (Family Zingiberaceae) is an important rhizomatous medicinal herb found in tropical countries, including Sri Lanka, India, Thailand and Malaysia. The drugs prepared from the *A. calcarata* are used in the treatment of rheumatism, bronchial catarrh, asthma and in reducing pain. It is used to stimulate digestion, purify blood, improve voice and to treat inflammation. It is reported that the properties and uses of the rhizomes of *Alpinia calcarata* are similar to those of *Alpinia galanga* and can be used as its substitute. Five germplasm collections of *Alpinia calcarata* from different regions of Kerala were conserved in the field repository at NBPGR Regional Station, Thrissur. These germplasm collections were screened for their quality traits at NBPGR, Delhi. The essential oil extracted from rhizomes were analyzed for essential oil content and aroma constituents by GC and GC-MS. Major aroma constituents identified in these collections were 1,8–cineole, α-fenchyl acetate, camphor, camphene, α-pinene, β-pinene, α-terpineole. Among these IC210421 collected from Erattupetta village of Pathanamthitta district of Thrissur was found to contain highest 1,8-cineole (37.21%) and α-fenchyl acetate (19.87%) contents.

IC210421 is a perennial, branched, cylindrical aromatic rhizomatous herb. The rhizomes are 11.5-13.4 mm thick, prostrate, dull white with dry scales from node. Leafy pseudo stem is aromatic, basal region red 90-151 cm tall, with 10-15 leaves per pseudo stem. Lamina is 3-4.6 cm broad and 19.7-40.3 cm long with shortly bifid ciliate with lingual with 0.7-1.4 cm long. Inflorescence is aromatic, paniculate, unbranched, 10-15 cm long, densely pubescent peduncle, light green. Flowers are shortly pedicellate, ovary densely pubescent. Labellum is variegated with dark purple and yellow venation, glabrous and fruits are not formed. The rhizomes and roots are rich in essential oils.

IC210421 was found to contain high 1,8-cineole content of 37.21% which is an important aroma chemical reported to possess expectorant, antiseptic and anesthetic properties and is widely used in pharmaceutical preparations. The oil of *A. calcarata* or its constituents namely 1,8-cineole and α-fenchyl acetate hold promise as a possible pest control agents. Recently 1,8-cineole has been found effective against the mosquito A*edes aegypti* larvae and the whitefly *Bemisia ergentifolii.* Cinmethylin, a product based on 1,8-cineole has also been developed as a commercial herbicide. Thus, *A. calcarata* collection IC 210421 rich in 1,8-cineole and α-fenchyl acetate can be exploited for use in pharmaceutical and agrochemical industry.

Reference

Raina Archana P, Suresh Walia, KK Sharma, Z Abraham and SK Mishra (2007) Essential oil constituents of rhizome oil of *Alpinia calcarata* from South India. *Indian Perfumer* **51(2):** 27-29.

Table1. Salient quality attribute of the essential oil content of *Alpinia calcarata* IC210421

Accession/ collector no.	Essential oil content (%)	1,8-cineole (%)	α-fenchyl acetate(%)	α-pinene (%)	Camphene(%)	Camphor (%)	a-ter-pineole (%)
IC210421(VU/97-82)	1.26	37.21	19.87	4.13	6.02	4.38	5.71

52. Co 97016 (IC565018; INGR09052), a Sugarcane (*Saccharum* spp. hybrid) Germplasm with High Cane and Sugar Yield and Tolerance to Water-logging, Salinity and Drought

Bakshi Ram, G Hemaprabha, BK Sahi and N Vijayan Nair
Sugarcane Breeding Institute Reg. Centre, Karnal

A source of high cane yield and sugar yield and tolerance to water-logging, salinity and drought. The clone is a genetic stock with par/better cane yield and juice quality with CoS767 (the major midlate variety in North-western zoneand for its additional merits, *viz*, its tolerance to abiotic stresses. The genotype possess the blood of the wild species, *S. robustum* (57NG80), which is rarely represented in commercial gene pool. Hence, this clone would provide a new and diverse genetic base when used as a parent).

53. SCGS 00-0402 (IC565019; INGR09053), a Sugarcane (*Saccharum* spp. hybrid) Germplasm with High Levels of Juice Sucrose

RM Shanthi and S Alarmelu
Sugarcane Breeding Institute, Coimbatore-641 007, Tamil Nadu

Sugarcane cultivars with substantially higher levels of juice sucrose suitable for early harvest are very less in the present breeding populations. New parental clones that are capable of accumulating much higher levels of sucrose than found in the local commercial varieties are to be developed. Successful efforts to improve sucrose content through the adoption of different selection strategies coupled with the choice of appropriate parents have been reported (Legendre, 1995; Lo and Chen, 1995).

SCGS 00-0402 is an early high sugar clone identified from the first selection cycle of a simple recurrent selection scheme. The clone has registered a substantial gain for all the juice parameters *viz.*, juice brix %, sucrose %, CCS % and purity % compared to the zonal standards under the early maturity group. SCGS 00-0402 was developed at the Sugarcane Breeding Institute, Coimbatore has been registered as a source of high levels of juice sucrose at 240 days of crop age by the Plant Germplasm Registration Committee of ICAR vide registration number INGR. 09053.

Morpho-agronomic Characters

The clone SCGS 00-0402 has a semi-erect stool habit and yellowish red cane colour. Internode alignment is zig-zag with a cane diameter of 2.7 cms. Exposed root zone is yellowish red in colour. Leaf sheath clasping is medium and canopy is semi-drooping type. The genotype flowers during mid season (November) and flowering intensity is 90%. Pollen fertility is less than 5% and can be used as a safe female parent.

Performance of SCGS 00-0402 for Juice Traits

At 240 days of crop age, SCGS 00-0402 recorded an average juice brix of 22.57% against the early checks CoC 671 (20.73%) and Co 85004 (19.85%). It registered an improvement of 13.71% compared to Co 85004 and 8.88% as compared to CoC 671. SCGS 00-0402 recorded an average juice sucrose of 21.62% at 240 days compared to the standards CoC 671 (19.37%) and Co 85004 (18.42%). The clone recorded an improvement of 17.35% over Co 85004 and 11.62% over CoC 671. For commercial cane sugar percent, SCGS 00-0402 recorded an average of 15.51% as compared to 13.74% in the check variety CoC 671 and 13.03% in Co 85004. It showed an improvement of 18.97% compared to Co 85004 and 12.82% as compared to CoC 671.

The potential of SCGS 00-0402 as a donor for juice quality is evident from the progeny evaluation for juice characters. The best progeny, *viz.*, 03-0402 recorded a maximum of 23.00% juice brix against the standard CoC 671 with 12.20% improvement over the early check Co 85004 and 9.52% over the other check variety CoC 671. Early sucrose accumulation is a promising characteristic in sugarcane improvement programmes. Hence, the clone SCGS 00-0402 is a potential pre-breeding stock and its use in hybridization is expected to generate more number of segregants for early high sugar content in sugarcane.

References

Legendre BI (1995) Potential of increasing the sucrose content of sugarcane: An assessment of recurrent selection in Louisiana. *Sugarcane* **3:** 4-8.

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54. LG 95053 (IC553283; INGR09054), a sugarcane (*Saccharum* spp. hybrid) Germplasm with High Sugar Content and Utility as a Female Parent

BL Srivastava, Raman Kapur, SK Duttamajumder and Ram Kumar
Indian Institute of Sugarcane Research, Lucknow

The present-day cultivated sugarcane is a cross-pollinated, highly heterozygous, polyploid, species-hybrid (*Saccharum* sp. hybrid). The inherent genetic complexity of sugarcane makes its breeding rather empirical. The present material, LG 95053, is the product of a concerted effort to develop breeding stocks for high sugar accumulation potential in the subtropical agro-climate. This approach is aimed at lending precision to the process of breeding in sugarcane.

Morpho-agronomic Characteristics

LG 95053 is the result of selection in the progeny of a biparental mating (Co 89003 x CoC 671) effected in 1994. It was originally selected in 1996 as N_2-17-7 and was evaluated subsequently for its early high sugar accumulation potential. Its cane is medium-thick and medium-tall with moderate cane yield. Its canes are erect, purple yellow with cylindrical internodes, and ovate buds. It is early maturing with high juice purity. Sucrose content in juice ranges from 17-19 % during November to January. It was identified as a promising high sugar breeding stock (1-3) and sent to National Hybridization Garden (NHG), Sugarcane Breeding Institute, Coimbatore in 1997-98.

Associated Characters and Cultivation Practices

LG 95053 flowers in the third week of October at Coimbatore and registers very low pollen fertility (< 5%) making it an ideal female parent in a highly cross pollinated system (4). Over the years, it has proven its merit as a female parent (Table 1) in transmitting high sugar traits to its progenies (5).

Fig. 1: LG 95053; • Early maturing, high sugar clone with regular flowering, • Good female parent giving high proportion of progeny with early high sugar accumulation potential

Table 1. Progeny performance

Type of mating	Size of seedling population	Family mean (% brix)	Percent seedlings above CoJ 64 (>21%)	Percent seedlings at par with CoJ 64 (20-21%)	Percent seedlings with high sugar content
LG 95053 Self	22	20.00	18.2	40.9	59.1
LG 95053 GC	27	20.05	48.2	14.8	63.0
LG 95053 x HR 83-65	50	20.50	36.0	32.0	68.0
LG 95053 x LG 94184	61	20.19	32.8	32.8	65.6

55. VL 876 (IC565010; INGR09055), a Wheat (*Triticum aestivum*) Germplasm, with High Bread Loaf Volume and Good Quality Bread

Laksmi Kant, Vinay Mahajan, HS Gupta, BD Pandey and Daya Shanker, SK Pant and RK Gupta
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

Bread Loaf volume >575 ml highly desirable for good quality bread making. Bread Loaf volume (ml) / Dough weight (g) > 3.5 is considered appropriate for a good quality bread. Bread quality score between 7.1-8.0 (out of 10) is very good for a good quality bread.

54. LG 95053 (IC553283; INGR09054), a sugarcane (*Saccharum* spp. hybrid) Germplasm with High Sugar Content and Utility as a Female Parent

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56. VL 852 (IC565011; INGR09056), a Wheat (*Triticum aestivum*) Germplasm, a Diverse Source of Chapatti Quality

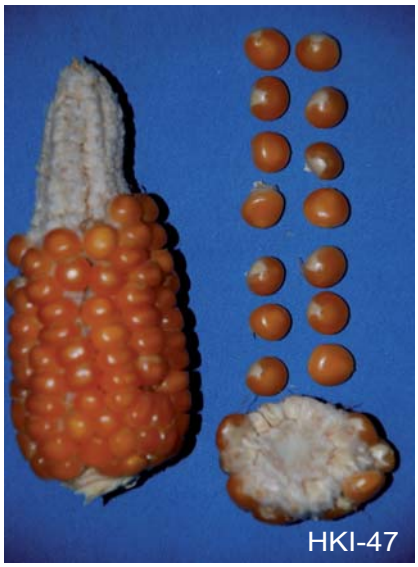
Laksmi Kant, Vinay Mahajan, HS Gupta, BD Pandey, Daya Shanker, SK Pant and RK Gupta
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora

Excellent chapatti quality (8 out of 10). Diverse source of chapatti quality than C 306.

57. HKI-47 (IC563953; INGR09057), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

A late maturing normal maize grain line derived from CIMMYT highland single cross hybrid (ET 38146 x 38147) after 7-8 years of continuous inbreeding following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.



HKI-47

HKI-47 is medium stature plant type with medium to long cob. It takes 60 days for 50% silking. It has sparse tassel branches and is a good pollen shedder, which is a merit of a good pollen parent. The grain rows arrangement is straight and the Anthocyanin colouration of glume is white. It has very attractive orange flint grain colour.

The four year data from 2003 to 2006 with respect to common rust and Maydis Leaf Blight (MLB) reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM600 for Maydis Leaf blight and common rust against susceptible check CM202. The disease reaction for Maydis Leaf Blight in HKI-47 ranged from 1.0 to 1.5 and for common rust it showed consistently 1.0. This can be utilized as a source of stable resistance against the above mentioned diseases for the development of disease free hybrids and deriving new inbred lines.

It is also a good combiner. When it was crossed with temperate material the line produced very productive hybrids; it can also be used as good pollen parent for tropical and sub-tropical lines.

Criteria for Registration [Unique feature(s)]

1. Resistant to common rust,
2. Attractive grain colour,
3. Sparse tassel branches, good pollen shedder,
4. Good combiner.

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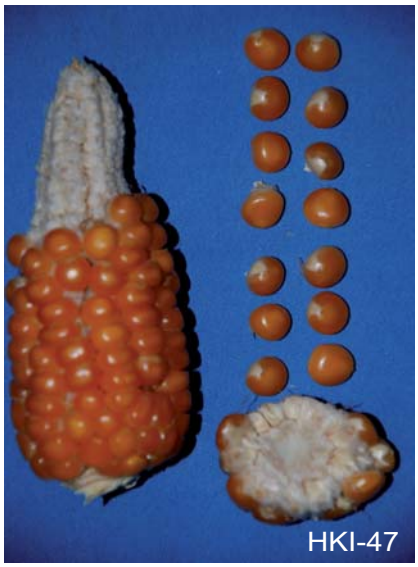


HKI-47

HKI-47 is medium stature plant type with medium to long cob. It takes 60 days for 50% silking. It has sparse tassel branches and is a good pollen shedder, which is a merit of a good pollen parent. The grain rows arrangement is straight and the Anthocyanin colouration of glume is white. It has very attractive orange flint grain colour.

The four year data from 2003 to 2006 with respect to common rust and Maydis Leaf Blight (MLB) reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM600 for Maydis Leaf blight and common rust against susceptible check CM202. The disease reaction for Maydis Leaf Blight in HKI-47 ranged from 1.0 to 1.5 and for common rust it showed consistently 1.0. This can be utilized as a source of stable resistance against the above mentioned diseases for the development of disease free hybrids and deriving new inbred lines.

It is also a good combiner. When it was crossed with temperate material the line produced very productive hybrids; it can also be used as good pollen parent for tropical and sub-tropical lines.

Criteria for Registration [Unique feature(s)]

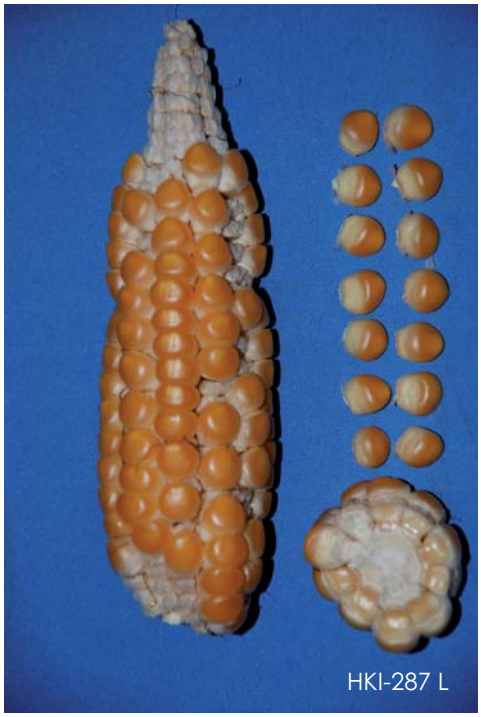
1. Resistant to common rust,
2. Attractive grain colour,
3. Sparse tassel branches, good pollen shedder,
4. Good combiner.

58. HKI-287L (IC563954; INGR09058), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

HKI-287 L

A late maturing line derived from CIMMYT line CML-287 which was not uniform with respect to many traits. Phenotypically superior plants were selected and were subjected to 7-8 years of selfing following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal. The line was evaluated during *kharif* and *rabi* seasons, it has shown very high level of resistance for MLB and common rust, respectively, under normal field conditions. The four-year data, during 2003-2006, with respect to common rust and Maydis Leaf Blight (MLB) reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM600 for Maydis Leaf blight and common rust against susceptible check CM202. The disease reaction for Maydis Leaf Blight in HKI-287L ranged from 1.0 to 2.0 and for common rust ranged from 1 to 1.5. This can be utilized as a source of stable resistance against the above mentioned diseases for development of disease free hybrids.



HKI-287L is tall growing plant with medium to long cob. Based on four year data (2003-2006) in rabi and kharif evaluated for various morphological traits revealed that it takes 60-64 days for silking. The height ranged from 150-160 cm. The test weight is more than 200 g/1000 grains and productivity is > 2.5 ton in the both the seasons. It has sparse tassel branches and a good pollen shedder. It can be used as a pollen parent in developing single cross hybrids. The grain row arrangement is straight and the Anthocyanin coloration of glume is white. It has very attractive orange flint grain colour.

It is also a good combiner. It has given good hybrids when crossed with HKI-1128, HKI-1126, HKI-288-2, HKI-1105, HKI-326, HKI-326-1 etc. This line has useful genes for productivity and is good combiner, hence can be used by breeders for the production of Single cross hybrids.

Criteria for Registration [Unique feature(s)]

1. Late maturing,
2. Attractive orange grain color,
3. Dark green leaves, productive.

59. HKI-327 T (IC563955; INGR09059), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

A late maturing line derived from CIMMYT line CML-327 which was not a uniform line and varied for many traits. Superior plants were selected after 7-8 years of selfing following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

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Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

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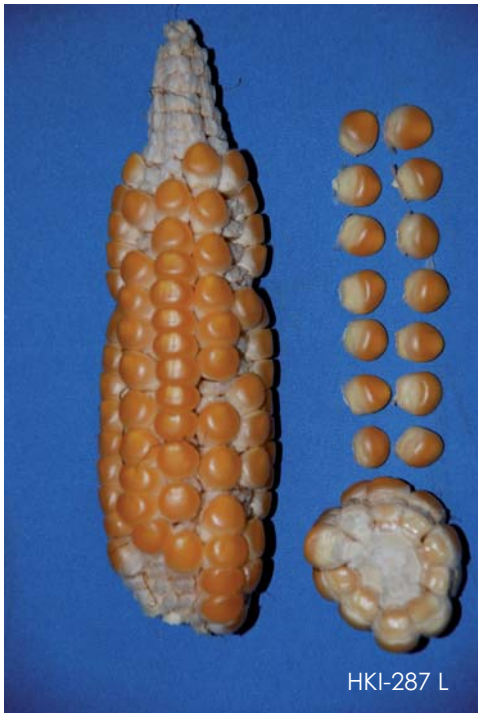

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Criteria for Registration [Unique feature(s)]

1. Late maturing,
2. Attractive orange grain color,
3. Dark green leaves, productive.

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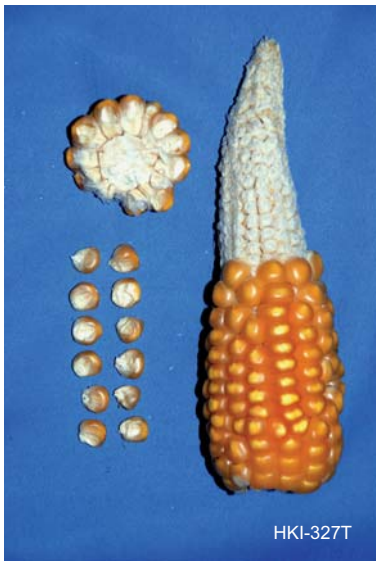


HKI-327T

HKI-327T is tall stature plant type with medium to long cob. Based on four years data the line takes 56-59 days to flower and height goes upto 160 cm. Grains are very bold and line is very productive. Yield is up to 2.7 t/ha in kharif and 2.8 t/ha in winter season. This line has shown high level of resistance for MLB and common rust under artificial condition continuously for four years. This line will be useful for maize breeders for developing single cross hybrids.

Criteria for Registration [Unique feature(s)]

1. Tall, dark green, broad leaves,
2. Resistant to MLB and common rust,
3. Late maturing, productive.

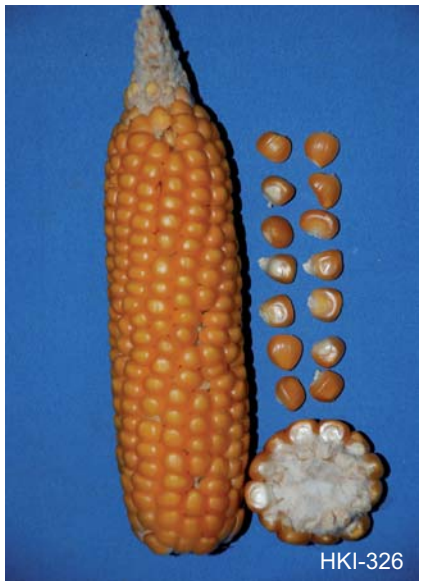
60. HKI-326 (IC563957; INGR09060), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rrust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

A late maturing line derived from CIMMYT line CML-326 which was not uniform and was variable for various traits. A few good plants were selected which were selfed for 7-8 years following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

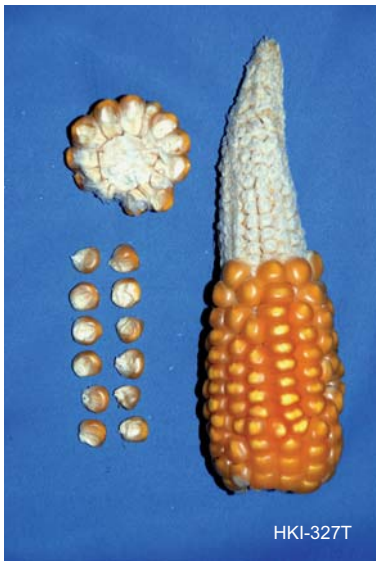
It has very long cob with thin, white gully, this will contribute to high harvest index and high shelling percentage. It comes to flowering within 55-58 days. It reaches to the height of 140 cm. It has sparse tassel branches. It has very attractive orange flint grain colour.

In *kharif* season the productivity of this line is near 2 t/ha and in *rabi* season it is more than 2 t/ha. It can be used in both ways as male and as well as female in combination breeding. Extensive testing for four years (2003 to 2006) has shown high level of resistance to major diseases like Maydis Leaf Blight and common rust in *kharif* and *rabi*, respectively, under natural field condition.The line can be made available to different centers of the country for its extensive use in breeding single cross hybrids.



Criteria for Registration [Unique feature(s)]

1. Attractive orange grain colour,
2. Late maturing, green leaves,
3. Very long cobs and good combiner, productive.



HKI-327T

HKI-327T is tall stature plant type with medium to long cob. Based on four years data the line takes 56-59 days to flower and height goes upto 160 cm. Grains are very bold and line is very productive. Yield is up to 2.7 t/ha in kharif and 2.8 t/ha in winter season. This line has shown high level of resistance for MLB and common rust under artificial condition continuously for four years. This line will be useful for maize breeders for developing single cross hybrids.

Criteria for Registration [Unique feature(s)]

1. Tall, dark green, broad leaves,
2. Resistant to MLB and common rust,
3. Late maturing, productive.

60. HKI-326 (IC563957; INGR09060), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rrust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

A late maturing line derived from CIMMYT line CML-326 which was not uniform and was variable for various traits. A few good plants were selected which were selfed for 7-8 years following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

It has very long cob with thin, white gully, this will contribute to high harvest index and high shelling percentage. It comes to flowering within 55-58 days. It reaches to the height of 140 cm. It has sparse tassel branches. It has very attractive orange flint grain colour.

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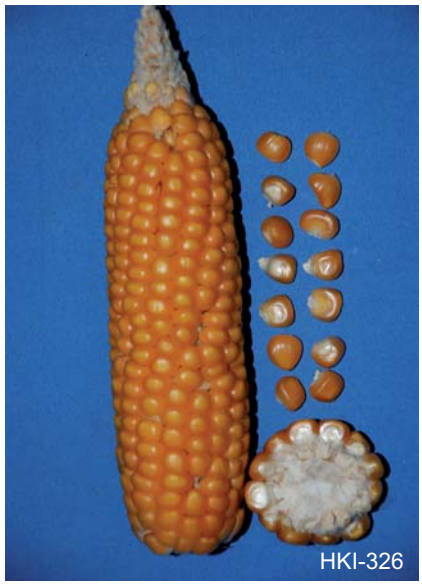


Criteria for Registration [Unique feature(s)]

1. Attractive orange grain colour,
2. Late maturing, green leaves,
3. Very long cobs and good combiner, productive.

61. HKI-1040-5 (IC563960; INGR09061), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

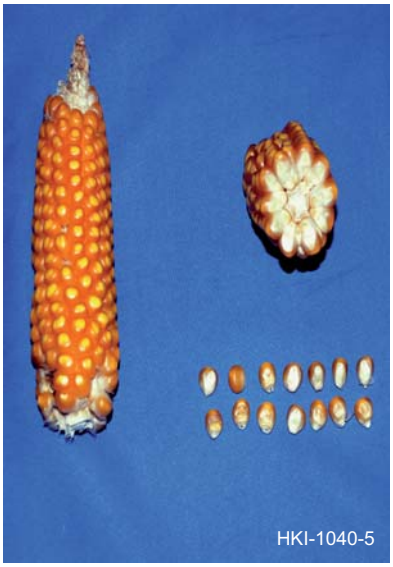
Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

It is medium maturing line derived from the Brazilian extra early single cross hybrid BC-318 through the process of selfing and selection. The hybrid was continuously selfed for 7-8 generations following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

HKI-1040-5

HKI-1040-5 is medium tall plant with long cob. The plant height varies from 110 to 145 cm. In winter season the height is around 100 cm. The 50% silk emergence is between 50-54 days depending upon weather conditions.

It is orange flint with purple glumes. is purple silk and the sheath is also purple. Tassel is purple with purple anther colour. Under natural field conditions, this inbred line line is resistant to MLB and common rust but under artificial condition it showed moderate resistance to these diseases.



Criteria for Registration [Unique feature(s)]

1. Attractive orange grain colour,
2. medium maturing, dark green leaves,
3. Good combiner.

62. HKI-1341 (IC563962; INGR09062), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

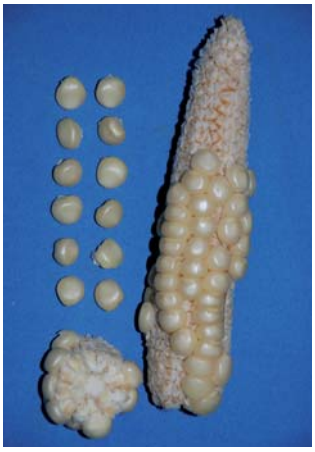
It is a white shiny grain line with high level of resistance to common rust under artificial disease conditions. The disease score is1.0 against the highly susceptible check CM-202.

This was derived from a variable CIMMYT line CML-6. 7-8 generations of selfing and selection has resulted in the development of this line.

The tassel has sparse branches, late in maturity. It has flint grain and kernel row arrangement is straight and has white glume.

HKI-1341

This line can be used in winter season as a source of resistance to common rust for the derivation of elite resistant lines and as well as in combination breeding.



Criteria for Registration [Unique feature(s)]

1. Attractive shining white grain,
2. Late maturing, dark green leaves,
3. Resistant to common rust and productive.

61. HKI-1040-5 (IC563960; INGR09061), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

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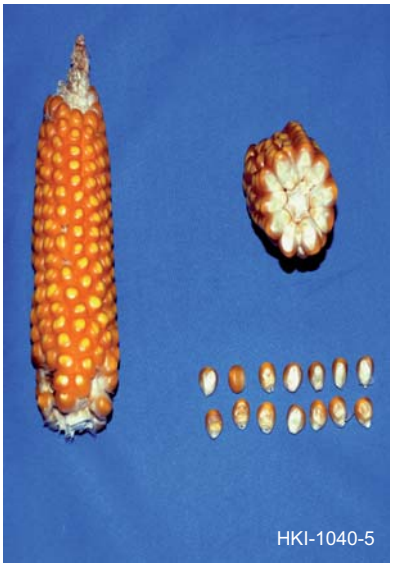
HKI-1040-5

HKI-1040-5 is medium tall plant with long cob. The plant height varies from 110 to 145 cm. In winter season the height is around 100 cm. The 50% silk emergence is between 50-54 days depending upon weather conditions.

It is orange flint with purple glumes. is purple silk and the sheath is also purple. Tassel is purple with purple anther colour. Under natural field conditions, this inbred line line is resistant to MLB and common rust but under artificial condition it showed moderate resistance to these diseases.



Criteria for Registration [Unique feature(s)]

1. Attractive orange grain colour,
2. medium maturing, dark green leaves,
3. Good combiner.

62. HKI-1341 (IC563962; INGR09062), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

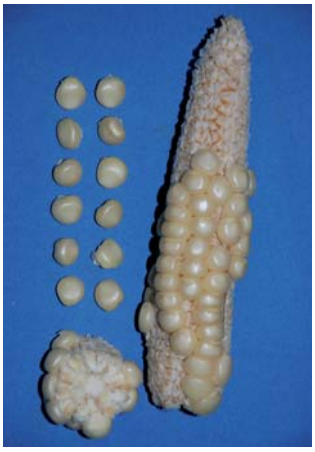
It is a white shiny grain line with high level of resistance to common rust under artificial disease conditions. The disease score is1.0 against the highly susceptible check CM-202.

This was derived from a variable CIMMYT line CML-6. 7-8 generations of selfing and selection has resulted in the development of this line.

The tassel has sparse branches, late in maturity. It has flint grain and kernel row arrangement is straight and has white glume.

HKI-1341

This line can be used in winter season as a source of resistance to common rust for the derivation of elite resistant lines and as well as in combination breeding.



Criteria for Registration [Unique feature(s)]

1. Attractive shining white grain,
2. Late maturing, dark green leaves,
3. Resistant to common rust and productive.

63. HKI-1342 (IC563963; INGR09063), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

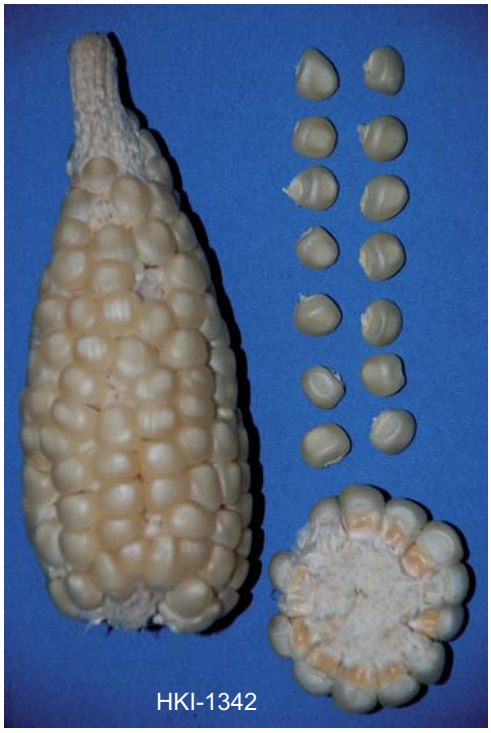
A late maturing line derived from CIMMYT line CML 6 after 7-8 years of inbreeding following by ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

HKI-1342

HKI-1342 is medium stature plant type with medium long cob. It has sparse tassel branches and a good pollen shedder, which is a merit of a good pollen parent. The grain row arrangement is straight and the Anthocyanin coloration of glume is white. It has very attractive white flint grain colour.

The four year data with respect to common rust and Maydis Leaf Blight (MLB) reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM600 for Maydis Leaf blight and common rust against susceptible check CM202. The disease reaction for Maydis Leaf Blight and common rust in HKI-1342 was consistently 1.0. This can be utilized as a source of stable resistance against the above mentioned diseases for development of disease free hybrids.

It is also a good combiner. When it was crossed with temperate material the line produced very productive hybrids, it can also be used as good pollen parent for tropical lines.



Criteria for Registration [Unique feature(s)]

1. Resistant to rust and MLB,
2. Late maturing, dark green leaves and productive,
3. White with shiny grain.

64. HKI-170 (1+2) (IC563967; INGR09064), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

A late maturing line derived from CIMMYT line CM170 after 7-8 years of inbreeding following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

HKI-170 (1+2)

HKI-170 (1+2) is medium stature plant type with medium long cob. It has sparse tassel branches and a good pollen shedder, which is a merit of a good pollen parent. The grain row arrangement is straight and the Anthocyanin coloration of glume is white. It has very attractive yellow flint grain colour. HKI-170 (1+2) is a QPM inbred and has high tryptophan (>0.6%) content in its endosperm.

The four year data with respect to common rust and Maydis Leaf Blight (MLB) reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM600 for Maydis Leaf blight and common rust against susceptible check CM202. The disease reaction for Maydis Leaf Blight in HKI-170 (1+2) was consistently 1.0 and for common rust the range was 1.0 to 1.5. This can be utilized as a source of stable resistance against the above mentioned diseases for development of disease free hybrids.

63. HKI-1342 (IC563963; INGR09063), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

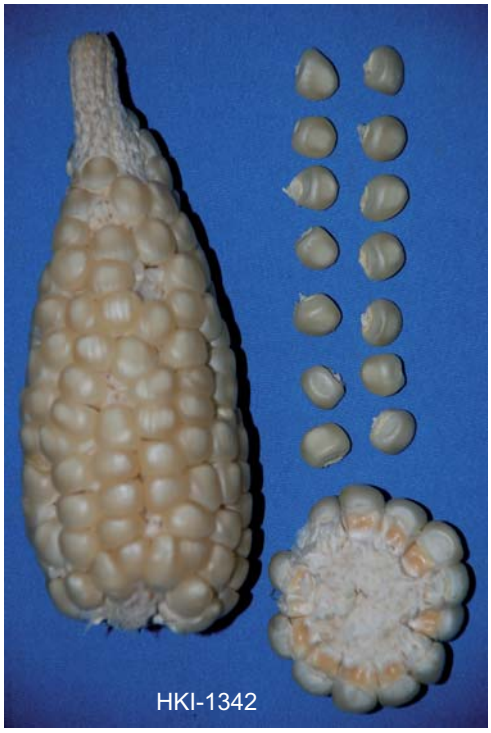
A late maturing line derived from CIMMYT line CML 6 after 7-8 years of inbreeding following by ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

HKI-1342

HKI-1342 is medium stature plant type with medium long cob. It has sparse tassel branches and a good pollen shedder, which is a merit of a good pollen parent. The grain row arrangement is straight and the Anthocyanin coloration of glume is white. It has very attractive white flint grain colour.

The four year data with respect to common rust and Maydis Leaf Blight (MLB) reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM600 for Maydis Leaf blight and common rust against susceptible check CM202. The disease reaction for Maydis Leaf Blight and common rust in HKI-1342 was consistently 1.0. This can be utilized as a source of stable resistance against the above mentioned diseases for development of disease free hybrids.

It is also a good combiner. When it was crossed with temperate material the line produced very productive hybrids, it can also be used as good pollen parent for tropical lines.



Criteria for Registration [Unique feature(s)]

1. Resistant to rust and MLB,
2. Late maturing, dark green leaves and productive,
3. White with shiny grain.

64. HKI-170 (1+2) (IC563967; INGR09064), a Maize (*Zea mays*) Germplasm, a Good Pollen Shedder, Attractive Grain Color, Resistant to Rust

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju, Rishi Pal and Dharam Pal Singh
Chaudhary Charan Singh, HAU, Karnal

A late maturing line derived from CIMMYT line CM170 after 7-8 years of inbreeding following ear-to-row selection at Haryana Agriculture University, Regional Research Station, Uchani, Karnal.

HKI-170 (1+2)

HKI-170 (1+2) is medium stature plant type with medium long cob. It has sparse tassel branches and a good pollen shedder, which is a merit of a good pollen parent. The grain row arrangement is straight and the Anthocyanin coloration of glume is white. It has very attractive yellow flint grain colour. HKI-170 (1+2) is a QPM inbred and has high tryptophan (>0.6%) content in its endosperm.

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When it was crossed with temperate material the line produced very productive hybrids, it can also be used as good pollen parent for tropical lines.

Criteria for Registration [Unique feature(s)]

1. Attractive yellow grain colour,
2. Late maturing,
3. Good combiner.

65. NBPGR Tomato-1 (IC564448; INGR09065), a Tomato (*Lycopersicon esculentum*) Germplasm, a High TSS (60.B)

SK Yadav, KK Gangopadhyay, SK Mishra, Gunjeet Kumar, Chitra Pandey, BL Meena, RK Mahajan, Mathura Rai, SK Sharma, Rajesh Kumar, HC Prasanna and Nagender Rai

National Bureau of Plant Genetic Resource, New Delhi-110 012

Tomato (*Lycopersican esculantum* L.) is one of the important vegetable crops widely grown all over India during winter and spring season. It is known for its use in salad, cooked and processed products. Tomato fruits with high TSS are highly demanding in processing industries for making tomato paste, puree, ketch-up, chutney etc. For processing, high TSS (Total soluble solids) is an important character for crop improvement and there is not many lines/ varieties available to suitable for processing. Therefore, identification of lines having high TSS will be useful in quality improvement of tomato. The experiment was conducted at IIVR, Varanasi as a part of multiplication evaluation of vegetable crops germplasm AICRP (Vegetable Crops) during winter 2005-06. The TSS of the said accession (NBPGR Tomato-1) has been found 6.0^0 Brix which is much higher than the normal (3-4^0 B).

The other parameters of this selection are Days to first flowering-44.0 days, Days to first maturity-79.0 days, Fruit length-3.6 cm, Fruit width-3.4 cm, Fruit weight-130.0 g, Number of fruit per plant-60.0, Number of branches per plant 5.0 and fruit yield per plant 900 g.

When it was crossed with temperate material the line produced very productive hybrids, it can also be used as good pollen parent for tropical lines.

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66. ANSR-1 (IC385843; INGR09066), a Kawaunch (*Mucuna pruriens*) Germplasm, High L-DOPA Content (6.30%)

Anil Kumar Singh, SK Pareek, Ashok Kumar, SK Singh, SS Malik and YS Tomer
National Bureau of Plant Genetic Resource, New Delhi-110 012

The genus *Mucuna pruriens* has a wide distributed in tropics/subtropical regions of the world. In India, 14 species are found in the foot hills of Himalayas, plains of West Bengal, Madhya Pradesh, Karnataka, Kerala, Andhra Pradesh and Andaman and Nicabar. Commonly it is "Kawanch" a trible pulse, velvet bean, cow-itch plant, mostly sown as alley cropping pattern. It conserves soil and improves the agro-forestry system. In particular, the seed and the root of *M. pruriens* are used in the India sustem of medicine as effective nervine tonic and aphrodisiac. It has diuretic property and consequently is used in kindly troubles and dropsy.

The seed contain L-DOPA (L-3:4-dihydroxy phenylalanine) which is the active principal responsible for treatment of Parkinson's disease and hypertension. In addition the seeds have fats, sterols, alkaloids and other amino acids.

67. D4 (IC567213; INGR09067), a Potato (*Solanum tuberosum*) Germplasm, a Male Fertile and Drogenic (Di)haploid of Tetraploid Potato Flowering

Sushruti Sharma, Debabrata Sarkar and Suman Kumar Pandey
Central Potato Research Institute, Shimla

The extraction of androgenic (di)haploids ($2n = 2x = 24$) from tetraploid potatoes (*Solanum tuberosum* L.; $2n = 4x = 48$) is frustratingly difficult. Androgenic potato (di)haploids extracted till date are either non-flowering or male sterile (Rokka, 2009). At the Central Potato Research Institute (CPRI), Shimla (India), two first-ever male-fertile androgenic (di)haploids-D4 (INGR 09067) and C-13 (INGR 09068) of tetraploid Indian potato cvs JTH/C-107 (a TPS parental line) and Kufri Chipsona-2 (a processing variety) respectively-have been developed through anther culture (Sharma *et al.*, 2009). Whereas C-13 is highly resistant to late blight, D4 is a flower colour (from intense purple to white) mutant.

Morpho-agronomic Characteristics

C-13 ($2n = 2x = 24$) is a dwarf and late-maturing, with a semi-compact bushy appearance (Fig. 1), short internodes, small lighter green leaves, white semi-stellate four-lobed corollas, pale yellow anther, short anther length and bilobed stigma. Its tubers are cylindrical with white flesh colour and closed sprout tip. D4 ($2n = 2x = 24$) has an open canopy structure, with short internodes, small dark-green narrow leaves (Fig. 1) without midrib pigmentation, no anthocyanin coloration of floral bud, floral stalk, calyx and pedicel, white corolla and pale yellow anthers. Its tubers are kidney-shaped with shallow eye depth, white predominant and vascular ring-type secondary flesh colour, and white-cream skin colour. Both D4 and C-13 yield on an average 3.4 and 7.8 tubers per plant, with 7.1 and 7.6 g avergae tuber weight and 14.1 and 21.1% tuber dry matter, respectively.

Associated Characters and Cultivation Practices

C-13 and D4 [endosperm balance number (EBN) 2] are invaluable (di)haploid breeding material for potato (Sharma *et al.*, 2009). They are recommended for introgressing various agronomic traits and disease resistance and/or abiotic stress tolerance attributes from 1 EBN diploid potato species, such as *S. bulbocastanum*, *S. circaeifolium*, *S. commersonii*, *S. etuberosum* and *S. pinnatisectum* into the gene pool of cultivated Indian tetraploid potatoes (4 EBN) through symmetric/ asymmetric somatic hybridization (Sharma *et al.*, 2008). C-13 can be used not only as an important source of late blight resistance in a potato breeding programme, but also to generate an appropriate biparental segregating population (F_1) for QTL-mapping of late blight resistance.

References

Rokka VM (2009) Potato haploids and breeding. In: A Touraev, BP Forster and SM Jain (eds) *Advances in Haploid Production in Higher Plants*. Springer Science + Business Media B.V., Dordrecht, pp 199-208.

Sharma S, D Sarkar and SK Pandey (2008) Symmetric somatic hybridization between *Solanum bulbocastanum* and *Solanum tuberosum* utilizing an effective protoplast isolation and culture system. In: J Gopal, D Pattanayak, D Kumar, PM Govindakrishnan and B Singh (eds) *Global Potato Conference 2008. Opportunities and Challenges in the New Millennium*. Indian Potato Association, Shimla, p 189.

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Associated Characters and Cultivation Practices

C-13 and D4 [endosperm balance number (EBN) 2] are invaluable (di)haploid breeding material for potato (Sharma *et al.*, 2009). They are recommended for introgressing various agronomic traits and disease resistance and/or abiotic stress tolerance attributes from 1 EBN diploid potato species, such as *S. bulbocastanum*, *S. circaeifolium*, *S. commersonii*, *S. etuberosum* and *S. pinnatisectum* into the gene pool of cultivated Indian tetraploid potatoes (4 EBN) through symmetric/ asymmetric somatic hybridization (Sharma *et al.*, 2008). C-13 can be used not only as an important source of late blight resistance in a potato breeding programme, but also to generate an appropriate biparental segregating population (F_1) for QTL-mapping of late blight resistance.

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68. C-13 (IC567214; INGR09068), a Potato (*Solanum tuberosum*) Germplasm, a Highly Resistant to Late Blight

Sushruti Sharma, Debabrata Sarkar and Suman Kumar Pandey
Central Potato Research Institute, Shimla

The extraction of androgenic (di)haploids (2*n* = 2*x* = 24) from tetraploid potatoes (*Solanum tuberosum* L.; 2*n* = 4*x* = 48) is frustratingly difficult. Androgenic potato (di)haploids extracted till date are either non-flowering or male sterile (Rokka, 2009). At the Central Potato Research Institute (CPRI), Shimla (India), two first-ever male-fertile androgenic (di)haploids-D4 (INGR 09067) and C-13 (INGR 09068) of tetraploid Indian potato cvs JTH/C-107 (a TPS parental line) and Kufri Chipsona-2 (a processing variety) respectively, have been developed through anther culture (Sharma *et al.*, 2009). Whereas C-13 is highly resistant to late blight, D4 is a flower colour (from intense purple to white) mutant.

Morpho-agronomic Characteristics

C-13 (2*n* = 2*x* = 24) is a dwarf and late-maturing, with a semi-compact bushy appearance (Fig. 1), short internodes, small lighter green leaves, white semi-stellate four-lobed corollas, pale yellow anther, short anther length and bilobed stigma. Its tubers are cylindrical with white flesh colour and closed sprout tip. D4 (2*n* = 2*x* = 24) has an open canopy structure, with short internodes, small dark-green narrow leaves (Fig. 1) without midrib pigmentation, no anthocyanin coloration of floral bud, floral stalk, calyx and pedicel, white corolla and pale yellow anthers. Its tubers are kidney-shaped with shallow eye depth, white predominant and vascular ring-type secondary flesh colour, and white-cream skin colour. Both D4 and C-13 yield on an average 3.4 and 7.8 tubers per plant, with 7.1 and 7.6 g avergae tuber weight and 14.1 and 21.1% tuber dry matter, respectively.

Associated Characters and Cultivation Practices

C-13 and D4 [endosperm balance number (EBN) 2] are invaluable (di)haploid breeding material for potato (Sharma *et al.*, 2009). They are recommended for introgressing various agronomic traits and disease resistance and/or abiotic stress tolerance attributes from 1 EBN diploid potato species, such as *S. bulbocastanum*, *S. circaeifolium*, *S. commersonii*, *S. etuberosum* and *S. pinnatisectum* into the gene pool of cultivated Indian tetraploid potatoes (4 EBN) through symmetric/asymmetric somatic hybridization (Sharma *et al.*, 2008). C-13 can be used not only as an important source of late blight resistance in a potato breeding programme, but also to generate an appropriate biparental segregating

Fig. 1: Androgenic (di)haploids C-13 (left) and D4 (right) of tetraploid Indian potato cvs Kufri Chipsona-2 and JTH/C-107, respectively, flowering under long-day conditions (May-August) of Shimla hills in northern India

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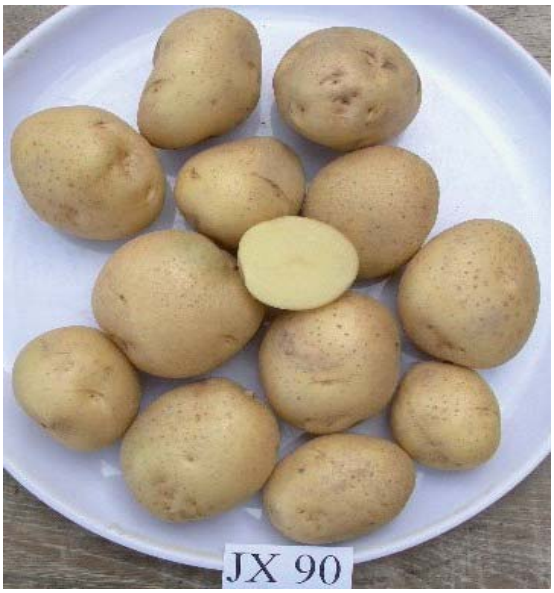
69. JX 90 (INGR09069), a Potato (*Solanum tuberosum*) Germplasm, a Horizontal Resistant to Late Blight and Early Blight, High Yield under Early (75 days) and Medium (90 days) Crop Duration

Raj Kumar, GS Kang, SK Pandey and Jai Gopal
Central Potato Research Station, Jalandhar-144 003

JX 90 was approved for registration as a source of resistance to late blight and early blight by Germplasm Registration Committee in its XIXth meeting held on 13th March 2009. Late blight caused by the fungus *Phytophthora infestans* (Mont.) de Bary is one of the most devastating diseases of cultivated potatoes worldwide. The disease is responsible for important economic losses and high levels of fungicide use (Singh and Shekhawat, 1999). Early blight (*Alternaria solani*) is a disease of potato across the crop's geographic range (Pavek and Cornisi, 1994). The disease is prevalent in many potato growing areas and is of economic importance in plains of India (Lakra, 1997).

JX 90 possess high horizontal resistance to late blight, high general combining ability for horizontal resistance to late blight; early blight resistance and high yield under early (75 days) and medium (90 days) harvests. At early (75 days) harvest it has performed at par with best control variety Kufri Ashoka for yield. Generally early bulking varieties are susceptible to late blight. However, JX 90 combines high horizontal resistance to late blight with early bulking. Under All India Coordinated Research Ptoject on Potato (AICRP Potato) trials JX 90 have shown resistance to late blight and early blight and its horizontal resistance to late blight has been confirmed in the study carried out by us during the years 2005 and 2006 (Kumar *et al*., 2007). It is well known that while vertical resistance to late blight may not be stable, horizontal resistance to late blight is a known stable character due to its multi-genic inheritance.



JX 90 is a selection from the progeny of the cross CP 1346 (Krirrinee) x MS/78-62. The cross was made at during 1985. The clone was selected from the progeny of this cross at Central Potato Research Station Jalandhar, Punjab. The breeding methodology is clonal selection from the cross between selected parents.

Morpho-agronomic Characteristics

Tubers of JX 90 are oval shape, with brownish skin colour, large sized, with shallow eyes and yellow flesh colour. JX 90 flower profusely at Kufri. The flower is white. Plant is medium compact. Leaflets are oval.

population (F_1) for QTL-mapping of late blight resistance.

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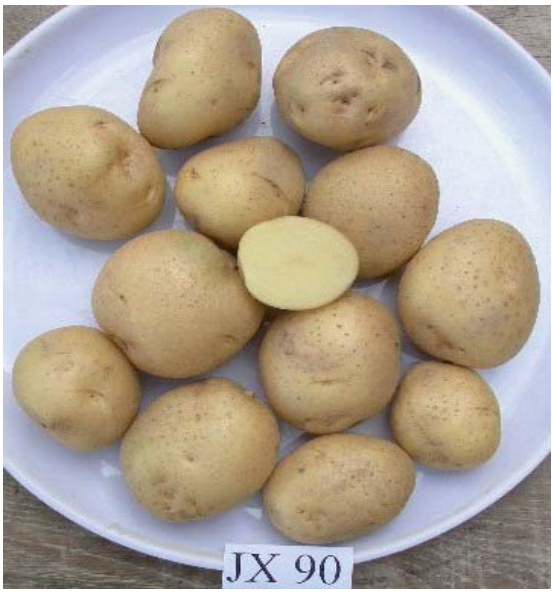

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Morpho-agronomic Characteristics

Tubers of JX 90 are oval shape, with brownish skin colour, large sized, with shallow eyes and yellow flesh colour. JX 90 flower profusely at Kufri. The flower is white. Plant is medium compact. Leaflets are oval.

Anthers are pale yellow with stylar length more than stamen column. Sprouts are bulbous and white-green in colour. For yield at early and medium maturity harvest this culture have performed consistently well over the years under multilocation trials under AICRP (Potato) from 1999-2000 to 2002-2003.

Associated Characters and Cultivated Practices

This line performs well for yield under early (75 days) and medium (90 days) harvest in Indian plains and plateau region.

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In Memoriam – A Tribute to Dr Norman Ernest Borlaug

(March 25, 1914- September 12, 2009)

The World Food Prize Organization has rightly described this eminent scientist as "The man who has saved more lives than any other person who has ever lived" while conferring the honor to him. In his passing away, the world has lost a famous agricultural scientist and a friend of developing nations like India. His life and achievements were a testimony to the contributions of his towering intellect, persistence and scientific vision. Dr. Norman Ernest Borlaug was an American agronomist, humanitarian, and a Nobel laureate who has been deemed the father of the Green Revolution. Dr. Borlaug was one of only six people to have won the Nobel Peace Prize, the Presidential Medal of Freedom and the Congressional Gold Medal. He was also the recipient of the Padma Vibhushan, India's second highest civilian honor. He received his Ph.D. in plant pathology and genetics from the University of Minnesota in 1942 and took up an agricultural research position in Mexico. He left his footprints in agriculture through his personal and professional commitment to fight hunger and poverty and the pioneering work in the development of semi-dwarf, high-yielding, and disease-resistant wheat varieties. During the mid-20th century, he was instrumental in introducing these high-yielding varieties combined with modern agricultural production techniques to Mexico, Pakistan, and India. Dr. Borlaug is credited with saving over a billion people worldwide from starvation and was awarded the Nobel Peace Prize in 1970 in recognition of his outstanding contributions to world peace through increasing food supply. The Nobel Prize Committee, while identifying him for this high recognition, concluded "More than any other single person of this age, he has helped to provide bread for a hungry world. We have made this choice in the hope that providing bread will also give the world peace…" The day the award was announced, Dr. Borlaug, vigorous and slender at 56, was working in a wheat field outside Mexico City when his wife, Margaret, drove up to tell him the news. His renowned Literary work includes Wheat *in the Third World* (1982), L*and use, food, energy and recreation* (1983), *Feeding a human population that increasingly crowds a fragile planet* (1994), Norman

Borlaug on World Hunger (1997), The Green Revolution Revisited and the Road Ahead *(*2000), Ending World Hunger, The Promise of Biotechnology and the Threat of Antiscience Zealotry (2000), Feeding *a World of 10 Billion People (*2003), and Prospects *for world agriculture in the twenty-first century* (2004). Dr. Norman Borlaug's remarkable lifetime efforts to feed millions of less fortunate around the world will continue to inspire all those concerned with hunger and malnutrition. His legacy includes billions of lives saved from the misery of starvation and the education of thousands of scientists worldwide (who carry on his work today. For fifty-two years, Dr. Norman Borlaug helped to provide more food to the neediest areas of the world. But perhaps of greater importance, this distinguished scientist-philosopher has been demonstrating practical ways to give people of the entire world a higher quality of life. The passion that drives Dr. Borlaug's life is an inspiration for all of us to follow, said Jimmy Carter, 39th President of the United States and 2002 Nobel Peace Prize Laureate.

In his demise, the world has lost a great visionary, a humanitarian and a champion in the battle against world hunger. The PGR scientific community pays its respect and homage to this great human being.

Editors
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