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The Wild Genepool of Pigeonpea at ICRISAT Genebank - Status and Distribution

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Wild pigeonpea genepool is a promising source for various biotic and abiotic stress resistances, and important agronomic and nutritional traits. The genebank at ICRISAT, Patancheru, India, conserves 13,771 accessions of pigeonpea from 74 countries, including 555 accessions of wild relatives belonging to 66 species of six genera from 41 countries. Out of 11 genera now recognized in *Cajaninae*, only six are available at ICRISAT genebank. Of the 32 species recognized in genus *Cajanus,* ICRISAT genebank holds a total of 213 accessions of 19 species and *C. scarabaeoides* has largest number of accessions (102 accessions). Genebank has 303 accessions of genus *Rhynchosia* represented by 33 species and largely represented by *R. minima* (186 accessions). Genus *Paracalyx* has two accessions of one species; genus *Dunbaria* has 12 accessions of two species; genus *Eriosema* has seven accessions of three species and genus *Flemingia* is represented by 18 accessions of eight species.

Key Words: *Cajanus,* Genepool, Germplasm, *Rhynchosia,* Wild species

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) is one of the important grain legume crops of tropics and subtropics. Because of its multiple uses, pigeonpea cultivation is extended to about 82 countries as a field or as backyard crop. Due to high seed protein content (up to 25%), pigeonpea is an important protein source for the vegetarian population especially, in the Indian sub-continent. Considerable progress in pigeonpea improvement has been made by using variability within the cultivated species. However, the crop still suffers from several biotic stresses like pod borer (*Helicoverpa armigera* Hubner), podfly (*Melanagromyza obtusa* Mall), sterility mosaic disease (SMD), wilt (*Fusarium udum* Butler) and phytophthora blight (*Phytophthora drechsleri* Tucker); and abiotic stresses such as salinity and water logging conditions. Many wild relatives (WR) including those of pigeonpea have survived drought, floods, extreme heat and cold, and have developed resistance to various biotic and abiotic stresses. Wild relatives are more important when they possess traits of agronomic importance in addition to biotic and abiotic stress resistance especially, those that can be hybridized easily with cultivated species. Despite their importance, the wild relatives have not received due attention from germplasm collectors and plant breeders, and remain under-represented, accounting for less than two percent of the global germplasm collections of major food crops (Kameshwara Rao, 2003). The knowledge on existing collections of wild relatives is meager and poorly documented. Therefore, the present study was aimed at reviewing the world collection of pigeonpea wild relatives conserved at the genebank of International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India, for their geographical distribution, useful traits and crossability relationships to enhance their utilization in pigeonpea improvement.

Materials and Methods

ICRISAT genebank serves as world repository for pigeonpea germplasm and conserves 13,771 accessions originated in 74 countries, including 555 accessions of wild relatives. Wild accessions introduced from different sources and collected in different countries were identified and by using passport information, summarized belonging to 66 species of six genera. Number of accessions in each species, genepool affinity, geographical distribution, identification of promising species and studies on crossability relationships were discussed for enhanced utilization of wild relatives' germplasm in pigeonpea improvement.

Results and Discussion

Germplasm Assembly

The wild relatives of many crop plants including those of pigeonpea are disappearing at an alarming rate due to rapid urbanization, shifting cultivation, forest fires, climate change, natural calamities, over grazing etc. (Upadhyaya and Gowda, 2009). The genebank at ICRISAT,

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Patancheru, India assembled and is conserving 13,771 accessions of pigeonpea from 74 countries including 555 accessions of wild relatives belonging to 66 species of six genera, from 41 countries (Table 1). The assembly of wild relatives' germplasm includes introductions from different organizations and the germplasm collected by ICRISAT in collaboration with NARS partners, universities, NGOs, Bioversity International (formerly IPGRI) *etc.,* by launching collection missions in priority areas. A total of 314 accessions of wild relatives were introduced from various organizations located in different countries. Australia was the major donor providing 254 accessions that originated in different countries. The collection strategy for wild species involves identification of geographic distribution of species, precise location, time of fruiting etc., which need to be gathered from different herbaria and through correspondence. As the wild relatives are uncommon in natural vegetation and location data are often old and not precise, hence, it is always not feasible to follow the collection strategy recommended for the cultivated species (Remanandan, 1981). ICRISAT and partners have launched a total of 216 germplasm collection missions in 62 countries for its mandate crops and their wild relatives including those of pigeonpea and collected 241 samples of pigeonpea wild relatives during 40 collection missions in nine countries. India being the primary center of diversity for pigeonpea resulted in 154 accessions from 26 collection missions.

The assembled species are summarized by number of accessions and traits of importance in Table 1. Out of 11 genera now recognized in *Cajaninae*, only six are available at ICRISAT genebank. Among six genera, *Cajanus* and *Rhynchosia* have largest number of accessions. Of the 32 species recognized in genus *Cajanus,* the cultivated species (*Cajanus cajan)* and 19 wild species are assembled at ICRISAT genebank. Out of 213 accessions of all these wild species, *C. scarabaeoides* is represented by largest number of accessions (102 accessions). Genus *Rhynchosia* represented by 33 species has 303 accessions largely represented by *R. minima* (186 accessions). The remaining 117 accessions belong to 32 other species. Genus *Paracalyx* has only one species with two accessions; *Dunbaria* has two species with 12 accessions; *Eriosema* has three species with seven accessions and genus *Flemingia* represented by eight species with 18 accessions. (Table 1). Species classification for three accessions of genus *Flemingia* and seven accessions of genus *Rhynchosia* is not yet known. The summary of wild relatives' germplasm at ICRISAT genebank indicates wide taxonomical gaps in the collection and urgency of filling these gaps.

All the species assembled at ICRISAT genebank are seed producing and are conserved as active collection in medium-term cold store maintained at 4ºC and 35% RH. Species with critical seed quantity are multiplied by growing in the botanical garden. The passport information on the collection is available at http://www.icrisat.org/ICRISAT.crops.htm. ICRISAT genebank has served as a major source for pigeonpea wild relatives' germplasm. Limited seeds of all in-trust accessions with FAO are available under Standard Material Transfer Agreement (SMTA) of the International Treaty for research and utilization globally. So far, the genebank has provided 4,633 seed samples of 56 species for research use in 31 countries.

Geographical Distribution

The geographical distribution of different species is presented in Table 2. Asian countries are the predominant source and accounted for a total of 285 accessions belonging to 50 species of six genera in the collection. India is represented by 201 accessions of 35 species belonging to six genera. Oceania was another important region for pigeonpea wild relatives accounting for 78 accessions of 13 species and three genera. Australia alone is represented by 73 accessions of 13 species of three genera. Twelve African countries, particularly, the eastern and southern Africa have accounted for 69 accessions of 16 species belonging to *Dunbaria, Eriosema* and *Rhynchosia*. Mexico is represented by 59 accessions of six species of *Rhynchosia*. Eight countries each of Central America and South America contributed 61 accessions belonging to 24 species of three genera and United Kingdom represented as a donor for one *Cajanus* accession.

Promising Sources

The collection of pigeonpea wild relatives at ICRISAT genebank has not been characterized and evaluated systematically, which involves participation of multidisciplinary scientists and additional resources. However, screening and evaluation of limited species by researchers indicated wild pigeonpea genepool as a promising source for various biotic and abiotic stresses in addition to possessing some important agronomic traits (Reddy *et al*., 2000). The major constraints

Table 1. Summary of pigeonpea wild relatives' germplasm assembled at the ICRISAT genebank, Patancheru, India.

Genus	Species	No. of accs.	Genepool*	Traits of importance	References
Cajanus	*acutifolius* (F.v. Muell.) van der Maesen	12	2	Drought and salinity tolerant	Remanandan (1981); Srivastava *et al*. (2006)
	albicans (W. & A.) van der Maesen	20	2	Resistance to SMD, alternaria blight; drought and salinity tolerance, high seed protein (> 30%), and crossable with pigeonpea	Pundir and Singh (1985a); Reddy *et al*. (2000)
	cajanifolius (Haines) van der Maesen	5	2	Salinity tolerant, tolerant to pod borer, podfly and pod wasp, source for A5 cytoplasm and crossable with pigeonpea	Singh *et al*. (1990); Pundir and Singh (1985a); Reddy *et al.* (2000); Sharma *et al*. (2006)
	cinereus (F.v. Muell.) F.v. Muell.	1	–		
	confertiflorus F.v. Muell.	1	3		
	crassus (Prain ex King) van der Maesen	10	3	Source for A3 Cytoplasm	
	elongatus (Benth.) van der Maesen	1	3		
	goensis Dalz.	1	3	High seed number per pod	van der Maesen, (1986)
	lanceolatus (W.V. Fitzg.) van der Maesen	1	2		
	latisepalus (Reynolds & Pedley) van der Maesen	1	2		
	lineatus (W. & A). van der Maesen	10	2	Resistance to SMD and alternaria blight; drought tolerance, early flowering, source for A6 cytoplasm and crossable with pigeonpea	Pundir and Singh (1985a); Reddy *et al*. (2000)
	marmoratus (R. Br. Ex Benth.) F. von Mueller	2	3		
	mollis (Benth.) van der Maesen	8	3	High seed protein content (33.4%) and high seed number per pod	Remanandan (1990); van der Maesen (1986)
	platycarpus (Benth.) van der Maesen	17	3	Resistance to phytophthora and alternaria blight; salinity tolerance; annuality, rapid seedling growth, photoperiod insensitivity, extra early flowering and maturity, high harvest index; high seed protein (27-31.6%), high cystine + methionine (> 29%) and a source for A7 cytoplasm	Reddy *et al*. (2000); Srivastava *et al*. (2006)
	reticulatus (Dryander) F.v. Muell.	8	2	Hardy, fire-tolerant, resistant to pod borer, high seed protein (33%) and a source for A8 cytoplasm	Akinola *et al*. (1975); Reddy *et al*. (2000)
	rugosus (W and A) van der Maesen	6	3		
	scarabaeoides (L.) Thouars	102	2	Early flowering, resistance to wilt, sterility mosaic disease (SMD), phytophthora blight (both for P2 and P3 isolates), alternaria blight, pod borer, podfly, pod wasp, cyst nematode, and possesses combined resistance to diseases and insects; water logging tolerance; high seed protein (> 28%), source for A2 cytoplasm and crossable with pigeonpea	Pundir and Singh (1985a); Reddy *et al*. (2000)

** 2=Secondary genepool, 3=Tertiary genepool, 4=Quaternary genepool*

Genus	Species	No. of accs.	Genepool	Traits of importance	References
	sericeus (Benth. Ex Bak.) van der Maesen	4	2	Resistance to SMD, phytophthora, and alternaria blight; pod borer, podfly, pod wasp; drought and salinity tolerance ; high seed protein content (> 29%), source for A1 cytoplasm and crossable with pigeonpea	Remanandan (1990); Sharma, (2006); Upadhyaya (2006)
	trinervius (DC.) van der Maesen	3	2	Crossable with pigeonpea	Pundir and Singh (1985a); Reddy *et al*. (2000)
	Total	**213**			
Dunbaria	*ferruginea* Wight & Arn	7	4	Salinity tolerant	Singh *et al*. (1990)
	heynei Wight & Arn	5	4	Green manure	Arora and Chandel (1972)
	Total	**12**			
Eriosema	*ellipticum* Wel. Ex Beker	1	4	Medicinal use	Abbot and Lowore (1995)
	glomeratum (Guill. & Perr.) Hook. f	1	4		
	sporaleoides (Lam.) G. Don.	2	4		
	unknown	3	4		
	Total	**7**			
Flemingia	*bracteata* Roxb.	2	4		
	involucrate Benth.	1	4		
	macrophylla Benth.	6	4		
	nana Roxb.	1	4		
	paniculata Benth.	1	4		
	semialata Roxb.	1	4		
	stricta Roxb.	1	4		
	strobilifera (L.) W.T. Aiton	5	4	Cover crop and medicinal use	Ambasta (1986)
	Total	**18**			
Paracalyx	*scariosa* Roxb.Ali.	2	4		
	Total	**2**			
Rhynchosia	*americana* (Houst. Ex Mipp.) M.C. Metz.	1	4		
	aurea (Willd.) DC.	8	4		
	bracteata Baker	6	4	Tolerant to pod borer, podfly and pod wasp	Sharma (2006)
	burkartii Fortunato	1	4		
	cana (Willd.) DC.	6	4		
	candida (Hiern) Torre	1	4		
	caribaea (Jacq.) DC.	1	4		
	cyamosperma	2	4		
	densiflora (Roth) DC.	5	4		
	edulis Griseb.	9	4		
	filipes Benth.	2	4		
	heynei Wight & Arn.	1	4		

Genus	Species	No. of accs.	Genepool	Traits of importance	References
	himalensis Benth. Ex Baker	1	4		
	hirta (Andrews) Meikle & Verdc.	3	4		
	kilimandscharica Harms	1	4		
	longiracemosa M. Martens & Galeotti	2	4		
	malacophylla (Spreng.) Bojer	1	4		
	micrantha (Harms)	5	4		
	minima (L.) DC.	186	4	Medicinal use and pasture	Morris (1999)
	pyramidalis (Lam.) Urb.	1	4	Narcotic properties	Farnsworth *et al*. (1967)
	reticulata (Sw.) DC.	1	4	Early flowering, photoperiod insensitivity, protease inhibitor	Reddy *et al*. (2000)
	rothii Benth. Ex. Aitch	11	4	High seed protein content	Remanandan (1981)
	rufescens (Willd.) DC.	7	4		
	schimperi Bioss.	2	4		
	senna Gillies ex. Hook.	2	4		
	suaveolens (L.f.) DC.	2	4		
	sublobata (Schumach.)	9	4		
	totta (Thumb.) DC.	11	4		
	velutina Wight & Arn	1	4		
	venulosa (Hiern) K. Schum.	1	4		
	verdcourtii Thulin	3	4		
	viscidula Steud.	2	4		
	viscose (Roth) DC.	1	4		
	Unknown	7			
	Total	**303**			
	Grand Total	**555**			

to pigeonpea production among the insect pests are pod borer and podfly. Among the diseases, fusarium wilt, sterility mosaic and phytophthora blight are economically important. Sources of resistance identified by different researchers for various biotic and abiotic stresses and agronomic traits in different species include *C. scarabaeoides* for wilt; *C. albicans, C. lineatus, C. scarabaeoides, C. sericeus* and *C. crassus* var. *crassus* for sterility mosaic disease (Reddy *et al*., 2000; Lava Kumar *et al*., 2005); *C. platycarpus, C. scarabaeoides* and *C. sericeus* for phytophthora blight; *C. albicans, C. lineatus, C. platycarpus, C. scarabaeoides* and *C. sericeus* for alternaria blight (Reddy *et al*., 2000); *C. albicans, C. scarabaeoides, C. sericeus, C. reticulatus* and *R. bracteata* for pod borer, podfly and pod wasp (Sharma, 2006); *C. scarabaeoides*, *R. aurea*, *R. minima* and *R. rothii* for nematodes (*Rotylenchulus reniformis*) (Sharma *et al*., 1993); *C. acutifolius, C. albicans, C. lineatus* and *C. sericeus* for drought (Reddy *et al*., 2000); *C. acutifolius, C. albicans, C. cajanifolius, C. platycarpus, C. scarabaeoides, C. sericeus* and *D. ferruginea* for salinity (Srivastava *et al*., 2006); *C. scarabaeoides* for water logging; *C. lineatus* for cleistogamy (Saxena *et al*., 1992) and *C. reticulatus* var *grandifolius* for fire tolerance (Reddy *et al*., 2000) (Table 1). *C. platycarpus* and *C. scarabaeoides* for early flowering; *C. platycarpus* and *R. reticulata* for photoperiod insensitivity (Reddy *et al*., 2000);

Table 2. Geographical distribution of pigeonpea wild relatives germplasm assembled at the ICRISAT genebank, Patancheru, India

Region	Country	No. of accessions	Species
Africa	Angola	1	*R. candida*
	Botswana	3	*R. minima* and *R. totta*
	Kenya	5	*R. edulis, R. micrantha, R. rothii, R. totta* and *R. velutina*
	Malawi	4	*E. ellipticum, Eriosema* sp. and *R. sublobata*
	Mali	4	*R. minima*
	Mozambique	1	*R. totta*
	Namibia	5	*R. minima* and *R. totta*
	Senegal	1	*E. glomeratum*
	South Africa	15	*R. cyamosperma, R. densiflora, R. minima, R. sublobata, R. totta* and *R. venulosa*
	Tanzania	13	*R. aurea, R. densiflora, R. micrantha, R. minima, R. sublobata, R. verdcourtii* and *D. ferruginea*
	Zambia	7	*R. minima* and *R. sublobata*
	Zimbabwe	10	*R. minima, R. sublobata* and *R. totta*
Asia	China	1	*R. minima*
	India	201	*C. albicans, C. cajanifolius, C. crassus, C. elongatus, C. goensis, C. lineatus, C. mollis, C. platycarpus,, C. rugosus, C. scarabaeoides, C. sericeus, C. trinervius, D. ferruginea, D. heynei, Eriosema* sp., *F. macrophylla, F. nana, F. semialata, F. stricta, F. strobilifera, P. scariosa, R. aurea, R. bracteata, R. cana, R. cyamosperma, R. densiflora, R. filipes, R. heynei, R, himalensis, R. hirta, R. minima, R. rothii, R. rufescens, R. schimperi, R. suaveolens,* and *R. viscidula*
	Indonesia	36	*F. bracteata, F. involucrata, F. strobilifera, R. minima, R. rufescens, Rhynchosia* sp. and *C. scarabaeoides*
	Myanmar	8	*C. crassus, C. scarabaeoides, F. paniculata* and *R. bracteata*
	Oman	3	*R. kilimandscharica* and *R. minima*
	Pakistan	1	*Rhynchosia* sp.
	Philippines	2	*C. scarabaeoides*
	Sri Lanka	33	*C. albicans, C. rugosus, C. scarabaeoides, C. trinervius, R. cana, R. viscose* and *Rhynchosia* sp.
Europe	United Kingdom	1	*C. scarabaeoides*
North America	Mexico	59	*R. americana, R. caribaea, R. edulis, R. longeraemosa, R. minima, R. pyramidalis* and *Rhynchosia* sp.
Central America	Antigua and Barbuda	4	*R. minima*
	Belize	2	*R. longeraemos* and *R. minima*
	Costa Rica	1	*R. minima*
	Cuba	6	*R. minima*
	Honduras	1	*R. minima*
	Nicaragua	4	*R. minima*
	Panama	2	*R. minima* and *R. reticulata*
	Trinidad and Tobago	1	*F. bracteata*
South America	Argentina	8	*R. burkartii, R. edulis, R. minima* and *R. senna*
	Bolivia	8	*R. edulis* and *R. minima*
	Brazil	10	*R. edulis* and *R. minima*
	Colombia	3	*R. minima*

Region	Country	No. of accessions	Species
	Ecuador	1	*R. minima*
	Paraguay	5	*R. edulis* and *R. minima*
	Peru	2	*R. minima*
	Venezuela	3	*R. minima*
Oceania	Australia	73	*C. acutifolius, C. cinereus, C. confertiflorus, C. lanceolatus, C. latisepalus, C. marmoratus, C. reticulatus, C. scarabaeoides, C. sericeus, E. sporaleoides, R. edulis, R. minima* and *R. viscidula*
	Fiji	2	*C. scarabaeoides*
	Papua New Guinea	3	*C. reticulatus* and *R. minima*
No information		2	*C. scarabaeoides* and *R. malacophylla*

C. aromaticus, *C. goensis* and *C. mollis* for high seed number per pod (van der Maesen, 1986) and *C. scarabaeoides* for high pod setting (74%) (Upadhyaya, 2006) are the important sources for agronomic traits. The highest seed protein content in the entire collection of cultivated pigeonpea was 30.8% (Remanandan, 1990) and evaluation of different species for seed protein content revealed that *C. lineatus* (34.2%), *C. crassus* (33.8%), *C. cajanifolius* (33.6%), *C. mollis* (33.4%), *C. platycarpus* (33.3%), *C. scarabaeoides* (up to 34%) and *C. albicans* (32.5%) as the best sources (Reddy *et al*., 1997; Reddy *et al*., 2000) (Table 1). Genetic male sterility is available in *C. cajanifolius* (van der Maesen, 2006). Most of the *Cajanus* species are palatable to cattle and goats and many wild species of pigeonpea are useful in rearing lac insects. Some wild species of pigeonpea were found as the sources of cytoplasmic and genetic male sterility system (CGMS). *C. sericeus* for A1 cytoplasm (Ariyanayagam *et al*., 1995; Saxena *et al*., 1996), *C. scarabaeoides* for A2 cytoplasm (Tikka *et al*., 1997; Saxena and Kumar, 2003), *C. volubilis* for A3 cytoplasm (Wanjari *et al*., 2001), *C. cajanifolius* for A4 cytoplasm (Saxena *et al*., 2008), *C. cajan* for A5 cytoplasm, *C. lineatus* for A6 cytoplasm, *C. platycarpus* for A7 cytoplasm and *C. reticulatus* for A8 cytoplasm are the known sources of CGMS cytoplasm (Saxena *et al*., 2010). Wild relatives of pigeonpea offered avenues for the development of CGMS system, which led to development of hybrids, a major shift in pigeonpea improvement work.

Crossability Relationships

The main efforts of crossability studies have been interspecific hybridization with pigeonpea. Depending upon the crossability relationships, Harlan and de Wet (1971) placed all species which intercross readily to produce fertile hybrids in to the primary genepool. All cultivated pigeonpeas (*Cajanus cajan)* are included in primary genepool. Species such as *C. acutifolius*, *C. albicans, C. cajanifolius, C. lanceolatus, C. latisepalus, C. lineatus, C. reticulatus, C. scarabaeoides, C. sericeus* and *C. trinervius,* which produce partially fertile hybrids with the cultivated species are placed in secondary genepool. *C. cajanifolius*, which has close affinity to cultivated pigeonpea placed in this genepool is the progenitor of cultivated pigeonpea (Mallikarjuna *et al*., 2011). Tertiary genepool comprises of the all *Cajanus* species, which are not crossable with cultivated species or crossable by using biotechnology tools. Wild species placed in the quaternary genepool belong to genera such as *Flemingia, Rhynchosia, Dunbaria, Eriosema, Paracalyx, Adenodolichos, Bolusafra, Carissoa, Chrysoscias, Baukea* (Mallikarjuna *et al*., 2011) (Table 1). Limited attempts to cross *Rhynchosia* and *Dunbaria* species with *Cajanus cajan* so far have not been successful. Reddy *et al*. (1981) reported that six species (*C. lineatus, C. sericeus, C. scarabaeoides var. scarabaeoides, C. albicans, C. trinervius* and *C. cajanifolius*) cross with cultivated pigeonpea. Pundir and Singh (1985a) reported the crossability of *C. albicans*, *C. cajanifolius*, *C. lineatus, C. scarabaeoides* and *C. trinervius* with cultivated pigeonpea. Within the genus *Cajanus*, *C. lineatus* crossed with *C. albicans* and *C. scarabaeoides* with *C. sericeus*. Three species, (*C. platycarpus*, *C. volubilis* and *R. rothii*) did not cross with any other species. Biosystematic studies encompassing morpho-cytological and electrophoretic analysis of *Cajanus cajan*, seven species of *Cajanus* and one of *Rhynchosia* revealed that *C. cajanifolius* is closest to *C. cajan*, followed by *C. lineatus, C. scarabaeoides, C. sericeus, C. albicans, C. volubilis, C. platycarpus* and *R. rothii*, in that order (Pundir and Singh, 1985b). Tissue culture and embryo

rescue techniques have provided an opportunity for the utilization of tertiary genepool in breeding programmes. Hybrids between *C. platycarpus* and cultivated pigeonpea have been obtained by using embryo rescue technique followed by chromosome doubling through colchicine treatment (Mallikarjuna *et al*., 2006).

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Meddling Wheat Germplasm to Augment Grain Protein Content and Grain Yield

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Association of grain protein content with grain yield components was critically examined in (*Triticum aestivum* L.) to facilitate development of genetic resources blended with yield and protein. Investigations carried out for four years on 400-450 line/year, revealed that grain weight plays a defining role in augmenting protein content with grain yield. Even though the extent of variability matched in the four populations, negative association between grain size and protein content was not registered when population mean improved and the trend remained unchanged even when shrivelled or poorly developed grains were removed. Negative association between grain size and protein content also weakened when very small grains were separated. A population with increased grain weight enhanced protein yield and it made selection easier. Population with improved grain weight provided an equal opportunity of selecting genotypes of improved grain yield and grain protein with no deficit on genetic variability. The study demonstrated that grain weight can be articulated to combine yield and grain protein content more efficiently.

Key Words: Bread wheat, Diversity, Grain protein content, Grain weight, Protein yield, Selection efficiency, Yield components

Introduction

The wheat research in India is getting increasingly endowed to grain quality. Genetic improvement in grain protein content of bread wheat (*Triticum aestivum* L.) is crucial for nutritional security and for also improving bread-making quality and the flour yield. A strong inverse relationship between grain protein content and grain yield has been a problem in blending these two traits in high proportion (O'-Brien and Ronalds, 1984; Levy and Feldman, 1987, 1989; Beiquan *et al.*, 1994; Fabrizius *et al*., 1997; Asseng and Milroy, 2006). Any morphological trait useful in removing negative association between yield and protein content shall be immensely useful in selecting genotypes blended with protein and yield but such a possibility has been negated by Martre *et al.* (2007). Since yield and protein are influenced by grain weight in disparate directions, any strategy to augment grain yield and protein content in wheat has to ensure a delicate balance with grain weight. A critical association between grain weight and grain protein content has been articulated for enhancing grain protein content in the background of high yield.

Materials and Methods

Germplasm consisting of entries from the national and international programmes was examined for four successive crop seasons during 2004-07. The material under study was developed as the germplasm-enrichment efforts focussed on quality improvement. Each year some new entries were added to the genetic resource retained from the previous year. The selections were exercised basically to discard the entries which exhibited late flowering, poor development, tendency to lodge, high susceptibility to rust diseases and very low grain protein content. The resource saved each year was augmented with new accessions next year and re-examined for the traits under study. The testing material in the final year therefore, had a good proportion of genotypes superior in 1000 grain weight (TGW) and grain protein content (GPC). Planting was done under irrigated conditions in the middle of November in plot size of 1.2 m^2 *i.e.* (two rows of 2m row length spaced at 30 cm) with recommended agronomic practices, under Augmented Block Design to adjust components under study as per block variations. GPC recorded on Infra-Tec 1255 instrument was converted to 14% grain moisture. The instrument based on infra-red transmission was calibrated with universal software updated for Indian wheat and had been used earlier in several thousand Indian wheat samples for estimation of GPC. Observations were recorded on grain yield, plant height, days to heading, maturity period and TGW. Simple correlations were derived between protein and targeted yield components. Based on average grain weight, the material was further

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assorted into two groups, and the pattern of variability and yield protein relationship was compared each year as suggested by Cochran and Cox (1957).

Results and Discussion

Morphological Traits and Protein Content

The germplasm evaluated during experimental period (four years) exhibited wide range of variability, for all the traits (Table 1). During this period, the coefficient of variability ranged from 6.58 to 7.26% for GPC and 21.5 to 28.6% for grain yield. Early heading and early ripening was noted in the first year material (Set I). Germplasm evaluated in the second year *i.e.* Set II exhibited more diversity and higher GPC but the seeds were small. This difference could be attributed to i) the suppressing growth conditions in the second crop year as expressed through lower yield resulting from less number of grains and poor grain weight which resulted in elevated GPC, and ii) the new accessions augmented in the Set II. Material in the third year (Set III) appeared more uniform and improved for important field characteristics, particularly the phenological attributes, plant height and TGW but protein content was low due to more number of grains. The final year material (Set IV) was characteristically different with high GPC as well as TGW. Selection during past three years led to higher TGW and GPC as negative linkage was broken between these two traits and +ve alleles for both got accumulated in the final year material. In the first two years of Set I and II, the grain yield was negatively correlated with grain weight. On the contrary, when grain weight improved as in Set III and IV, there was no association between grain yield and grain weight. In those populations, it was the grain number which regulated the grain yield with negative correlation between them. As per convention, a negative association between yield and protein was too obvious in all the years. As reported earlier by Beiquan *et al.* (1994), some of the phenological traits also registered association with GPC in some of the years but it appeared totally germplasm specific. Amongst all the traits under study, there was some consistency between grain weight and protein content. A strong negative correlation between GPC and TGW was observed in Set I and II, the populations possessing low TGW. However in improved grain weight populations of Set III and Set IV, such an association was not observed. Strong inverse relationship between TGW and GPC has been reported by Nagarajan *et al.* (2007) and absence of such an association is also not so uncommon (Levy and Feldman, 1987).

It can be concluded that negative association between TGW and GPC was not due to shrivelled grains alone because the trend remained negative in Set I (N: 259, r: -0.28**) and Set II (N: 372, r: -0.35**) and unrelated in Set III (N: 479, r: -0.08) and Set IV (N: 369, r: 0.10) even after delimiting the four populations from late heading and long duration. Multiple regression analysis revealed that indices based upon the morphological traits alone could not be devised to aid selection of high protein genotypes. Though the regression coefficient was significant in each population, the six characters under study could explain very little variability for GPC as the R^2 value varied from 0.08 (Set IV) to 0.23 (Set I). Also, there was no consistency regarding components contributing significantly to high protein in the individual

Table 1. Variability in lines for yield contributing traits and their association with protein content

Characters	SET I 2004 (373 lines)			SET II 2005 (450 lines)			SET III 2006 (523 lines)			SET IV 2007 (428 lines)		
	Mean	CV	r value	Mean	CV	r value	Mean	CV	r value	Mean	CV	r value
GPC (%)	12.6	6.58	1.00	13.1	7.26	1.00	12.5	7.04	1.00	12.9	6.41	1.00
GY (g/m^2)	435.0	21.50	-0.18**	407.0	28.6	-0.24**	487.0	23.00	-0.29**	402.0	25.4	-0.21**
TGW (g)	33.5	14.10	-0.39**	32.1	15.5	-0.36**	36.9	12.50	-0.07	39.5	13.3	0.08
GPM ('000)	13.1	21.20	0.04	12.8	28.4	-0.06	13.3	23.40	-0.24**	10.3	25.6	-0.23**
PH (cm)	104.0	9.50	0.18**	107.0	9.92	0.07	102.0	8.68	0.18**	99.0	10.0	0.04
HD (days)	90.0	6.07	0.28**	93.0	8.80	0.13**	95.0	4.06	0.03	93.0	6.38	-0.03
GGP (days)	43.0	10.90	-0.27**	52.0	12.6	-0.04	45.0	6.73	-0.07	48.0	11.5	-0.02

CV = Coefficient of variability (%), r value = Correlation coefficient with grain protein content,
** = Significant at P 0.01, GY = Grain yield, GPM = Grains per m^2, PH = Plant height, HD = Heading days,
GGP = Grain growth period

populations. It was TGW, height and grain growth period (GGP) in Set I, heading and GGP in Set II, height in Set III, and TGW and GGP in Set III.

Grain Weight and Protein Relationship

Balance between grain weight and grain yield has always been crucial in wheat. Since yield in wheat is derived through number of grains per unit area and grain weight, negative relationship between TGW and GPC is bound to hamper breeding efforts aimed to blend high protein content and high grain yield. An understanding of the magnitude and direction of the association between TGW and GPC is, therefore, very crucial in breeding for high protein content without compromising TGW. It was observed that instead of linear, the polynomial trend fitted better between these two important grain traits (Fig. 1). R^2 value improved in all the four populations when polynomial trend line of the order 2 was plotted. It is evident from the present study that in the populations with low TGW, negative association between these traits existed only in the lot where TGW fell below 32-33g. Therefore, negative association between grain weight and protein content should not always be taken as disincentive in quality improvement efforts.

Selection for Protein Yield

Grain yield and grain protein concentration are two important parameters in breeding for high protein content in wheat. Independent segregation of the genes controlling grain yield and protein concentration had been reported to suggest simultaneous selection for the two components (O'-Brien and Ronalds, 1986, Fabrizius *et al.,* 1997). It has also been suggested that overemphasis on selection for high protein content can reduce yield in the following generation (O'-Brien and Ronalds, 1986). Alternatively, selection for protein yield per unit area has also been in practice since long (Bhatia, 1975; McNeal *et al.,* 1982). In the present study, the path analysis was done to ascertain importance of component traits. Since protein yield is a function of GPC and yield, high direct effects of GPC and grain yield were quite obvious in each population. However, importance of grain weight

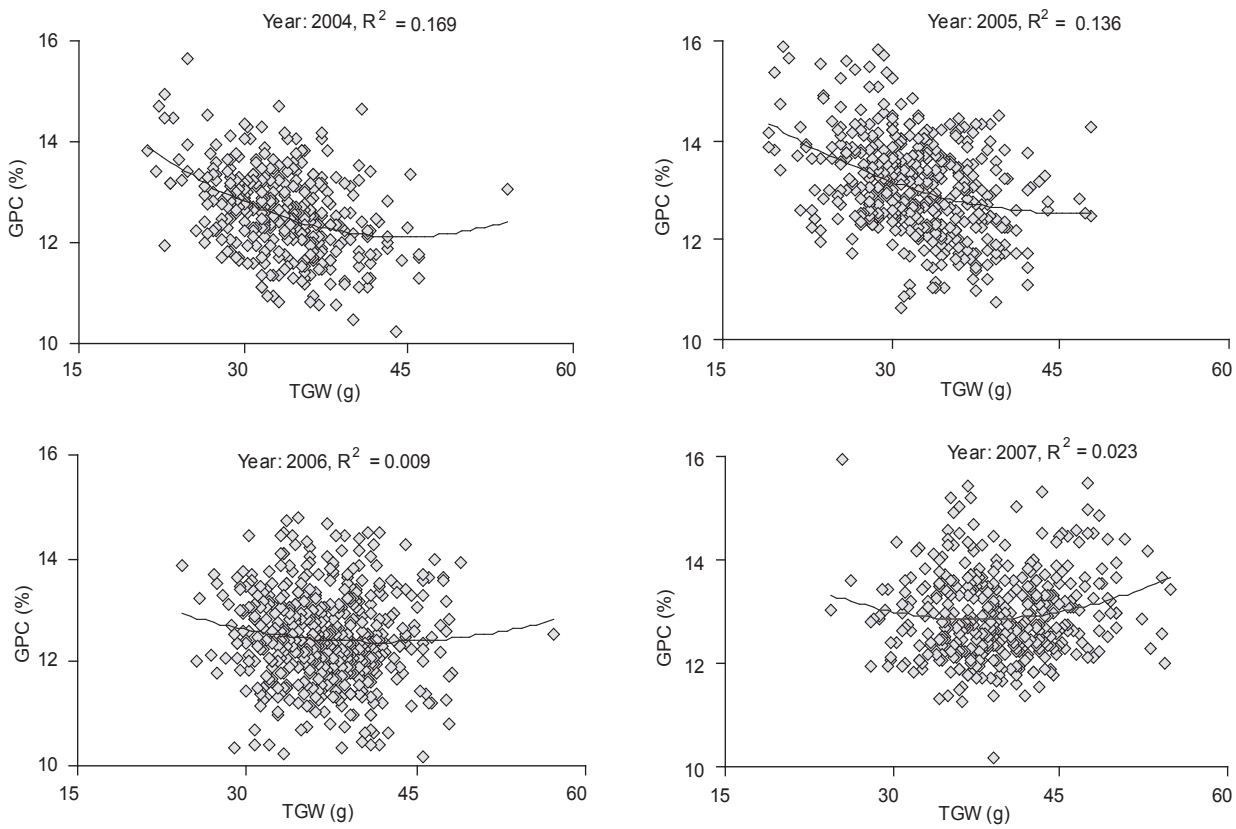

Fig. 1: Relationship between grain weight and protein content

and number of grains per unit area was also noticeable in Set I and Set II, the two populations with poor grain size. In Set III and Set IV, the grain number and grain size had negligible direct contribution. It implied that if populations are improvised for grain size, protein yield can be augmented with ease by selection based upon GPC and grain yield.

Table 2. Direct effects on protein yield in wheat

Components	2004	2005	2006	2007
Grain protein content	0.296	0.256	0.319	0.246
Grain weight	0.077	0.080	0.039	0.001
Grains/ m^2	0.117	0.142	0.072	0.011
Grain yield	0.893	0.883	0.971	1.010
Plant height	-0.000	0.001	-0.003	-0.006
Heading days	-0.005	0.014	-0.003	-0.009
Grain ripening duration	-0.000	0.017	-0.001	-0.005
Residual	0.004	0.006	0.005	0.004

Multiple regression analysis further confirmed the utility of the material improvised for TGW. Besides GPC and yield, grain number and grain weight were again significant constituents of protein yield when populations were low in TGW, whereas a population with improved TGW (Set IV) derived protein yield from GPC and grain yield only.

Table 3. Regression analysis for protein yield

Regression Statistics	2004	2005	2006	2007
R^2 value	0.996*	0.994*	0.995*	0.996*
Intercept	-60.320	-66.030	-62.940	-45.970
Regression coefficient				
Grain protein content (%)	4.241*	4.053*	4.839*	3.804*
Grain yield (g/m^2)	0.113*	0.114*	0.116*	0.127*
1000 Grain weight	0.192*	0.238*	0.112*	0.004
Grains/ m^2 ('000')	0.500*	0.583*	0.304*	0.061
Plant height (cm)	-0.001	0.001	-0.005	-0.007
Heading days	-0.009	0.025	-0.009	-0.020
Grain growth period (days)	0.001	0.037	-0.004	-0.013

*Significant at P 0.001

Diversity in Grain Weigh-improvised Populations

Importance of grain weight in augmenting protein content was further investigated by assorting the study material of each year into two groups and the average TGW of that season was used as the dividing line. The group with improved TGW in each population was labelled 'Elite' and the extent of variability was compared with that of the total population (Set). It was observed that even after sieving the population, the elite populations registered no loss in the extent of variability for both GPC as well as protein yield (Table 4). Therefore, equal opportunity persisted while selecting the right type of genotype for GPC and protein yield. The elite groups had an inbuilt advantage with respect to protein yield, over the years.

Step-down multiple regression analysis further suggested that selection for protein yield was easier in the grain weight improvised populations (elite groups) as it was based solely on two traits i.e. yield and GPC. Unlike the parental populations, characters like grain weight and number of grains per unit area (represented by number of spikes, spikelets and spike length) had marginal influence in the elite groups (Table 5).

Conclusions

High grain weight, an important yield component, is regarded as a bottleneck in enhancing grain protein content and this adverse relation can not just be attributed to shrivelled grains. A strong correlation in positive direction with grain yield and in negative direction with that of GPC makes TGW a very tricky characteristic in wheat breeding. However, it can be made to serve as stratagem to improvise the selection methodology required for selecting genotypes with high GPC or protein yield. It can be articulated by sieving the working populations against low TGW i.e. $\leq$ 30-35g (depending upon the crop season). A large and diverse population might pose problems in selection but such an assortment downsizes the base population with no bearing on variability for protein content and protein yield and no fear of inverse relationship between TGW and GPC. In this improvised population, selection gets easier and more effective, especially in case of protein yield. Route to protein yield is also different in such elite populations. Grain weight and grain number per unit area accumulating from tillering, spike length and number of spikelets becomes redundant and unlike original populations, protein yield just becomes direct function of yield and protein content. Such a selection technique therefore may pave way for harnessing enhanced grain protein content in the background of high yield.

Table 4. Extent of variability for protein content and protein yield in improvised populations

Group	2003-04		2004-05		2005-06		2006-07	
	Total	Elite	Total	Elite	Total	Elite	Total	Elite
Lines	373	189	450	230	523	257	428	211
TGW	21.2-54.0	33.6-54.0	19.2-47.6	32.1-47.6	24.3-57.1	37.0-57.1	24.4-54.8	39.1-54.8
Grain protein content (%)								
Range	10.2-15.6	10.2-14.6	10.6-15.9	10.8-14.5	10.2-14.8	10.2-14.7	10.1-16.1	11.4-16.1
CV (%)	6.58	6.35	7.26	6.75	7.04	7.24	6.41	6.25
Mean	**12.6***	12.3	**13.1***	12.8	12.4	12.4	12.9	13.0
Protein yield (g/m^2)								
Range	18.6-97.0	25.6-97.0	19.7-120.5	21.5-111.5	21.2-101.0	21.2-101.0	15.6-87.3	20.5-87.3
CV (%)	21.7	21.9	28.4	26.2	22.1	20.9	24.8	23.8
Mean	54.6	56.3	53.0	55.5	60.4	**63.1***	51.8	**54.5***

*Significant at P 0.05 (Bold)

Table 5. Step-down regression analysis for protein yield in elite groups

Regression Statistics	Elite group		
	2003-04	2004-05	2005-06
R^2 value	0.997*	0.996*	0.995*
Intercept	-56.130*	-56.480*	-62.210*
Coefficients			
Protein %	4.464*	4.345*	5.009*
Grain yield	0.126*	0.130*	0.124*
1000-grain weight	Nil	Nil	Nil
Grains/m^2	Nil	Nil	Nil
Plant height	Nil	Nil	Nil
Heading days	Nil	Nil	Nil
Maturity period	Nil	Nil	Nil

*Significant at P 0.001

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Validation of Biometrical Principles for Genetic Enhancement of Chickpea (*Cicer arietinum* L.)

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In the present investigation, the degree of heterosis for seed yield varied considerably. Parent such as ICC 7315, ICC 13124, ICC 15697 and ICC 6877 were good general combiners and could be of use in breeding for improved productivity in chickpea. The top three crosses *viz.*, ICC 11944 x ICC 13124 (16.95), ICC 9137 x ICC 13124 (16.63) and ICC 2507 x ICC 2072 (13.10) exhibited highly significant positive (specific combining ability) effect with high *per se* performance for seed yield/ plant. This indicated that the heterotic performance of these hybrids were mainly due to additive gene action. Further, these crosses are having parents with good x good general combiners. The high Holics effects in these crosses was mainly through additive x additive type of interaction causing heterosis. Hence, direct selection for higher values of seed yield can be made in the advanced generations of the heterotic crosses involving such parents, as a large portion of the total variation is a result of additive gene effects. Considering F_2 performance of these hybrids, three of the six highly heterotic F_1's in high diversity group and high mean (ICC 6877 x ICC 7315, ICC 6877 x ICC 2072 and ICC 6877 x ICC 10755) followed by high coefficient of variation and range. The mean F_2 values of these hybrids range from 25.6 to 37g, from 32.2 to 39.0% coefficient of variation and the higher value of range from 41.2 to 43 g/ plant. While in case of medium diversity group, three hybrids (ICC 15697 x ICC 7315, ICC 3776 x ICC 7315 and ICC 3776 x ICC 10755) showed relatively high mean values and higher coefficient of variation with reasonably high range of expression but these figures were lower than those of the hybrids in high diversity group. These facts indicate that parents with high diversity have a better chance of showing high heterosis and better performance.

Key Words: Chickpea, Combining ability, Heterosis, Heterotic crosses

Introduction

Chickpea (*Cicer arietinum* L.) is the world's third largest legume crop with a total annual production of 8.8 million tonnes. The cultivated area is over 10 million hectare. Major chickpea production worldwide is predominantly under rainfed conditions, grown on residual, progressively declining soil moisture. Chickpea is a self pollinated crop and it needs intensive studies to investigate and exploit the existing variability. Realizing the importance of diversity, the breeders are now looking for more diverse forms from various sources to augment the yield potential. Selection of parent is very crucial step in breeding programmes for generating potential breeding populations with high variability. This will ensure success of the breeding programme by employing proper and meticulous selection scheme in such population. Selection of parent can be done in different ways. It is suggested that parental diversity is important to generate productive breeding population. It is often suggested that the extent of diversity between the parents involved in hybridization programme assume greater importance in developing potential breeding populations. Though it was suggested that the extent of diversity should be high for realizing high heterosis and potential cross combination, Arunachalam *et al*., (1984) based on their experimentation in groundnut reported that the level of diversity between parents should be medium. To verify such concept minicore will provide an excellent opportunity to identify parents with varying levels of diversity. Similarly concept of combining ability, though highly used, in practical crop improvement programmes of cross pollinated species, its use in self pollinated crops is very minimal. It is also known that combining ability of the parent is important. But unfortunately information on either diversity or combining ability are hardly used for planning and developing breeding population in self pollinated crops. Although these quantitative genetic principles are routinely used in cross pollinated crops such as maize. It is important that such quantitative genetic principles should also be used in self pollinated

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crops, not only to make the exercise more scientific but also to increase the probability of success of breeding programmes. It is often reported that high diversity is pre requisite in generating highly heteriotic and potential population. But very often the reports are based on the studies conducted in limited number of accessions, consequently represent the traunkated information on diversity. Therefore, if at all any generalization is to be made to provide a guideline then it is essential that the hypothesis relating to desired level of diversity has to be made on the basis of the studies on the entire spectrum of variability of the species concerned. It is however a very difficult task to conduct the studies on thousands and lakhs of germplasm accessions. Hence, the present study aims at generating information on the usefulness of biometrical principles for genetic enhancement of chickpea.

Materials and Methods

The experimental material for this study was constituted by a set of lines and testers selected based on diversity analysis. Twelve genotypes selected as lines which are having high *per se* and to some extent higher seed weight belong to high, medium and low diversity groups from different inter and intra clusters and four genotypes selected as testers having high *per se* productivity. Each of these lines were crossed to four testers used as male in a line x tester mating design to produce 48 F_1 hybrids. The experimental material consisting of 48 F_1 hybrids and 17 (12 lines+ 4 testers + A1 check) parents was grown in a Randomized Block design with two replications at the Genetics and Plant Breeding garden, College of Agriculture, Dharwad during *rabi* 2007-08. Each entry was represented by a single two meter long row with a spacing of 60 cm between rows and 10 cm between plants within a row. Both parents and F_1s were randomized completely among themselves but grown in a continuous block. The experiments were laid out in medium black soils. The soils are rich in available nitrogen, potash and poor in available phosphorous. The soil pH is 7.6 and contains high amount of clay, silt and sand with a bulk density of 1.33 g/cc. The field experiments were carried out in a Randomized Complete Block Design with two replications.The following observations were recorded on each of the five plants selected at random per treatment or genotype in each replication and averaged separately in all the experiments. 1. Days to 50% flowering (DFF), 2. Plant height (PLHT) (cms), 3. Primary branches/ plant (PB), 4. Secondary branches/plant (SB), 5. Tertiary branches/plant (TB), 6. Pods/plant (PPP), 7. 100-seed weight (SDWT) (g), 8. Yield/plant (YPP) (g).

The magnitude of heterosis was estimated in relation to mid parental, better parental and standard check values. They were thus, calculated as percentage increase or decrease of F_1's over the mid-parent (MP), better parent (BP) and standard check (SC) using the methods of Turner (1953) and Hayes *et al.* (1955).The variation among the hybrids was further partitioned into genetic components attributed to general combining ability (gca) and specific combining ability (sca) following the method suggested by Kempthorne (1957).

Parents and crosses were scored for gca and sca effects, respectively. A parent showing positive or negative (significant or non significant) gca effect for a character was multiplied with their genotypic correlation value and put the value as positive or negative to that character. A total of the values obtained by a parent for all the characters under study was obtained by adding these values. Mean of the total values of the parents was worked out and used as a norm for classifying parents into high and low combiners. Similar procedure was followed to score and categorize the crosses with respect to their sca effects. The F_1s so generated were evaluated and the gca, sca and heterosis were all computed. The criteria of advancing the crosses showing yield performance of above mean $\pm$ 2 SD. Totally 16 crosses were evaluated during *rabi* 2007-08. The observation on 50 plants in each F_2's were studied. The performance of F_2 populations giving mean, range and coefficient of variation were computed.

Results and Discussion

With 203 accessions all possible (203×202/2 D^2 values) pair wise D^2 values were obtained. Taking the minimum D^2 value and maximum D^2 value, the mean D^2 value was computed. This provided the base for classifying the F_1s either as highly diverse or as low depending upon the D^2 value being more than or less than the mean, respectively. Further taking productivity of popular check cultivar A-1 and it's seed size as the criteria parents were chosen in such a way that pair wise they would represent high, medium and low diversity. They were then crossed following L x T design so that their combining ability status could also been estimated. In the present investigation, the degree of heterosis for seed yield varied considerably. Parent such as ICC 7315, ICC 13124, ICC 15697 and ICC 6877 were good

general combiners and could be of use in breeding for improved productivity in chickpea. The superiority of the hybrids in crosses was estimated over mid parent (MP), better parent (BP) and standard check (SC) for all the eight characters studied. The range of heterosis over mid parent, better parent and standard check and top three desirable hybrids in respect of each of the character studied are presented (Table 1-4).

The over all gca status of parents studied across the characters (Table 5).The parent having high gca effects for productivity and productivity related traits was determined. On the basis of this, parents ICC 15697, ICC 5878, ICC 11944, ICC 6877, ICC 3776, ICC 2507, ICC 13124 and ICC 7315 had high gca effects for yield/ plant, number of pods/ plant, seed weight and days to 50 per cent flowering. This suggests that, parent such as

Table 1. *Per se* performance and heterosis of top three potential hybrids in respect of eight quantitative characters in chickpea

Characters	Potential hybrids	Mean	MP (%)	BP (%)	SC (%)
DFF	ICC 6279 × ICC 13124	37.50	-3.23	-3.85	-8.54
	ICC 6877 × ICC 7315	39.50	-25.47	-24.76	-3.66
	ICC 6877 × ICC 10755	39.50	-22.55	-18.56	-3.66
PLHT (cm)	ICC 6877 × ICC 10755	67.30	20.77	2.44	63.15
	ICC 6877 × ICC 13124	67.10	38.55	31.83	62.67
	ICC 9137 × ICC 7315	66.15	20.38	5.08	60.36
PB	ICC 15697 × ICC 7315	9.15	150.68	131.65	200.00
	ICC 1180 × ICC 2072	8.95	167.16	184.13	193.44
	ICC 6877 × ICC 10755	8.80	121.38	120.00	188.52
SB	ICC 1180 × ICC 2072	18.95	67.70	59.24	69.20
	ICC 11944 × ICC 2072	18.90	83.05	76.64	68.75
	ICC 9137 × ICC 13124	18.80	51.00	17.50	67.86
TB	ICC 2969 × ICC 7315	37.10	123.83	112.61	136.31
	ICC 2969 × ICC 2072	30.35	106.81	122.34	93.31
	ICC 15697 × ICC 7315	28.55	78.72	63.61	81.85
PPP	ICC 5878 × ICC 7315	195.40	106.77	117.77	133.37
	ICC 11944 × ICC 13124	187.85	94.61	50.58	124.30
	ICC 11944 × ICC 7315	173.55	119.61	93.37	107.22
SDWT (g)	ICC 15697 × ICC 7315	38.40	29.84	12.78	144.59
	ICC 2507 × ICC 2072	37.00	124.58	127.69	135.67
	ICC 15697 × ICC 2072	36.90	78.48	127.08	135.07
YPP (g)	ICC 6877 × ICC 2072	64.40	136.76	100.62	152.05
	ICC 2507 × ICC 2072	61.00	83.05	90.03	138.75
	ICC 6877 × ICC 7315	60.55	90.86	47.14	136.99

ICC 7315, ICC 13124, ICC 15697 and ICC 6877 were good general combiners and could be of use in breeding for improved productivity in chickpea.

Productivity is the ultimate trait of interest to the breeder. In the present study, the top three crosses *viz.*, ICC 11944 x ICC 13124 (16.95), ICC 9137 x ICC 13124 (16.63) and ICC 2507 x ICC 2072 (13.10) exhibited highly significant positive sca effect with high *per se* performance for seed yield/ plant. This indicated that the heterotic performance of these hybrids were mainly due to additive gene action. Further these crosses are having parents with good × good general combiners. The high sca effects in these crosses was mainly through additive × additive type of interaction causing heterosis. Hence, direct selection for higher values of seed yield can be made in the advanced generations of the heterotic crosses involving such parents, as a large portion of the total variation is a result of additive gene effects. For this trait, similar results have been reported by Sarode *et al.,* (2000), Jeena and Arora (2000) and Mali *et al.* (2006). The over all sca status of hybrids studied across the characters (Table 6).

Table 7 gives the mean, seed yield, heterosis over mid parent and standard check, combining ability status of parents and hybrids, parental GCA status, SCA status of hybrids and the performance of respective F_2 populations giving mean, range and coefficient of variation. The number of hybrids with high as well as low heterosis occurring in the high, medium and low diversity groups have been listed. It may be seen from the table that there were as many as six highly heterotic crosses under high diversity class while their was none with low heterosis. In medium diversity group there were five hybrids showing high heterosis while two hybrids were with

Table 2. Percent heterosis in respect of seed yield of heterotic hybrids with different parental diversity in chickpea

S. No.	Hybrids	Per se performance			D^2 value	Percent heterosis over		
High diversity groups		Female	Male	F_1		MP	BP	SC
1	ICC 6877 × ICC 2072	57.05	39.88	54.65	695.04	136.76	100.62	152.05
2	ICC 6877 × ICC 7315	57.05	36.38	64.40	695.04	115.16	91.75	113.89
3	ICC 6877 × ICC 10755	57.05	38.17	60.55	695.04	90.86	47.14	136.99
4	ICC 5878 × ICC 7315	45.93	39.88	37.00	868.60	46.25	29.82	44.81
5	ICC 5878 × ICC 13124	45.93	40.60	50.30	868.60	57.68	20.62	96.87
6	ICC 5878 × ICC 10755	45.93	38.17	57.95	868.60	83.24	40.83	126.91
7	ICC 506 × ICC 7315	37.81	39.88	47.30	566.99	72.47	65.96	85.13
8	ICC 506 × ICC 13124	37.81	40.60	43.20	566.99	26.97	3.6	69.08
9	ICC 2507 × ICC 7315	50.28	39.88	47.25	968.70	49.88	65.79	84.93
10	ICC 2507 × ICC 2072	50.28	36.38	61.00	968.70	83.05	90.03	138.75
Medium diversity groups								
1	ICC 3776 × ICC 7315	45.10	39.88	57.10	488.90	99.83	100.35	123.48
2	ICC 3776 × ICC 10755	45.10	38.17	55.85	488.90	60.03	35.72	118.59
3	ICC 15697 × ICC 7315	40.39	39.88	52.90	292.28	110.55	85.61	107.05
4	ICC 15697 × ICC 2072	40.39	36.38	42.55	292.28	58.03	32.55	66.54
5	ICC11944 × ICC 13124	38.85	40.60	57.65	232.80	69.43	38.25	125.64
6	ICC 11944 × ICC 7315	38.85	39.88	39.95	232.80	45.67	40.18	56.36
Low diversity groups								
1	ICC 1431 × ICC 13124	31.94	40.60	35.15	10.62	12.84	-15.71	37.57
2	ICC 1431 × ICC 7315	31.94	39.88	36.30	10.62	47.88	27.37	42.07
3	ICC 1431 × ICC 2072	31.94	36.38	32.25	10.62	22.39	0.47	26.22
4	ICC 2969 × ICC 2072	28.03	36.38	29.80	3.16	3.38	-7.17	16.63

Table 3. Heterosis index of heterotic hybrids in chickpea

S. No.	Hybrids	Heterosis index									
		DFF	PLHT	PB	SB	TB	PPP	SDWT	YPP	Total score	Class
	High diversity groups										
1	ICC 6877 × ICC 2072	0.01	0.006	0.02	0.0004	-0.01	0.14	0.11	1.37	1.65	High
2	ICC 6877 × ICC 7315	0.01	-0.004	0.12	0.007	-0.002	0.15	0.01	1.15	1.44	High
3	ICC 6877 × ICC 10755	0.01	0.03	0.15	0.01	0.17	0.15	0.02	0.91	1.45	High
4	ICC 5878 × ICC 7315	0.006	-0.002	0.15	0.01	0.16	0.35	-0.06	0.46	1.07	High
5	ICC 5878 × ICC 13124	0.003	0.000	0.02	0.002	0.002	0.07	-0.08	0.58	0.60	High
6	ICC 5878 × ICC 10755	-0.005	-0.000	0.15	0.006	0.05	0.02	-0.02	0.83	1.04	High
7	ICC 506 × ICC 7315	-0.002	0.01	0.03	-0.001	0.06	0.17	0.02	0.72	1.07	High
8	ICC 506 × ICC 13124	-0.005	-0.00	0.15	0.006	0.05	0.02	-0.02	0.83	1.04	High
9	ICC 2507 × ICC 7315	0.01	-0.002	0.01	0.003	0.04	0.09	-0.008	0.50	0.64	High
10	ICC 2507 × ICC 2072	0.01	0.02	0.09	0.002	=0.02	0.06	0.31	0.83	1.30	High
	Medium diversity groups										
1	ICC 3776 × ICC 7315	-0.003	0.008	0.180	0.010	0.20	0.17	0.08	1.11	1.75	High
2	ICC 3776 × ICC 10755	-0.010	0.020	0.110	0.008	0.16	0.02	0.19	0.58	1.08	High
3	ICC 15697 × ICC 7315	0.008	0.006	0.020	0.010	0.09	0.13	-0.06	0.99	1.19	High
4	ICC 15697 × ICC 2072	0.010	-0.030	0.020	-0.009	0.14	0.08	-0.04	0.60	0.77	High
5	ICC 11944 × ICC 13124	0.006	0.010	0.004	-0.004	0.06	0.17	-0.09	0.69	0.84	High
6	ICC 11944 × ICC 7315	0.001	0.005	0.000	-0.004	0.00	0.22	-0.06	0.46	0.62	High
	Low diversity groups										
1	ICC 1431 × ICC 13124	0.005	0.020	0.100	-0.001	-0.01	0.10	-0.05	0.13	0.29	Low
2	ICC 1431 × ICC 7315	0.009	0.007	0.140	0.006	0.03	0.14	-0.08	0.48	0.73	High
3	ICC 1431 × ICC 2072	0.004	0.002	0.040	0.003	0.03	0.03	0.04	0.22	0.37	Low
4	ICC 2969 × ICC 2072	0.000	0.006	0.186	0.006	0.27	0.06	0.06	0.034	0.62	High

Table 4. Heterosis index for eight characters in chickpea

S. No.	Hybrids	Heterosis index score									
		DFF	PLHT	PB	SB	TB	PPP	SDWT	YPP	Total score	Class
1	ICC 2969 × ICC 13124	-0.01	0.01	0.02	-0.01	0.16	-0.08	0.08	-0.03	0.14	Low
2	ICC 2969 × ICC 7315	-0.00	0.05	0.05	0.04	0.31	-0.01	0.01	-0.06	0.39	High
3	ICC 2969 × ICC 2072	0.00	0.01	0.19	0.01	0.27	0.06	0.06	0.03	0.62	High
4	ICC 2969 × ICC 10755	-0.00	0.01	0.07	0.00	0.15	0.04	-0.03	-0.27	-0.05	Low
5	ICC 9137 × ICC 13124	-0.00	0.01	0.10	0.01	0.19	0.09	0.02	0.47	0.88	High
6	ICC 9137 × ICC 7315	0.01	0.02	0.05	0.01	0.13	0.02	0.01	-0.03	0.22	Low
7	ICC 9137 × ICC 2072	0.01	-0.01	0.03	0.02	0.12	-0.05	-0.04	-0.14	-0.06	Low
8	ICC 9137 × ICC 10755	0.01	-0.01	0.00	-0.00	0.08	-0.09	0.01	-0.22	-0.23	Low
9	ICC 6279 × ICC 13124	0.00	0.03	0.01	0.00	0.07	-0.07	-0.03	-0.25	-0.24	Low
10	ICC 6279 × ICC 7315	-0.00	0.03	0.03	0.02	0.12	0.03	-0.05	-0.06	0.12	Low
11	ICC 6279 × ICC 2072	0.00	0.00	0.07	0.02	0.26	0.07	0.12	-0.29	0.25	Low
12	ICC 6279 × ICC 10755	0.01	0.02	0.01	0.01	0.17	-0.02	0.02	-0.08	0.13	Low
13	ICC15697 × ICC 13124	0.01	0.01	0.11	0.00	0.01	0.06	-0.05	-0.08	0.07	Low
14	ICC15697 × ICC 7315	-0.00	0.01	0.18	0.01	0.20	0.17	0.08	1.11	1.75	High
15	ICC15697 × ICC 2072	-0.01	0.02	0.11	0.01	0.16	0.02	0.19	0.58	1.08	High
16	ICC15697 × ICC 10755	0.01	-0.01	0.13	0.01	0.09	-0.04	0.06	0.18	0.43	Low
17	ICC 506 × ICC 13124	-0.01	0.01	0.00	-0.01	0.04	0.03	-0.07	0.27	0.26	Low
18	ICC 506 × ICC 7315	-0.00	0.01	0.03	-0.00	0.06	0.17	0.02	0.72	1.01	High
19	ICC 506 × ICC 2072	0.00	-0.02	0.03	0.00	0.13	-0.02	0.01	0.24	0.38	Low
20	ICC 506 × ICC 10755	-0.00	0.00	0.03	0.01	0.08	-0.03	0.05	-0.27	-0.14	Low
21	ICC 5878 × ICC 13124	0.00	0.00	0.02	0.00	0.00	0.07	-0.08	0.58	0.60	High
22	ICC 5878 × ICC 7315	0.01	-0.00	0.15	0.01	0.16	0.35	-0.06	0.46	1.07	High
23	ICC 5878 × ICC 2072	0.01	0.00	0.09	0.01	0.16	0.13	0.01	0.42	0.82	High
24	ICC 5878 × ICC 10755	0.01	-0.00	0.15	0.01	0.05	0.02	-0.02	0.83	1.04	High
25	ICC11944 × ICC 13124	0.01	0.01	0.00	-0.00	0.06	0.17	-0.09	0.69	0.84	High
26	ICC11944 × ICC 7315	0.00	0.01	0.00	-0.00	0.00	0.22	-0.06	0.46	0.62	High
27	ICC11944 × ICC 2072	0.01	-0.00	0.17	0.02	0.16	0.08	0.01	-0.18	0.26	Low
28	ICC11944 × ICC 10755	0.03	-0.00	0.09	0.01	0.08	-0.02	0.08	0.00	0.24	Low
29	ICC 1180 × ICC 13124	0.01	-0.00	0.01	-0.01	0.01	0.00	0.07	-0.00	0.08	Low
30	ICC 1180 × ICC 7315	0.01	0.02	0.14	0.01	0.05	0.00	-0.09	-0.13	0.01	Low
31	ICC 1180 × ICC 2072	0.01	0.01	0.20	0.01	0.21	0.02	-0.01	-0.18	0.27	Low
32	ICC 1180 × ICC 10755	0.01	-0.02	0.16	0.01	0.18	-0.01	0.01	-0.12	0.21	Low
33	ICC 6877 × ICC 13124	0.01	0.05	0.04	-0.00	-0.01	0.04	0.04	0.52	0.69	High
34	ICC 6877 × ICC 7315	0.01	-0.00	0.12	0.01	-0.00	0.15	0.01	1.15	1.44	High
35	ICC 6877 × ICC 2072	0.01	0.01	0.02	0.00	-0.01	0.14	0.11	1.37	1.65	High
36	ICC 6877 × ICC 10755	0.01	0.03	0.15	0.01	0.17	0.15	0.02	0.91	1.45	High
37	ICC 3776 × ICC 13124	0.01	0.01	0.03	0.01	0.05	0.06	-0.05	-0.05	0.06	Low
38	ICC 3776 × ICC 7315	0.01	0.01	0.02	0.01	0.09	0.13	-0.06	0.99	1.19	High
39	ICC 3776 × ICC 2072	0.01	0.02	0.03	0.00	0.05	0.01	-0.02	0.13	0.23	Low
40	ICC 3776 × ICC 10755	0.01	-0.03	0.02	-0.01	0.14	0.08	-0.04	0.60	0.77	High
41	ICC 1431 × ICC 13124	0.01	0.02	0.10	-0.00	-0.01	0.10	-0.05	0.13	0.29	Low
42	ICC 1431 × ICC 7315	0.01	0.01	0.14	0.01	0.03	0.14	-0.08	0.48	0.73	High
43	ICC 1431 × ICC 2072	0.00	0.00	0.04	0.00	0.03	0.03	0.04	0.22	0.37	Low
44	ICC 1431 × ICC 10755	0.01	-0.03	0.03	0.00	0.04	0.02	-0.09	-0.22	-0.24	Low
45	ICC 2507 × ICC 13124	0.01	0.01	-0.03	-0.01	-0.04	-0.06	-0.04	0.16	-0.002	Low
46	ICC 2507 × ICC 7315	0.01	-0.00	0.01	0.00	0.04	0.09	-0.00	0.50	0.64	High
47	ICC 2507 × ICC 2072	0.01	0.02	0.09	0.00	-0.02	0.06	0.31	0.83	1.30	High
48	ICC 2507 × ICC 10755	0.01	-0.01	0.09	-0.00	-0.02	-0.05	-0.03	0.28	0.27	Low
										Mean	0.50

Table 5. Overall gca status of lines and testers evaluated in Line × Tester experiment in chickpea

S. No.	Lines/ Testers	Combining ability effects									
		DFF	PLHT	PB	SB	TB	PPP	SDWT	YPP	Total score	class
Lines											
1	ICC 2969	-0.28	-0.008	-0.03	-0.04	2.23	-4.55	0.08	-10.73	-13.32	Low
2	ICC 9137	-0.08	0.04	-0.11	-0.001	0.32	-6.70	1.16	-5.83	-11.20	Low
3	ICC 6279	0.10	-0.04	0.18	0.03	0.59	-2.68	-0.37	-10.72	-12.91	Low
4	ICC 15697	-0.006	0.04	0.19	0.01	0.24	-2.42	2.24	1.63	1.93	High
5	ICC 506	-0.23	-0.12	-0.15	0.04	-0.18	-1.41	-0.26	-0.95	-3.26	Low
6	ICC 5878	0.12	-0.52	0.11	0.03	0.04	7.98	-1.67	7.12	13.20	High
7	ICC 11944	0.10	-0.34	-0.009	-0.02	-0.57	4.40	-0.49	0.09	3.16	High
8	ICC 1180	-0.07	0.07	0.19	0.03	0.18	-1.96	-0.56	-9.99	-12.07	Low
9	ICC 6877	0.24	0.11	0.07	-0.009	-0.42	8.06	-2.13	18.29	24.21	High
10	ICC 3776	0.01	0.18	-0.19	0.01	-0.53	0.27	-1.34	6.34	4.75	High
11	ICC 1431	-0.11	-0.04	0.12	0.01	-0.72	2.74	-1.50	-6.82	-6.32	Low
12	ICC 2507	0.15	0.66	-0.008	0.002	-1.17	-1.99	-0.35	11.52	1351	High
									Mean	**0.14**	
Testers											
1	ICC 13124	0.11	-0.15	-0.11	-0.03	-0.47	-0.49	0.03	1.85	0.74	High
2	ICC 7315	-0.11	0.33	0.05	0.002	0.23	3.47	-0.09	1.12	5.00	High
3	ICC 2072	-0.08	0.01	-0.005	0.006	-0.13	0.48	-0.64	-2.38	-2.74	Low
4	ICC 10755	0.07	-0.20	0.06	0.02	0.37	-3.46	0.700	-0.57	-3.01	Low
									Mean	**-0.003**	

Table 6. Overall sca status of hybrids evaluated in Line × tester experiment in chickpea

S. No.	Hybrids	Combining ability effects									
		DFF	PLHT	PB	SB	TB	PPP	SDWT	YPP	Total score	Class
1	ICC 2969 × ICC 13124	-0.06	-0.19	-0.11	-0.06	-0.21	-5.81	1.93	2.68	-1.83	Low
2	ICC 2969 × ICC 7315	0.04	-0.22	-0.13	0.02	0.11	-5.83	0.27	-3.84	-9.58	Low
3	ICC 2969 × ICC 2072	0.08	-0.14	0.27	0.03	0.04	5.80	-0.80	4.15	9.43	High
4	ICC 2969 × ICC 10755	-0.05	0.54	-0.04	0.02	-1.20	5.85	-1.39	-2.19	0.74	High
5	ICC 9137 × ICC 13124	-0.11	0.23	0.34	0.12	1.74	10.53	1.24	16.63	30.72	High
6	ICC 9137 × ICC 7315	0.02	1.13	-0.00	0.01	-0.18	-3.31	0.66	-6.69	-8.36	Low
7	ICC 9137 × ICC 2072	0.06	-0.76	-0.11	-0.01	-0.69	-3.88	-2.17	-4.70	-12.26	Low
8	ICC 9137 × ICC 10755	0.02	-0.13	-0.22	-0.13	-0.87	-3.33	0.27	-5.24	-9.63	Low
9	ICC 6279 × ICC 13124	0.22	-0.14	0.07	-0.01	-0.41	-6.17	-0.28	-2.33	-9.05	Low
10	ICC 6279 × ICC 7315	-0.22	0.33	-0.03	0.03	-0.60	-1.87	-0.81	-0.86	-4.03	Low
11	ICC 6279 × ICC 2072	-0.10	-0.78	0.09	0.03	0.91	6.45	0.74	-2.81	4.53	High
12	ICC 6279 × ICC 10755	0.11	0.59	-0.13	-0.05	0.10	1.59	0.23	6.00	8.44	High
13	ICC15697 × ICC 13124	0.26	-0.28	0.05	0.02	-0.86	-5.86	-2.59	-13.18	-22.42	Low
14	ICC15697 × ICC 7315	-0.51	0.02	0.15	-0.01	1.21	7.69	1.13	11.39	21.07	High
15	ICC15697 × ICC 2072	0.13	0.69	-0.16	-0.04	0.18	-0.19	1.30	4.54	6.45	High
16	ICC15697 × ICC 10755	0.12	-0.43	-0.04	0.03	0.53	1.63	0.16	-2.75	-4.01	Low
17	ICC 506 × ICC 13124	0.11	-0.10	0.04	-0.05	-0.08	1.42	-1.41	3.54	3.47	High
18	ICC 506 × ICC 7315	0.02	0.48	-0.02	-0.05	0.33	6.10	1.03	8.37	16.26	High
19	ICC 506 × ICC 2072	0.17	-0.91	-0.02	0.03	-0.41	-5.46	-0.97	0.77	-7.57	Low
20	ICC 506 × ICC 10755	0.07	0.53	-0.00	0.06	0.16	-2.06	1.35	-12.68	-12.57	Low
21	ICC 5878 × ICC 13124	0.05	-0.35	-0.17	0.01	-0.62	-0.60	-0.41	2.53	0.44	High
22	ICC 5878 × ICC 7315	0.06	-0.24	0.13	0.03	-1.20	2.45	-0.01	-10.04	-8.82	Low
23	ICC 5878 × ICC 2072	-0.02	0.03	-0.11	0.03	0.15	2.24	-0.01	-5.09	-2.78	Low
24	ICC 5878 × ICC 10755	-0.09	0.57	0.16	-0.01	0.72	-4.09	0.42	12.61	10.29	High
25	ICC11944 × ICC 13124	-0.02	0.22	-0.11	-0.03	-0.57	-8.62	-1.61	16.95	6.21	High
26	ICC11944 × ICC 7315	0.14	-0.20	-0.27	-0.11	1.24	2.09	0.11	-0.02	2.98	High

Contd……

S. No.	Hybrids	Combining ability effects									
		DFF	PLHT	PB	SB	TB	PPP	SDWT	YPP	Total score	Class
27	ICC11944 × ICC 2072	0.03	-0.06	0.30	0.11	-0.75	-2.77	-0.80	-12.32	-16.26	Low
28	ICC11944 × ICC 10755	-0.16	0.31	0.08	0.03	-0.08	-7.95	2.30	-4.41	-9.88	Low
29	ICC 1180 × ICC 13124	0.08	-0.16	-0.31	-0.07	-0.78	1.82	2.54	3.39	6.51	High
30	ICC 1180 × ICC 7315	-0.03	0.06	0.02	-0.01	-1.13	-5.07	-1.54	-4.78	-12.48	Low
31	ICC 1180 × ICC 2072	-0.11	0.22	0.17	0.06	0.90	1.04	-1.20	-1.23	0.15	High
32	ICC 1180 × ICC 10755	0.06	-0.12	0.12	0.03	1.01	2.20	0.19	2.62	6.11	High
33	ICC 6877 × ICC 13124	-0.22	0.44	-0.05	0.00	-0.08	-5.39	0.67	-10.30	-14.93	Low
34	ICC 6877 × ICC 7315	0.18	-0.36	0.14	0.01	-0.91	-3.65	-0.30	-3.52	-8.11	Low
35	ICC 6877 × ICC 2072	0.04	-0.08	-0.30	-0.07	-1.13	1.86	0.11	9.73	10.16	High
36	ICC 6877 × ICC 10755	0.00	-0.01	0.21	0.06	2.12	7.18	-0.48	4.09	13.10	High
37	ICC 3776 × ICC 13124	0.00	-0.01	0.15	0.05	0.25	1.93	0.44	-13.60	-10.77	Low
38	ICC 3776 × ICC 7315	0.02	-0.03	-0.05	0.03	-0.04	-1.37	0.04	10.88	9.46	High
39	ICC 3776 × ICC 2072	-0.07	0.13	-0.04	-0.10	-0.91	-5.68	-0.33	-8.62	-15.62	Low
40	ICC 3776 × ICC 10755	0.04	-0.09	-0.06	0.02	0.70	5.12	-0.15	11.34	16.92	High
41	ICC 1431 × ICC 13124	0.03	-0.07	0.24	0.02	0.14	5.06	0.61	1.37	7.40	High
42	ICC 1431 × ICC 7315	0.14	-0.27	0.23	0.03	0.01	0.14	-0.14	3.25	3.39	High
43	ICC 1431 × ICC 2072	-0.22	0.43	-0.21	-0.02	-0.22	-4.43	0.89	2.69	-1.09	Low
44	ICC 1431 × ICC 10755	0.05	-0.09	-0.26	-0.02	0.07	-0.76	-1.36	-7.30	-9.65	Low
45	ICC 2507 × ICC 13124	-0.13	0.26	-0.17	-0.00	0.18	-5.56	-1.15	-7.65	-14.22	Low
46	ICC 2507 × ICC 7315	0.15	-0.30	-0.15	0.03	0.65	2.64	-0.45	-4.14	-1.57	Low
47	ICC 2507 × ICC 2072	0.00	-0.02	0.13	0.01	-0.40	5.03	3.22	13.10	21.07	High
48	ICC 2507 × ICC 10755	-0.03	0.06	0.19	-0.04	-0.44	-2.12	-1.62	-1.29	-5.29	Low
	Total										-17.86
	Mean										-0.37

Table 7. Mean, heterosis, combining ability of F_1 hybrids, their F_2 performance of combinations with representing different diversity levels in chickpea

Diversity class and heterotic status	F_1 performance			Parental combining ability status	SCA status	F_2 performance		
	Mean yield (g)	Heterosis (%)				Mean (g)	Range	CV (%)
		MP	SC					
I High diversity and high heterosis								
1. ICC 5878 × ICC 10755	57.9	83.2	126.8	H X L	H	13.2	11-17	21.5
2. ICC 6877 × ICC 13124	48.6	51.9	90.2	H X H	L	11.8	11-14	17.9
3. ICC 6877 × ICC 7315	54.6	115.2	113.9	H X H	L	27.4	12-43	39.3
4. ICC 6877 × ICC 2072	64.4	136.8	152.0	HXL	L	30.7	25-41	34.5
5. ICC 6877 × ICC 10755	60.6	90.9	136.9	HXL	H	25.6	19-42	33.2
6. ICC 2507 × ICC 2072	61.0	48.4	89.4	HXL	H	9.6	7-14	21.7
II High diversity and low heterosis	No cross showed heterosis in this class							
III Medium diversity and high heterosis								
1. ICC 11944 × ICC 13124	57.6	89.4	125.6	HXH	H	7.0	6-8	16.0
2. ICC 15697 × ICC 7315	52.9	110.6	107.0	HXH	H	27.4	18-32	27.8
3. ICC 15697 × ICC 2072	42.6	58.0	66.5	HXL	H	9.7	6-16	23.4
4. ICC 3776 × ICC 7315	57.1	99.8	123.5	HXH	H	16.4	12-21	25.7
5. ICC 3776 × ICC 10755	55.8	60.0	118.6	HXL	L	19.8	10-32	32.1
IV Medium diversity and low heterosis								
1. ICC 11944 × ICC 10755	33.8	0.30	32.5	HXL	L	9.5	7-13	19.9
2. ICC 1180 × ICC 13124	34.0	-3.75	33.1	HXL	L	8.4	6-10	18.3
V Low diversity and high heterosis	No crosses showed heterosis in this class							
VI Low diversity and low heterosis								
1. ICC 9133 × ICC 10755	27.1	-21.7	6.07	LXL	L	7.8	5-14	19.7

H-high L-low SCA- specific combining ability CV- coefficient of variation

low heterosis. In low diversity group no hybrid showed high heterosis while there was only one hybrid with low heterosis. This indicates that the probability of getting heterotic hybrids is high with high diversity. The mean performance of heterotic hybrid as well as the extent of mid parent heterosis and standard heterosis are slightly better with the hybrids in high diversity group. Further looking to the combining ability status of these heterotic crosses they were mostly of H x H type followed closely by H x L type. Considering F_2 performance of these hybrids, three of the six highly heterotic F_1's in high diversity group and high mean (ICC 6877 x ICC 7315, ICC 6877 x ICC 2072 and ICC 6877 x ICC 10755) followed by high coefficient of variation and range. The mean F_2 values of these hybrids range from 25.6 to 37 g, from 32.2 to 39.0% coefficient of variation and the higher value of range from 41.2 to 43 g/ plant. While in case of medium diversity group, three hybrids (ICC 15697 x ICC 7315, ICC 3776 x CC 7315 and ICC 3776 x ICC 10755) showed relatively high mean values and higher coefficient of variation with reasonably high range of expression but these figures were lower than those of the hybrids in high diversity group. These facts indicate that parents with high diversity have a better chance of showing high heterosis and better F_2 performance.

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Genetic Diversity in Farmers' Varieties and Some Advanced Lines of Aromatic Rice (*Oryza sativa* L.) from West Bengal

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The nature and magnitude of genetic diversity were estimated in 37 aromatic rice genotypes during the *kharif* (Aman) season under humid sub-tropic Terai Zone of West Bengal using Mahalanobis D^2 statistics. The genotypes were grouped into 10 clusters. The pattern of distribution of genotypes into different cluster is random and independent of geographical origin or region of adoption. The relative divergence of each cluster from other clusters displayed higher order of divergence between cluster VIII and X followed by clusters VII and VIII, clusters IX and X, and clusters III and IX. Maximum intra-cluster distance was observed among the genotypes, viz., Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1, Nunia in cluster X, indicating existence of wide genetic divergence among the constituent genotypes in it. Considerable variation in cluster mean values was observed for all the characters except seed thickness. Genotypes of clusters IX (KNS-6/2 and Chini Atap) and III [KNS-3-9(N) and KNS-2-1] exhibiting high seed yield may be directly used for adoption or in hybridization programme for yield improvement. Seed length, seed thickness, seed breadth, panicle length and seed yield were major contributing characters towards the total genetic divergence which may be used in selecting genetically diverse parents, particularly to exploit maximum heterosis or to execute efficient selection in highly segregating generations.

Key Words: Aromatic rice, Farmers' varieties, Genetic diversity

Introduction

Rice is the most important staple food grain and stands next to wheat in the global food grain production. India has the largest acreage under rice, about 44.6 m ha of land with a production of about 90.15 mt (Anonymous, 2009). The biodiversity of scented and non-scented rice in India is the largest in the world. The Indian subcontinent has the *natural gift* of basmati rice that has been accepted as the best scented, long and slender grain in the international markets and gets high price. In addition to the basmati rice, a large number of local landraces of scented rice perform equally in terms of aroma, cooking quality and yield as well. Most of these genotypes have short-bold to medium-bold grain. Their demand in the domestic market is greater than that of basmati. These are mainly used for special culinary preparation (such as *khir* in Bengal). Unfortunately, these have somehow not got the attention of the rice scientists, which has led to decline and/or extinction of this valuable wealth. Many patches of West Bengal and Assam are endowed with non-basmati rice cultivars which are cultivated casually, as way of life, with almost no bent towards their commercial exploitation. And this is not uncommon in the northern districts of West Bengal, wherein a score of outstanding landraces of such category, viz., Tulaipanji, Kataribhog, Kalobhog, Tulsibhog, Badshabhog, Khasha etc. are grown. These local cultivars posses the ability to tolerate biotic and abiotic stresses.

Germplasm constitute the foundation of any genetic improvement programme of crop. The pace and magnitude of genetic improvement generally depend on the amount of genetic variability present in a population. Further more, the spectrum of variability in segregating generations largely depend on the genetic diversity of the parents involved in the hybridization. Majority of the economically important characters including yield and its components are amenable to genetic improvisation through *inter-se* breeding among genetically diverse parents. It is, therefore, logical to assess the genetic divergence in the available germplasm, as the importance of genetic diversity for successful selection of parents to be used in hybridization has been emphasized earlier (Bansal *et al*., 1999; Soni *et al*., 1999). To unzip the genetic divergence and identify the character contributing towards the genetic divergence, a study was undertaken in 37 aromatic rice genotypes under Terai Zone of West Bengal.

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Materials and Methods

The experimental meterial comprised 37 aromatic rice genotypes consisting of 19 aromatic farmers' varieties, one basmati rice, six pure lines isolated from Kalobhog and 11 advanced aromatic lines derived from hybridization involving Kalobhog (Table 1). The experiment was conducted at University Farm, Pundibari, Cooch Behar. Single seedling (30 days old) was transplanted per hill in a plot measuring 3 x 1.5 m in randomized block design with two replications. The experiment was conducted for two years during rainy (*kharif*) season of 2010 and 2011. The inter- and intra-row spacing was 30 and 25 cm, respectively. Standard agronomic practices compatible to the humid sub-tropic of Terai Zone were adopted to ensure good crop growth. Observations were recorded for days to 50% flowering, plant height (cm), number of panicles/plant, panicle length (cm), number of fertile seeds/panicle, 100-seed weight (g), 100-kernel weight (g), seed length (mm), seed width (mm), seed thickness (mm) and seed yield (t/ha). The mean performance over two years was pooled and used for statistical analysis.

Data were subjected to multivariate analysis following Mahalanobis' D^2 statistics (Mahalanobis, 1928 and 1936) to measure the genetic divergence followed by the clustering of genotypes based on above mentioned 11 characters. D^2 statistics were performed using GenRes Statistical Software, (c) 1994 Pascal Intl Software Solutions, Version 3.01.

Results and Discussion

Analysis of variance showed highly significant mean sum of square for all the characters used in this study (Table 2). Based on the relative magnitude of D^2 values, 37 genotypes were grouped into 10 clusters (Table 3). Twelve genotypes were accommodated in cluster I, while clusters II, III, IV, V, VI and IX had two genotypes in each, clusters VIII contained three genotypes, finally the clusters VII and X retained five genotypes in each. Most of the aromatic farmers' varieties were accommodated in clusters I, VI, VII and VIII. Clusters II, III, IV and V retained only advanced lines derived from Kalobhog, whereas, the clusters VI, VII, VIII, IX and X contained both the advanced lines and farmers' varieties. The pattern of distribution of genotypes from diverse geographical region into different clusters was random, such as, Kalturey, Kagui, Jhapaka, Fudugey and Munimahnanri were collected from Kalingpong of Darjeeling district, distributed in cluster I and VII. It

Table 1. Place of collection or parentage of 37 genotypes of aromatic rice

Genotype	Place of collection or parentage	Genotype	Place of collection or parentage
Mohanbhog	Nadia, W.B.	KNS-5	Kalobhog/Pusa basmati-1
Kalojeera	Cooch Behar, W.B.	KNS-3-9(N)	Pure line of Kalobhog
Kalojeera-1	Nadia, W.B.	KNS-3	Kalobhog/Pusa basmati-1
Radhunipagal	Cooch Behar, W.B.	KNS-6	Kalobhog/Pusa basmati-1
Kalobhog	Cooch Behar, W.B.	KNS-2-1	Pure line of Kalobhog
Khasha	Maldah, W.B.	KNS-1(N)	Pure line of Kalobhog
Badshabhog	Maldah, W.B.	KNS-3-1	Kalobhog/Pusa basmati-1
Kalturey	Kalingpong, W.B.	KNS-4	Kalobhog/Pusa basmati-1
Kagui	Kalingpong, W.B.	KNS-2	Kalobhog/Pusa basmati-1
Jhapaka	Kalingpong, W.B.	KNS-2(N)	Pure line of Kalobhog
Chinikamani	Nadia, W.B.	KNS-1-2B	Kalobhog/Pusa basmati-1
Fudugey	Kalingpong, W.B.	KNS-5-1	Kalobhog/Pusa basmati-1
Munimahnanri	Kalingpong, W.B.	KNS-1-1	Kalobhog/Pusa basmati-1
Chakhao Poireiton	Imphal, Manipur	KNS-1-3(N)	Pure line of Kalobhog
Tulaipanji	Maldah, W.B.	KNS-1-2	Kalobhog/Pusa basmati-1
Gobindobhog	Nadia, W.B.	KNS-6/2	Kalobhog /IET4786
Radhunipagal-1	Nadia, W.B.	Chini Atap	Siliguri, W.B.
Pusa Basmati-1	IARI, New Delhi	Nunia	Kalingpong, W.B.
KNS-1	Pure line of Kalobhog		

Table 2. Pooled analysis of variance for grain yield and yield component character in 37 genotypes of aromatic rice

Source	d.f.	Mean sum of square					
		Days to 50% flowering	Plant height	No. of panicles/plant	Panicle length	No. of fertile seed/panicle	
Total	73	147.669	406.121	38.164	5.004	1778.194	
Replication	1	0.216	0.379	0.039	0.026	5.085	
Treatment	36	299.051**	817.280**	70.289**	8.457**	3385.351**	
Error	36	0.382	6.232	7.099	1.598	220.291	
		100-seed weight	100-kernel weight	Seed length	Seed breadth	Seed thickness	Seed yield
Total	73	0.116	0.082	1.319	0.006	0.026	0.813
Replication	1	0.001	0.002	0.006	0.008	0.003	0.466
Treatment	36	0.234**	0.165**	2.673**	0.105**	0.050**	1.529**
Error	36	0.003	0.001	0.003	0.067	0.003	0.107

Table 3. Cluster pattern, size and constituents of clusters involving 37 aromatic genotypes of rice through D^2 statistics

Cluster	No. of genotypes	Genotypes
I	12	Mohanbhog, Kalojeera, Kalojeera-1, Radhunipagal, Kalobhog, Khasha, Badshabhog, Kalturey, Kagui, Jhapaka, Chinikamani, KNS-1(N)
II	2	KNS-1, KNS5-1
III	2	KNS-3-9(N), KNS-2-1
IV	2	KNS-5, KNS-6
V	2	KNS-4, KNS-1-1
VI	2	Chakhao Poireiton, KNS-1-2B
VII	5	Fudugey, Munimahnanri, Tulaipanji, KNS-3-9(N), KNS-1-2B
VIII	3	Gobindobhog, Radhunipagal-1, KNS-2(N)
IX	2	KNS-6/2, Chini Atap
X	5	Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1, Nunia

showed that genotypes collected from same geographic region got distributed in several clusters. It might be due to selection differential or genetic drift under diverse environmental conditions within the same geographical region (Roy *et al*., 2002). Similarly, genotypes collected from different places coexisted in the same cluster, such as, cluster I. Mohanbhog, Kalojeera-1, Radhunipagal and Chiakamani were collected from southern parts of West Bengal; Kalobhog and Kalojeera were collected from Cooch Behar; Khasha and Badshabhog were collected from Madah and Kalturey and, Kagui and Jhapaka were collected from Darjeeling. Thus, the distribution of genotypes into different clusters was not associated with their geographical origin. Roy and Panwar (1993), Mehera *et al*. (1998) and Roy *et al*. (2002) reported the non-correspondence of genetic divergence with geographic diversity in rice. This tendency of genotypes occurring in the same cluster cutting across the geographical boundaries demonstrated that geographical isolation is not the only factor causing genetic diversity in rice (Bansal *et al*., 1999). Sinha *et al*. (1991) reported that geographical diversity might not always be a useful index in assessing genotypic diversity in rice.

The relative divergence (Table 4) of each cluster from other clusters displayed higher order of divergence between cluster VIII and X (D = 84.548) followed by clusters VII and VIII (D = 80.403), clusters IX and X (D = 77.329), and clusters III and IX (D = 70.210). Highly divergent genotypes deem to produce wide variability that may help further selection for genetic improvement (Rahaman *et al*., 1997). Hybrid developed from the genotypes within the limit of compatibility of those clusters may manifest high heterosis or desirable transgressive segregants, which would be beneficial for

Table 4. Average intra- and inter-cluster D^2 and D values among 37 aromatic genotypes of rice

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**1992.598 (44.639)**	1768.943 (42.059)	2379.483 (48.780)	1667.057 (40.830)	1743.835 (41.759)	1489.898 (38.599)	3636.560 (60.304)	2741.397 (52.358)	2354.313 (48.521)	4656.813 (68.421)
II		**75.337 (8.680)**	253.903 (15.934)	522.461 (22.587)	189.184 (13.754)	542.287 (23.287)	2256.036 (47.498)	2842.288 (53.313)	3767.885 (61.383)	2808.486 (52.995)
III			**108.291 (10.406)**	560.588 (23.677)	276.144 (16.618)	1002.625 (31.664)	2207.437 (46.983)	3651.724 (60.429)	4929.434 (70.210)	2553.670 (50.534)
IV				111.645 (10.566)	284.129 (16.856)	436.655 (20.896)	3037.185 (55.111)	1989.237 (44.601)	3566.569 (59.721)	3779.634 (58.988)
V					**121.552 (11.026)**	524.309 (22.898)	2372.981 (48.713)	2565.899 (50.655)	3561.843 (59.681)	2688.152 (51.847)
VI						**165.408 (12.861)**	3330.538 (57.711)	1656.536 (40.701)	3191.938 (56.497)	4194.745 (64.767)
VII							**3080.236 (55.500)**	6464.682 (80.403)	5040.680 (70.998)	3238.605 (56.909)
VIII								**2533.656 (50.335)**	3342.030 (57.810)	7148.374 (84.548)
IX									**1117.012 (33.422)**	5979.820 (77.329)
X										4028.527 (63.471)

genetic improvement. Dey *et al.* (2011) also suggested the use of divergent genotypes for development of lines with high yielding potential and better adaptability. Hybridization between genetically divergent parents to generate high heterotic segregants reported promising (Roy and Panwar, 1993; Vivekanandan and Subramanian, 1993; Sharma *et al*., 1997).

Maximum intra-cluster distance was observed among the genotypes, viz., Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1, Nunia in cluster X, indicating existence of wide genetic divergence among the constituent genotypes in it. High degree of divergence among the genotypes within a cluster would produce more segregating breeding materials and selection within such cluster might be executed based on maximum mean value for the desirable characters. Intra-cluster distance among the genotypes, viz., KNS-1 and KNS5-1, in cluster II was minimum. This indicates that unidirectional selection, which might have been practiced, could lead to uniformity with less divergence between the genotypes.

Considerable variation in cluster mean values was observed for all the characters (Table 5), except, seed thickness (mm) which did not show much variation among different clusters. In respects of days to 50% flowering, the genotypes (Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1 and Nunia) in the cluster X were early maturing, had comparatively shorter plant height and moderate number of fertile seeds per panicle. The genotypes (Fudugey, Munimahnanri, Tulaipanji, KNS-3-9(N) and KNS-1-2B) of cluster VII showed maximum number of panicles per plants along with high 100-seed weight, high seed length and high yield. Highest number of fertile seeds per panicle was observed for the genotypes (KNS-6/2 and Chini Atap) in the IX along with highest yield. Maximum number of panicles per plant was observed among the genotypes [Mohanbhog, Kalojeera, Kalojeera-1, Radhunipagal, Kalobhog, Khasha, Badshabhog, Kalturey, Kagui, Jhapaka, Chinakamani and KNS-1(N)] of cluster I along with tallest plants, moderate number of fertile seeds per panicle and moderate yield. Since the genotypes of clusters IX (KNS-6/2 and Chini Atap) and III (KNS-3-9(N) and KNS-2-1) possessed high seed yield, they may be directly used for adoption or used in hybridization programme for yield improvement. The genotypes with high mean value in any cluster for particular character may be directly used for adoption or in hybridization programme for improvement of that particular character.

The contribution of characters towards the total genetic divergence is important in deciding the characters for selection. Seed length, seed thickness, seed breadth, panicle length and seed yield were major contributing characters towards the total genetic divergence among the genotypes (Table 6). Whereas, number of panicles

Table 5. Cluster mean for 11 characters in 37 aromatic genotypes of rice

Clusters	Days to 50% flowering	Plant height (cm)	No. of panicles/ plant	Panicle length (cm)	No. of seeds/ panicle	100 seed weight (g)	100-kernel weight (g)	Seed length (mm)	Seed breadth (mm)	Seed thickness (mm)	Seed yield (t/ha)
I	177.07	126.66	28.23	26.63	150.72	1.291	0.839	6.220	2.066	1.753	2.128
II	173.80	136.25	26.45	27.90	143.60	1.489	1.351	7.009	2.148	1.781	1.800
III	175.00	139.50	26.30	27.85	148.50	1.507	1.122	7.319	1.993	1.697	2.662
IV	170.85	140.00	27.30	26.35	124.30	1.247	0.676	6.392	2.045	1.679	2.025
V	160.85	137.25	20.35	25.70	95.050	1.377	1.045	6.813	2.008	1.791	1.119
VI	172.40	135.50	23.47	24.90	82.85	1.716	1.003	5.964	2.288	1.731	1.325
VII	174.62	123.60	29.74	26.92	116.04	1.800	1.115	7.826	2.272	1.827	1.906
VIII	159.50	136.33	27.50	26.56	137.05	1.110	0.717	5.073	1.950	1.603	2.200
IX	149.02	113.00	24.92	26.15	172.55	0.934	0.776	5.884	1.969	1.771	2.775
X	145.92	127.60	24.13	26.02	157.14	1.554	1.135	8.091	2.126	1.791	1.845
CV (%)	1.49	0.48	9.98	4.77	10.73	3.790	3.850	0.780	3.850	3.150	16.350

Table 6. Contribution of different characters to total genetic divergence

Characters	No. of first rank	Contribution (%)
Days to 50% maturity	4	0.601
Plant height (cm)	79	11.862
Number of panicles/plant	1	0.150
Panicle length (cm)	1	0.150
Number of fertile seeds/panicle	9	1.351
100- seed weight (g)	20	3.003
100-kernel weight (g)	27	4.054
Seed length (mm)	167	25.075
Seed breadth (mm)	114	17.117
Seed thickness (mm)	138	20.720
Seed yield (t/ha)	106	15.916

per plant and panicle length were the characters, whose contributions were least in creating the total genetic divergence. These findings revealed that the seed shape was the major contributing factor towards total genetic divergence. The characters having high contribution towards the total genetic divergence may be used in selecting genetically diverse parents, particularly to exploit maximum heterosis or to execute efficient selection in highly segregating generations.

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Resistance to Spot Blotch in Barley Germplasm

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Multilocation evaluation of barley germplasm accessions for resistance to spot blotch was taken up under artificial epiphytotic conditions in four crop seasons at four locations (Varanasi, Faizabad, Kanpur and Karnal). The lines identified as resistant/ moderately resistant from the field screening were again screened in poly house for three more years. Disease data was recorded following the double digit system, indicating the percent area covered on the flag leaf and on the next below to flag leaf on 1 to 9 scale. Out of 5458 accessions screened in the field during four crop seasons, only 28 accessions could be termed as resistant. Another group of 58 accessions was observed as moderately resistant and rest of accessions were in susceptible to highly susceptible group. In order to further confirm their reaction the 86 accessions (resistant and moderately resistant) were screened under controlled conditions of temperature and humidity in poly house with artificial screening at Karnal. Out of the 86 accession 68 were observed as resistant and eight as moderately resistant, while rest 10 were either moderately susceptible or susceptible. The genotypes grouped as resistant were able to keep the disease level on the plant at very low level. These accessions may carry diverse resistance genes, making them useful for breeding programme. The study will provide opportunity for increased utilization of genetic resources maintained in active collection.

Key Words: Barley, Spot blotch, Germplasm, Resistance

Introduction

Barley (*Hordeum vulgare* L.) is an important cereal grain crop in India, grown since ancient times and has been traditionally considered as poor man's crop (Chandola, 1999) because of its low input requirement and better adaptability to harsh environments like drought, salinity, alkalinity and marginal lands. Presently barley occupies nearly 0.69 m ha area producing 1.54 m tones grain, with productivity of 2.23 t/ha (Anonymous, 2011) in India. In India, area is concentrated mainly in the states of Uttar Pradesh, Punjab, Rajasthan, Haryana, Bihar, Madhya Pradesh, in plains and Himachal Pradesh, Uttarakhand, Jammu & Kashmir in the hills. In recent years use of barley as industrial raw material for malting and brewing purposes is gaining more importance. Spot blotch or leaf spot, caused by *Bipolaris sorokiniana* (earlier *Helminthosporium sativum*) is the most common form of leaf blights of barley in India.

The occurrence of the spot blotch was common in north eastern plains zone (Eastern Uttar Pradesh, Bihar, Jharkhand and eastern part of Madhya Pradesh), because of the comparatively hot and humid climate during the crop season. In recent past, spot blotch has become more important disease on barley in north western plains zone (Punjab, Haryana, Western Uttar Pradesh, Delhi and Rajasthan except the dry belt) and also observed during the regular annual crop monitoring under All India Coordinated Wheat and Barley Improvement Project (AICW&BIP). This might be because of increased application of irrigation and fertilizers in barley (which was earlier mostly rainfed crop in the region) for better production of malt quality barley for industrial utilization as well as increased availability of these inputs resulting in the humid micro climate conducive for leaf blights development. The resistance breeding programme for spot blotch was not successful in India because there was no classified information available on the sources of effective resistance to the disease in the released cultivars and other collections. The new genotypes being evaluated for yield are also simultaneously screened in disease and pest screening nurseries under the barley network of AICW&BIP, but almost all of them are being classified as susceptible to highly susceptible under artificial inoculation at hot spot locations. Limited information (Verma *et al*., 2002; Singh *et al*., 2005) is available on resistance sources for spot blotch either

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based on single location screening or with a limited material. This led to the need of screening/ evaluation of the entire collection (5458 accessions) of barley genetic resources available in the DWR medium term storage module against the spot blotch disease to identify new sources of resistance, which can be utilized in barley improvement programme in country.

Material and Methods

The evaluation for resistance to spot blotch was taken up during 2003-04 to 2006-07 at Kanpur, Faizabad, Varanasi and Karnal, under artificial inoculation under the AP Cess Fund supported scheme of ICAR, New Delhi. The first three are considered to be the hot spot locations for the spot blotch where every year very heavy natural incidence of the disease is observed and Karnal gets moderate levels of natural incidence. Identical sets of germplasm accessions were supplied to all four centres for evaluation during crop seasons in each year (Table 1). The seed of a variety RD2503 was also supplied from one source every year to be used as infector. Similar layout was followed at all centres for sowing of test material and infector after every 50 rows as well as perpendicular to the test material in the field. Uniform application of irrigation and fertilizers was made at all the centres to maintain uniformity in all treatments of experimentation. The initial inoculum was supplied to all the centers from DWR, Karnal, to ensure proper disease development with sufficient inoculum load under artificial conditions as per Kumar *et al*. (1999) in addition to the natural incidence of the disease

The resistant and moderately resistant accessions identified during the field screening in first year were repeated in subsequent year for confirmation of reaction, along with a set of new accessions added every year. This provided an opportunity for at least two crop seasons screening at four centers in four crop seasons. The lines identified as resistant/ moderately resistant from the field screening over four years were then screened in poly house for three more years in 2007-08 to 2009-10 crop seasons at DWR Karnal. Disease data were recorded following the double digit system, indicating the percent area covered on the flag leaf and on the next below to flag leaf on 1 to 9 scale (Kumar *et al*., 1998; Nagarajan and Kumar, 1998). The reaction type of the genotype was also taken into consideration apart from the percent area covered on the leaf. Observations were recorded two to three times in the season at appropriate stages and the highest score on one genotype was reported based on final recording in the early dough stage.

The highest disease incidence score at any of the locations was considered to classify the entry in to resistant (R) up to 35, moderately resistant (MR) up to 46, moderately susceptible (MS) between 47-57 and susceptible (S) more than 57 in double digit scale. In addition to the percent area covered on the leaf, the type of lesion/ spot caused was also taken in to consideration for classification of accessions as resistant or moderately resistant. The typical eye shaped spot surrounded by a big hallow, spreading further continuously and covering major area of leaf by fusing with other spots were characteristics of susceptible genotypes. Contrary to this in the genotypes classified as resistant the size of individual spots was very small and remained almost static even at later stages in the season, while in moderately resistant genotypes the increase in spot size was there but the big hallow around the spots and necrosis of leaf tissue was not as prominent as in susceptible genotypes.

Results and Discussion

The susceptible variety RD 2503 used as check as well as infector in the study had disease score of 99 at all the four locations every year indicating the high disease development at all the locations. However at Karnal (NWPZ), where comparatively cooler climate persists longer, delayed initiation of spot blotch was observed in all years under field screening with comparatively lower disease scores than rest of the locations (NEPZ) indicating the environmental effects on the disease development. However in poly house screening at Karnal, the disease development started earlier than field screening due to controlled warmer conditions.

Table 1. Details of germplasm accessions evaluated in different years for spot blotch

Year / crop season	Number of accessions evaluated at each centre		Recorded as	
	New	Repetition from previous year	R/MR	MS/S
2003-04	1707	–	14	1693
2004-05	1921	14	135	1800
2005-06	1687	135	175	1647
2006-07	143	175	86	232
2007-10	-	86*	76	10
Total	5458		76	5382

R= resistant, S= susceptible, *Poly house screening at Karnal under artificial epiphytotics

Table 2. Germplasm lines observed as resistant and moderately resistant to leaf blight under field screening during 2003-04 to 2006-07

S. No.	BCU No.	Highest score in double digit			Overall Reaction
		Faizabad	Varanasi	Kanpur	
Resistant					
1	103	24	24	02	R
2	117	34	35	24	R
3	488	35	23	02	R
4	545	35	23	02	R
5	698	35	12	24	R
6	702	35	12	34	R
7	814	24	23	24	R
8	2156	35	24	34	R
9	4756	35	24	34	R
10	4916	35	35	24	R
11	4919	25	35	25	R
12	4920	35	35	24	R
13	4963	35	35	24	R
14	4966	35	35	24	R
15	5179	24	23	34	R
16	5180	35	23	34	R
17	5214	35	24	34	R
18	5459	35	35	34	R
19	5522	25	35	34	R
20	5527	35	25	34	R
21	5566	24	12	34	R
22	5569	35	12	34	R
23	5571	34	24	24	R
24	5593	35	35	24	R
25	5616	35	24	23	R
26	6031	24	24	34	R
27	6038	24	24	24	R
28	6079	35	24	23	R
Moderately Resistant					
1	76	46	35	46	MR
2	133	46	12	34	MR
3	572	46	12	34	MR
4	621	45	35	46	MR
5	625	46	12	24	MR
6	713	46	35	34	MR
7	716	47	24	02	MR
8	971	46	24	34	MR
9	1092	45	23	46	MR
10	1235	25	35	46	MR
11	1400	46	25	24	MR
12	1439	46	23	46	MR
13	2066	46	35	24	MR
14	3498	46	24	46	MR
15	3566	46	23	34	MR
16	3634	46	35	46	MR
17	3822	35	35	46	MR
18	3959	35	35	46	MR
19	3994	35	35	46	MR
20	4698	46	46	46	MR
21	4722	45	23	46	MR
22	4723	45	23	46	MR
23	4745	35	35	46	MR
24	4748	45	35	46	MR
25	4752	46	23	46	MR
26	4755	35	35	46	MR
27	4764	46	23	46	MR
28	4765	45	12	46	MR
29	4860	35	12	46	MR
30	4908	46	35	46	MR
31	4910	35	12	46	MR
32	4911	46	24	24	MR
33	4912	45	35	46	MR
34	4913	46	35	46	MR
35	4918	46	23	46	MR
36	4921	46	23	35	MR
37	4926	24	23	46	MR
38	4928	25	23	46	MR
39	4930	45	35	46	MR
40	4949	46	23	46	MR
41	4955	46	23	24	MR
42	4957	46	25	46	MR
43	5117	34	12	46	MR
44	5176	24	35	46	MR
45	5177	35	24	46	MR
46	5181	45	23	46	MR
47	5374	46	35	46	MR
48	5519	35	24	46	MR
49	5594	46	24	24	MR
50	5601	35	24	46	MR
51	5609	35	12	46	MR
52	5638	46	25	46	MR
53	6027	35	35	46	MR
54	6034	35	24	46	MR
55	6040	46	24	35	MR
56	6080	46	24	46	MR
57	6124	24	23	46	MR
58	6125	46	24	46	MR

** Highest score for each leaf in double digit system over the locations*
(R = up to 35, MR = 36-46, MS = 47-57, S = >57 score on double digit system *i.e.* % area covered on flag leaf and next below flag leaf)
BCU No. Barley Coordination Unit accession number

Table 3. Evaluation of selected germplasm accessions against spot blotch during 2007-10 under controlled conditions at DWR Karnal

S. No.	BCU No.	Name	Origin	Disease Reaction
1	76	BON-LRA-M (90-91)-86	E	R
2	103	KARAN-757	I	R
3	117	KARAN-1057	I	R
4	133	HBL 233	I	R
5	488	19th IBON (91-92)-28	E	R
6	545	19th IBON (91-92)-86	E	R
7	572	PUBEBLA	E	R
8	621	2nd IWFBON-18	E	MS
9	625	2nd IWFBON-23	E	R
10	698	2nd IWFBON -98	E	R
11	702	2nd IWFBON-103	E	MS
12	713	2nd IWFBON-114	E	MS
13	716	2nd IWFBON-117	E	R
14	814	BON-LRA-C (91-92)-12	E	R
15	971	1st HBSN 1	E	S
16	1092	BON-MRA(91-92)-93	E	R
17	1235	TOKAK	E	S
18	1400	ICB-94 (QUINN/BC//ATHS/ ANTARES)	E	R
19	1439	ICB-135 (WI2291/4/AVT/KI// AVT/3/TOLI/BZ)	E	R
20	2066	VLB 35	I	R
21	2156	Line 1243-3	I	R
22	3498	SEVIROWS(B)	I	R
23	3566	IC-25615	I	R
24	3634	IC-36899	I	R
25	3822	IC-58028	I	MS
26	3959	IC-61844	I	R
27	3994	IC-62765	I	R
28	4698	IC-79593	I	R
29	4722	20th IBYT-10	E	R
30	4723	20th IBYT-11	E	MS
31	4745	21st IBYT-7	E	R
32	4748	21st IBYT-10	E	R
33	4752	21st IBYT-14	E	R
34	4755	21st IBYT-17	E	R
35	4756	21st IBYT-18	E	R
36	4764	27th IBON-8	E	R
37	4765	27th IBON-9	E	R
38	4860	ISBCB-82 (ALANDA-01/3/ EMIR// ESP/SV. MARI ICB 89-0779-4L AP-4AP-OTR-3AP-OAP)	E	R
39	4908	29th IBON 3	E	R
40	4910	29th IBON 9	E	R
41	4911	29th IBON 11	E	R
42	4912	29th IBON 13	E	R
43	4913	29th IBON 20	E	R
44	4916	29th IBON 27	E	R
45	4918	29th IBON 41	E	R
46	4919	29th IBON 43	E	R
47	4920	29th IBON 44	E	MR
48	4921	29th IBON 49	E	R
49	4926	29th IBON 65	E	R
50	4928	29th IBON 70	E	R
51	4930	29th IBON 75	E	R
52	4949	29th IBON 170	E	MR
53	4955	10th EMBSN 5	E	R
54	4957	10th EMBSN 8	E	R
55	4963	10th EMBSN 20	E	R
56	4966	10th EMBSN 29	E	R
57	5117	IC-437886	I	MS
58	5176	IC-437955	I	R
59	5177	IC-437956	I	MS
60	5179	IC-437958	I	MR
61	5180	IC-437959	I	R
62	5181	IC-437960	I	R
63	5214	IC-437996	I	R
64	5374	IC-438160	I	MS
65	5459	IC-438257	I	R
66	5519	EC-492144	E	MR
67	5522	EC-492147	E	R
68	5527	EC-492152	E	R
69	5566	EC-492193	E	R
70	5569	EC-492196	E	R
71	5571	EC-492198	E	MR
72	5593	EC-492220	E	R
73	5594	EC-492221	E	R
74	5601	EC-492229	E	MR
75	5609	EC-492238	E	R
76	5616	EC-492254	E	R
77	5638	EC-492285	E	R
78	5960	DWR49	I	R
79	6027	VJM-360	I	R

Contd ...

S. No.	BCU No.	Name	Origin	Disease Reaction
80	6031	VJM-389	I	R
81	6034	VJM-507	I	R
82	6038	VJM-515	I	R
83	6040	VJM-522	I	R
84	6079	Keel	E	R
85	6080	Schooner	E	MR
86	6124	IC-438277	I	MR

BCU No. = Barley Coordination Unit accession number, E = Exotic, I = Indigenous

Of the entire material screened, none of the accessions could be termed as immune to leaf blights at any of the location. A number of lines were recorded as resistant or moderately resistant (Table 1). However differential response was observed at different locations at early stages of diseases spread. Many accessions were observed with slow disease spread as compared to others, though the highest disease score may be the same at the end of season. Based on the overall compilation, 28 accessions (based on at least two year's observations in field) could be termed as resistant out of 5458 accessions screened during four crop seasons. Another group of 58 accessions was observed as moderately resistant as indicated in the table 1. Rest of accessions were in susceptible to highly susceptible group, in some cases the extent of susceptibility was so high that it could not produce the spikes and grain with almost 100% yield losses. The details of the resistant and moderately resistant accessions under field screening are given in table 2.

These observations were further confirmed during poly house artificial inoculation screening in three crop seasons, leaving no chance of escape. The 28 resistant and 58 moderately resistant accessions identified under field screening were further evaluated under ploy house artificial inoculation for another three years. Under this screening, 68 accessions were confirmed as resistant and eight as moderately resistant. Another eight accessions were recorded as moderately susceptible and two as susceptible (Table 1). The variations observed between field and poly house screening for resistance as some of the moderately resistant accessions of field screening either recorded in resistant or moderately susceptible/ susceptible accessions in poly house screening. These variations either could be due host and pathogen interaction under conducive conditions in poly house or recording error at certain location under multilocation evaluation. Also in open screening at hot spot locations like Varanasi and Faizabad apart from the inoculum supplied from one source, the local more aggressive pathotypes of leaf spot might have been there which was not available in the ploy house recording. There is also possibility of differential recording of MR/MS reaction under field conditions by different persons, as it is only the visual recording and not a measurement character. Finally the repetitive recording in poly house for three seasons have confirmed the results as reported in Table 3 along with their names, source/origin and highest disease score observed during evaluation.

The results indicate that the resistance level as well as the number of resistant accessions is scanty in the barley germplasm material and unlike rusts there is nothing which can be termed as immune to the spot blotch in India. However the genotypes grouped as resistant were able to keep the disease level on the plant at very low level with very small spots which were not spreading further like the susceptible genotypes. These genotypes hold promise for utilization in the barley improvement for irrigated conditions having resistance to the spot blotch. All these sources are from different geographic regions/origin and may carry diverse resistance genes, making it useful for breeding programme. However their diversity at genetic level needs further confirmation by traditional inheritance studies or the molecular markers approaches.

The change in barley cultivation in India from traditional rainfed feed barley under minimal input conditions to irrigated optimally managed malt type barley is further making it important to incorporate resistance to leaf spot. The present study will provide very useful knowledge about the promising genetic resources maintained in our collection in the country and promote their utilization, as so far such material are lying unutilized in absence of proper evaluation.

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Introduction, Characterisation and Evaluation of Husk Tomato (*Physalis ixocarpa* Brot.) Genotypes under Temperate Climate

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The performance of 10 husk tomato genotypes under temperate conditions was observed during 2010-12. The result revealed significant variation for all the morphological, growth, fruiting and yield attributes in various genotypes. Maximum number of basal shoots was recorded in genotype EC467440 (7.0), whereas, number of prickles/shoot were recorded maximum (8.33) in EC467449. Maximum size of fully developed leaf (147.00 mm), plant height (168.33 cm) and maximum time taken for bud burst (29.33 days) was recorded in EC467459, whereas, maximum time taken from bud burst to flowering was found in EC467449 (37.67 days). Duration of fruit bloom was recorded maximum in EC467459 and EC467440 (66.0 days in each). Maximum days taken for maturity (75.0 days), maximum number of fruit/plant (260.67), maximum fruit weight (37.67 g), highest fruit husk ratio (1.21), maximum yield/plant (9.69 g) and maximum fruit firmness (RI) (44.10) were recorded in EC467459. Total soluble solid content ranged from 6.50-11.50 ˚B and highest value was recorded in EC467440 (11.50° B). The value of juice percentage of fruits ranged was recorded maximum (3.49%) in EC467459. The titrable acid content in fruits was estimated the lowest (0.36%) in EC467445. Ascorbic acid content was estimated maximum in EC467459 (24.27mg/100g). The maximum 'L' value indicating brightness was found in EC467439 (64.15), whereas 'a' value indicating redness was recorded highest in EC467435 (-2.44) and 'b' value indicating yellowness was observed maximum in EC467440 (35.50). Study reveals that genotypes EC467459, 467455, 467440, 467435, 467439, 467446 and 467450 can be used as elite selections for the temperate regions. However, further studies are required for development of complete package of practices for further commercial cultivation.

Key Words: Ecosystem, Genotypes, Growth, Husk tomato, Quality, Yield

Introduction

Introduction and adaptations of new crops contribute to an increase in diversity of agriculture systems offering new alternatives to farmers and markets, with crops that may have a high value and for which generally there is no over production (Prophens *et al.,* 2004). Therefore, new crops can result in an increase income for farmers, contribute to a more environment friendly agriculture, and reduce the risk of crop failure and also increases botanical knowledge. There are many new crops for tropical and subtropical region that can present desirable attributes to be introduced as new crops in temperate climates. Husk tomato (*Physalis ixocarpa* Brot.), also known as tomatillo, is an important herbaceous crop of family Solanaceae, grown for its edible fruits. It is usually cultivated as short cycle (4-5 months) annual crop, however, grows as perennial in absence of frost. Husk tomato is native to Mexico where many types and some named varieties are cultivated, with variability in berry size, colour and flavour (Heiser, 1975; Dremann, 1985; Hernando and Leon, 1994). In its region of origin it is adapted to a wide altitudal range (from sea level to 3200m) including erolytic and warm areas with an intense solar radiation to humid and cloudy environment (Nuez *et al.,* 1999). Husk tomatoes are bushy and spreading plants that may grow to a height of 90-120 cm with a similar spread. Plants are indeterminate; they keep flowering and bearing fruits until killed by frost. The plant is usually sprawling and needs support. Fruits of husk tomato are small 1-4.5 cm diameter; green round berry at maturing contains many tiny seeds (Chattopadhya, 1996). At maturity the fruits are yellowish-green, smooth and sticky. Plant can successfully set fruit if the minimum temperature is above 5°C (Person *et al*., 1989., Prophens and Nuez, 1994). Fruits are firmer than tomatoes and their flavour is similar to tangy lemon. The tomatillo fruit is surrounded by an inedible paper like husk formed from the calyx. The fruits are considered ready to harvest when they have achieved maximum size, forming the husk or calyx (Saray-Meza and Loya-Ramirez, 1974), but fruits from different stages of development can be mixed and marketed. The fruits can be eaten raw, as a dessert, and appetizer or used as

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dish decorator. It is rich in vitamin A, B, B_2, C and polyphenols (Gonzalez-Mendoza *et al*., 2010; Brazanti and Monaresi 1980; Sarangi *et al.,* 1989). Its wide range of adaptation and versatile use as table purpose and processing form and increasing demand in exotic fruit market gives good prospects for the expansion of husk tomato as a new cash crop in temperate region. Keeping its importance and scope for commercial production in consideration, ten genotypes collected from different agro-zones and NBPGR, Regional Station, Shimla were evaluated for their adaptation under temperate region grown in summer season. Further genetic differences in yield and fruit quality characters among accessions from different regions (Prophens and Nuez, 1994) can be exploited for husk tomato breeding.

Materials and Methods

The experiment was taken at experimental farm of Central Institute of Temperate Horticulture, Srinagar, (J&K), during summer months (May-September 2010-11 and 2011-12). Plants from nursery were transplanted during first week of May at a spacing of 30 x 30 cm and no training and pruning was done. The experiment was laid out in Randomized Block Design with three replications. Morphological characters, flowering and fruiting parameters of the plants were periodically recorded. Data on fruit length, diameter, firmness, husk fruit ratio, juice were recorded at appropriate maturity of fruits. Total soluble solids were recorded using digital refractometer. Acidity and ascorbic acid were determined by the method of AOAC (1990). Fruit firmness was measured using HP qualities digital firmness tester model no. 63776. Colour values for L (brightness), a (redness) and b (yellowness) were recorded using hunter lab refractometer model no. 45/0, serial no. CEEZ 0285, Colourflex-Ez. Statistical analysis was performed as per Panse and Sukhatme (1985). Soil status of experimental site and climatic parameters during the cropping season are given in table 1 and 2.

Table 1. Monthly average weather data for the year 2010-12

Month	Rain (mm)	Temperature ^oC		Humidity(%)
		Max	Min	
May	20.0	21.92	9.82	59.32
June	34.9	25.17	10.78	61.10
July	31.4	28.56	16.42	59.10
August	57.0	28.52	17.63	62.29
September	53.2	27.20	12.15	56.78
October	27.9	23.77	5.50	61.97

Table 2. Initial soil properties of the experimental soil

Soil properties	Inceptisol
pH	7.1
EC (ds m^{-1})	0.48
OC (%)	0.71
Available Nitrogen (kg ha^{-1})	420.0
Available phosphorus (kg ha^{-1})	28.2
Available Potassium (kg ha^{-1})	346.0
Zinc (kg ha^{-1})	1.2
Iron (kg ha^{-1})	5.7
Copper (kg ha^{-1})	0.8
Manganese (kg ha^{-1})	6.8

pH (1:2.5), EC (1:2.5), electrical conductivity (dS m^{-1})

Results and Discussion

Morphological Characters

These genotypes showed significant variation for morphological characteristics (Table 3). Maximum number of basal shoots was recorded in EC467440 (7.00), followed by EC467459 (7.0), 467445, while it was minimum in EC467449 (2.67). Maximum number of prickles/shoot (8.33) was recorded in EC467449, followed by EC467450 (7.33), while it was minimum in EC467459 (4.00). Maximum number of single (7.67), double (5.00) and triple prickles (3.00)/shoot were recorded in EC467449. The maximum number of points of attachment of prickles was found in EC467450 and EC467455(8.67 in each), while as minimum (4.67) in EC467435. The number of bristles on upper third of shoots was found maximum in EC467449 (9.0) followed by EC467449 and EC467455 (8.0 in each), while it was found minimum in EC467435 (5.0). Fully developed leaf size was recorded in EC467459 (147.0mm) followed by EC467439 (119.51mm), it was found minimum in EC467449 (65.0mm). Maximum plant height was recorded in EC467459 (168.33cm) followed by 126.33cm in EC-467449, while it was recorded minimum in EC467446 (70.33cm). Similar results showing variation in growth characteristics like number and size of the nodes on first bifurcation of the plant; size and number of teeth/leaf, branching of *Physalis ixocarpa* has been reported by Hernando and Leon (1994), which is possibly because of their self incompatibility. Variation in growth and yield attributes in *P. pereviana* cultivars under temperate conditions were also reported by Singh *et al.* (2011).

Flowering and Fruiting Characters

The data values for flowering and fruiting characteristics of husk tomato varied significantly (Table 4). Maximum time taken to bud burst was recorded in EC467459 (29.33 days) followed by 29.00 days in EC467455, while it was minimum in EC467435 and 467446 (21.00 days each). Maximum time taken for bud burst to flowering was found 37.67 days in EC467449 followed by 36.6 days in EC467450, while minimum was recorded in EC467435 (28.67 days). The predominant number of flowers was recorded maximum (26.67) in EC467455 followed by 26.67 in EC467455, while it was recorded minimum (20.00) in EC467435. The fruit length was recorded maximum in EC467435 (35.10 mm) and minimum was recorded in EC467446 (22.71 mm), while as fruit breadth was recorded maximum in EC467459 (38.49 mm) and minimum in EC467447 (25.62 mm). The fruit bloom character was recorded maximum in EC467446 and EC467440 (66.00 in each) followed by EC467459 (62.67) while minimum fruit bloom was recorded in EC467449 (46.00). Fruit elongation of base was recorded maximum in EC467435 (29.67 mm) followed by 29.16 mm in EC467459, and minimum was recorded in EC467446 (18.38mm). The length of fruit peduncle was recorded maximum in EC467440 (17.19 mm), however minimum length of fruit peduncle was recorded in EC467449 (12.98 mm). Number of fruits/plant was found maximum in EC467459 (260.67) followed

Table 3. Morphological characteristics of husk tomato genotypes

Genotype	No. of basal shoots	No. of prickle/ shoot	No. of single prickles/ shoot	No. of double prickles/ shoots	No. of triple prickles / shoots	No. of points of attachments of prickles	No. of bristles on upper third of shoots	Size of fully developed leaf (mm)	Plant height (cm)
EC467435	3.33	4.33	1.33	2.67	0.33	4.67	5.00	119.51	96.67
EC467439	4.33	5.33	1.33	4.00	1.67	7.00	6.67	93.00	99.33
EC467440	7.00	5.00	4.67	4.00	0.33	6.00	7.67	102.67	118.67
EC467445	5.33	6.33	3.00	3.00	2.00	5.33	5.67	66.33	92.00
EC467446	4.33	5.00	3.67	3.67	0.33	6.00	5.67	90.00	70.33
EC467447	3.33	6.67	5.00	2.67	2.00	8.00	8.00	103.33	110.00
EC467449	2.67	8.33	7.67	5.00	3.00	8.00	9.00	65.00	126.33
EC467450	4.00	7.33	6.00	3.00	0.33	8.67	7.33	94.67	105.00
EC467455	5.00	6.33	5.00	4.33	2.00	8.67	8.00	94.33	114.33
EC467459	6.33	4.00	3.33	3.00	0.67	7.67	6.67	147.00	168.33
CD at 5%	0.90	1.02	1.15	1.29	1.19	1.32	1.07	4.21	2.38
SEm	0.30	0.34	0.38	0.43	0.40	0.44	0.36	1.41	0.80

Table 4. Flowering and fruiting characters of husk tomato genotypes

Genotype	Time taken to bud burst (days)	Time taken to flowering (days)	Predominant no. of flowers	Fruit Size length (mm)	Fruit breadth (mm)	Fruit bloom (days)	Fruit elongation of base. (mm)	Length of fruit peduncle (mm)	No. of fruits/ plant	Days taken for maturity	Yield / plant (kg)
EC467435	21.00	28.67	20.00	35.10	34.56	60.00	29.67	16.74	199.67	70.00	5.42
EC467439	22.67	30.67	25.33	29.23	36.25	63.67	28.67	16.16	204.33	74.67	5.41
EC467440	24.33	32.67	25.67	31.69	37.38	66.00	24.63	17.19	230.00	71.67	6.44
EC467445	23.33	34.67	23.67	37.28	33.89	54.00	29.13	15.57	200.00	64.67	4.45
EC467446	21.00	34.33	20.67	22.71	27.32	66.00	18.38	14.52	187.00	74.67	4.62
EC467447	26.33	35.67	25.67	24.19	25.62	48.33	21.65	15.19	207.67	60.00	4.97
EC467449	28.33	37.67	23.33	28.30	33.44	46.00	23.50	12.98	183.33	60.00	3.52
EC467450	27.00	36.67	24.33	24.23	27.51	59.00	20.06	16.90	204.00	73.00	5.40
EC467455	29.00	36.00	26.67	25.45	31.33	65.00	26.23	15.52	240.33	70.00	6.88
EC467459	29.33	34.67	24.67	33.39	38.49	62.67	29.16	15.71	260.67	75.00	9.69
CD at 5%	1.57	0.87	1.09	1.49	3.97	183.67	1.18	1.22	3.43	1.43	0.02
SEm	0.52	0.29	0.37	0.50	1.33	61.81	0.40	0.41	1.15	0.48	0.01

by 240.33 in EC467455, while minimum in EC467449 (183.33). Maximum days taken for maturity (75.00 days) were recorded in EC467459 followed by EC467439 and 467446 (74.67 days in each), while it was minimum in EC467447 and EC467449 (60 days in each). The fruit yield/plant was recorded highest in EC467459 (9.69 kg) followed by 6.88 kg in EC467455, whereas lowest fruit yield was recorded in EC467449 (3.52 kg). Findings of Mazumdar (1979), Singh (1985), Pal (1991) and Chandi (2000) also confirm variability of different genotypes of *Physalis* species in terms of yields per plant and individual fruit weight. Hernando and Leon (1994) and Singh *et al.* (2011) also reported great variation in fruit weight, colour and size of *Physalis ixocarpa* and *P. pereviana* cultivars under different agro zones.

Physico-chemical Characters

The different physico-chemical characteristics were studied and data values recorded for average fruit weight, husk weight, fruit husk ratio, firmness, TSS Brix, juice percent, acidity percent and ascorbic acid varied significantly (Table 5). The maximum fruit weight was recorded in EC467459 (37.67 g) followed by EC467455 (29.33 g) and it was recorded minimum in EC467449 (20.00 g). Maximum husk weight was recorded in EC467455 (0.34 g) followed by 0.33 g in EC467450 and minimum was recorded in EC467449 (0.20 g). Fruit husk ratio was recorded highest in EC467459 (121.5) followed by EC467440 (110.2) and lowest husk ratio was recorded in EC467450 (84.84). Fruit firmness was recorded highest in EC467459 (44.10 RI) followed by EC-467455 (37.87 RI) and lowest firmness was recorded in EC467445 (25.87 RI). Total soluble solids content ranged from 6.50-11.50°Brix and highest value was recorded in EC467440 (11.50°B) followed by 9.47°B in EC467439 and EC467459, and its lowest value (6.50° B) was found in EC467450 and EC467455 Singh *et al*. (1976) also observed similar kind of results in the ripe berries but not in conformity with Pal (1991), who reported the TSS levels of the fruit different from strains of husk tomato. Similar variation in TSS, acidity and ascorbic acid contents of cape gooseberry cultivars were also reported by Singh *et al.* (2011). This may be due to variation in climatic and growing conditions. The value of juice percentage of fruits ranged between (2.11 to 3.49 %) and maximum value was found in EC467459 (3.49%) followed by EC467455 (3.38%) and minimum juice percentage was found in EC467447 (2.11%). Such variation in the level in juice percentage in husk tomato is due to varietal differences, the same has also been reported by Karrer and Kahlon (2005). The titrable acid content in fruits was estimated the lowest 0.36% in EC467445 and the highest in EC467440 (1.51%). More or less similar values of acidity in husk tomato have been reported by Singh *et al.* (1976) and Pal (1991). According to Wolf (1991), the lowest value of acidity to the extent of such variations may be due to environmental condition particularly during the peak of growth and development of fruits or varietal differences. Ascorbic acid content was estimated maximum in EC467459 (24.27 mg/100 g) followed by 22.40 mg/100 gm in EC467450, however lowest ascorbic acid was estimated in EC467445 (15.40 mg/100 g).

Table 5. Physico chemical characteristics of husk tomato genotypes

Variety	Average fruit weight (g)	Husk weight (g)	Fruit husk ratio	Firmness (RI)	TSS (°Brix)	Juice (%)	Acidity (%)	Ascorbic acid (mg/100gm)
EC467435	27.67	0.30	92.2	36.23	8.50	2.66	0.46	18.60
EC467439	27.00	0.30	90.0	27.67	9.47	2.90	0.48	17.27
EC467440	28.67	0.26	110.2	36.67	11.50	3.09	1.51	15.87
EC467445	22.80	0.26	87.6	25.87	8.40	2.45	0.36	15.40
EC467446	25.67	0.27	95.0	26.63	7.63	2.14	0.38	16.80
EC467447	25.00	0.27	92.5	27.20	6.50	2.11	0.42	17.27
EC467449	20.00	0.20	100.0	31.77	7.57	2.83	0.37	16.80
EC467450	28.00	0.33	84.84	30.23	6.50	2.54	0.41	22.40
EC467455	29.33	0.34	86.26	37.87	6.50	3.38	0.41	21.40
EC467459	37.67	0.31	121.5	44.10	9.47	3.49	0.62	24.27
CD at 5%	1.12	0.15	0.44	3.92	0.45	0.48	1.72	2.40
SEM	0.37	0.05	0.14	1.32	0.15	0.16	0.57	0.80

Colour Value

The colour value of husk tomato fruits taken for L (brightness), a (redness), and b (yellowness) varied significantly with different genotypes (Table 6). The maximum 'L' value indicating brightness was found in EC467439 (64.15) followed by EC467455 (62.40) while minimum was found in EC467447 (46.56). The 'a' value indicating redness was recorded highest in EC467435 (-2.44), minimum was noted in EC467440 (-11.04), the 'b' value indicating yellowness was observed maximum in EC467440 (35.50) followed by EC467435 (32.27) however, the minimum value was recorded lowest in EC467447 (17.82). Variation in colour of fruit in husk tomato genotypes is reported by Hernando and Leon (1994), Heiser (1975); Dremann (1985) and in cape goose berry by Singh *et al.* (2011). Based on this research study, it can be concluded that EC 467459, 467455, 467440, 467435, 467439, 467446 and 467450 can be used as elite selections for the temperate regions. However, further studies are required for these selections and their evaluation so that potential for better utilization in the future way be established by devising complete package of practices for commercial cultivation in temperate region.

Table 6. Colour value of husk tomato genotypes

Variety	L *	a*	b*
EC467435	61.56	-2.44	32.27
EC467439	64.15	-6.70	27.18
EC467440	55.17	-11.04	35.50
EC467445	55.56	-7.59	23.54
EC467446	59.26	-6.54	26.65
EC467447	46.56	-4.77	17.82
EC467449	57.01	-5.58	23.75
EC467450	53.18	-8.58	23.82
EC467455	62.40	-7.65	29.72
EC467459	59.59	-6.62	26.69
CD at 5%	5.62	0.34	0.37
SEm	1.89	0.11	0.12

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Path Coefficient Analysis for Husk and Contributing Traits in Isabgol (*Plantago ovata* Forsk.)

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The study was conducted at Udaipur, Rajasthan, India during rabi, 2009-11. The aim of study was to evaluate the inter-relationship of trait and husk recovery using path analysis with 24 isabgol genotypes collected from four major isabgol growing states namely Gujarat (4), Madhya Pradesh (1), Rajasthan (17) and Haryana (2) of India. The path coefficient analysis based on husk recovery, as a dependent variable implicated that seed yield/plant had the highest positive direct effect on husk recovery. This trait was followed by spikes/plant, leaf width and swelling factor. Biological yield/plant and harvest index had negative direct effect on husk recovery. The overall results demonstrated that seed yield/plant and spikes/plant were the most contributing traits on isabgol husk recovery and direct selection based on these traits would be advantageous.

Key Words: Husk recovery, Isabgol, Path analysis, *Plantago ovata*

Introduction

Ever since the dawn of human civilization, plants have been used as a source of medicines, and are a major component of Ayurvedic and Unani medicines (Chudiwal *et al.,* 2010). Out of a large number of medicinal plants known in present scenario, *Plantago ovata* Forsk. (family Plantaginaceae) commonly known as isabgol and commercially as blond psyllium (Dalal and Sri Ram, 1995) is grown in India for its use in ayurvedic medicines (Bist *et al.,* 2001). Economic value of isabgol is mainly related to mucilage content of the seed which mainly present in seed husk. A good crop may yield about 800-1000 kg of seeds per hectare. Harvested seed is processed through a series of grinding mills to separate the husk, about 30 per cent husk by weight is thus recovered. The seed husk, is not only a highly effective laxative but is also used in lowering blood cholesterol levels, ice cream making and cosmetics (Dhar *et al.,* 2005).

Complex trait like husk recovery is highly influenced by many genetic factors and environmental fluctuations. Path coefficient is an excellent means of studying direct and indirect effects of interrelated components of a complex trait (Sodavadiya *et al.,* 2009). Path coefficient analysis, a statistical device developed by Wright (1921), which measures the direct influence of one variable upon the other. Each correlation coefficient between a predictor variable and the response variable is partitioned into its component parts: the direct effect or path coefficient (a standardized partial regression coefficient) for the predictor variable and indirect effects, which involves the product of a correlation coefficient between two predictor variables with the appropriate path coefficient in the path diagram (Dewey and Lu, 1959). By determining the inter-relationships among husk recovery components, a better understanding of both the direct and indirect effects of the specific components can be attained and applied in isabgol improvement programmes. Therefore, this experiment was conducted to study the relations of certain agro-morphological traits with husk yield in isabgol.

Materials and Methods

The experiments were conducted at the instructional farm of the Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan) during *rabi* 2009-10 and 2010-11. The material for present study consisted of 24 genotypes of isabgol from four major isabgol growing states. During both the years, trials were laid out in randomized block design with three replications with plot size of 60 m^2. Row to row and plant to plant distance was kept at 30 and 15 cm, respectively. Fertilizers were applied 25 kg N: 20 kg P_2O_5 and 25 kg K_2O/ha at the time of sowing

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while 25 kg N/ha was top-dressed one month after sowing. Immediately after sowing a light irrigation was given. Second irrigation was given after three weeks and third one at the time of formation of spikes. Seven irrigations were given during the entire crop period. The plots were weeded manually to keep weed pressure low. Other recommended agronomic management practices were adopted for optimum crop growth and development. The data was recorded on fifteen agro-morphological traits. Five competitive plants were randomly selected and tagged from each replication in a genotype for recording detailed observations for 11 traits *viz.*, plant height, leaf width, effective tillers/plant, spikes/plant, weight of spike, weight of seeds/spike, spike length, test weight, seed yield/plant, biological yield/plant and harvest index (%). Days to 50% flowering and days to maturity were monitored as the number of days from sowing to when 50% of the plants flowered and 100% of the plants attained physiological maturity within a plot, respectively. Husk recovery (%) and swelling factor were calculated according to Kalyansundaram *et al.* (1982) and Kokate (1994), respectively.

The methodology proposed by Dewey and Lu (1959) was used to perform the path analysis for husk recovery and its components keeping husk recovery as resultant variable and its components as causal variables. For this purpose computer software Windostat (version 7.0) developed by Indostat Services Ltd., Hyderabad (India) was used.

Result and Discussion

The phenotypic as well as genotypic correlation coefficients between husk recovery and different traits were subjected to path coefficient analysis separately for partitioning these values into direct and indirect effects. The results obtained for direct and indirect effects of different traits on husk recovery at phenotypic and genotypic level are summarized in Table 1. The results of path analysis at genotypic and phenotypic level revealed that seed yield/plant (6.104 and 0.988) has maximum positive and significant direct effect on husk recovery followed by spikes per plant (1.297 and 0.583), leaf width (0.477 and 0.549) and swelling factor (0.293 and 0.461). This means that a slight increase in one of these traits may directly contribute to husk recovery. On the other hand, negative and significant direct effect of biological yield/plant (-6.026 and -1.259) and harvest index (-1.567 and -0.121) was observed on husk recovery. Effective tillers/plant showed negative and significant direct effect (-0.505) on husk recovery at genotypic level whereas, at phenotypic level its direct effect (0.042) on husk recovery was positive and significant. At genotypic level weight of seeds/spike and spike length exhibited positive and significant direct effect (0.453 and 0.929) with husk recovery. Days to maturity at genotypic level showed positive direct effect (1.407) on husk recovery with negative significant correlation.

Maximum positive indirect effects at genotypic and phenotypic level of biological yield/plant (5.721 and 0.902), spikes/plant (5.602 and 0.86), effective tillers/plant (3.904 and 0.57), harvest index (3.203 and 0.519), weight of seeds/spike (3.146 and 0.44), weight of spike (3.073 and 0.406), spike length (1.39 and 0.2), plant height (1.069 and 0.142) and leaf width (1.062 and 0.167) via seed yield/plant and biological yield/plant (1.224 and 0.516) and seed yield/plant (1.19 and 0.508) via spikes/plant were observed on husk recovery. Days to 50% flowering showed positive indirect effect (1.431) via days to maturity on husk recovery at genotypic level. Most of the traits showed their positive indirect effect only through seed yield/plant. Hence it may be concluded that seed yield/plant is the main trait which is responsible for manipulation of husk recovery in isabgol. Maximum negative indirect effect at both level of spikes/plant (-5.691 and -1.115), seed yield/plant (-5.647 and -1.15), effective tillers/plant (-3.043 and -0.577), weight of spike (-2.195 and -0.324), plant height (-1.853 and -0.39), weight of seeds/spike (-1.757 and -0.324), spike length (-1.346 and -0.244), days to 50% flowering (-1.274 and -0.23), harvest index (-1.212 and -0.178) and days to maturity (-1.167 and -0.16) *via* biological yield/plant were noticed on husk recovery. At genotypic level negative indirect effect of days to maturity (-1.497) via days to 50% flowering, weight of seeds/spike (-1.022) via weight of spike and weight of seeds/spike (-1.127) via harvest index was recorded on husk recovery. Days to maturity showed negative significant correlation with husk recovery due to indirect negative effect of days to 50 % flowering and biological yield/plant while, its direct effect was positive. The high values (R_g= 0.198 and R_p= 0.257) of residual effect towards husk recovery in the present study might be due to many other traits which were not studied, environmental factors and sampling errors (Sengupta and Karatia, 1971).

The path coefficient analysis revealed a clear idea about the highest contributing trait to husk recovery and

Table 1. Phenotypic (P) and genotypic (G) path coefficient analysis showing direct and indirect effects of different traits on husk recovery in isabgol

Trait		Plant height	Days to 50% flowering	Leaf width	Effective tillers/ plant	Spikes/ plant	Weight of spike	Weight of seeds/ spike	Spike length	Test weight	Seed yield/ plant	Biological yield/ plant	Harvest index	Days to maturity	Swelling factor	Correlation with husk recovery
Plant height	G	-0.110	-0.264	-0.029	-0.117	0.317	-0.029	0.007	0.455	0.009	1.069	-1.853	0.387	0.272	-0.091	0.023
	P	0.216	0.035	-0.043	0.007	0.083	0.017	0.000	0.044	0.011	0.142	-0.391	0.038	-0.023	-0.128	0.007
Days to 50% flowering	G	-0.020	-1.472	-0.133	0.010	0.155	0.212	-0.060	0.024	0.103	0.301	-1.274	0.607	1.431	-0.068	-0.185
	P	0.022	0.346	-0.117	0.000	0.105	-0.005	-0.009	-0.004	0.078	0.074	-0.230	0.026	-0.326	-0.062	-0.103
Leaf width	G	0.007	0.410	0.477	-0.004	0.024	-0.402	0.192	0.139	-0.022	1.062	-0.533	-0.494	-0.351	-0.049	0.456**
	P	-0.017	-0.074	0.549	0.001	0.034	-0.073	0.032	0.018	-0.026	0.167	-0.103	-0.034	0.041	-0.064	0.453**
Effective tillers/ plant	G	-0.026	0.029	0.004	-0.505	0.820	-0.110	0.118	0.271	0.009	3.904	-3.043	-0.852	-0.158	0.025	0.486**
	P	0.036	-0.003	0.008	0.042	0.332	-0.027	0.014	0.033	0.007	0.570	-0.577	-0.053	0.020	0.036	0.439**
Spikes/plant	G	-0.027	-0.176	0.009	-0.320	1.297	-0.016	0.040	0.102	0.025	5.602	-5.691	-0.466	0.043	0.028	0.451**
	P	0.031	0.062	0.032	0.024	0.583	-0.032	0.007	0.011	0.016	0.860	-1.115	-0.035	-0.050	0.060	0.453**
Weight of spike	G	-0.003	0.325	0.200	-0.058	0.021	-0.958	0.483	0.636	-0.090	3.073	-2.195	-0.846	-0.414	-0.015	0.159
	P	-0.020	0.009	0.217	0.006	0.101	-0.183	0.063	0.064	-0.087	0.406	-0.324	-0.057	-0.045	0.033	0.185
Weight of seeds/ spike	G	-0.002	0.196	0.203	-0.132	0.115	-1.022	0.453	0.449	-0.093	3.146	-1.757	-1.127	-0.167	-0.003	0.258*
	P	0.001	-0.039	0.210	0.007	0.045	-0.137	0.085	0.058	-0.084	0.440	-0.324	-0.065	0.028	0.004	0.229
Spike length	G	-0.054	-0.038	0.071	-0.147	0.142	-0.656	0.219	0.929	-0.033	1.390	-1.346	-0.236	0.005	0.013	0.260*
	P	0.059	-0.008	0.062	0.009	0.039	-0.074	0.031	0.159	-0.026	0.200	-0.244	-0.017	0.023	0.002	0.216
Test weight	G	0.005	0.768	0.054	0.023	-0.165	-0.438	0.214	0.156	-0.197	0.606	0.327	-0.689	-0.792	0.038	-0.090
	P	-0.011	-0.133	0.069	-0.001	-0.047	-0.078	0.035	0.021	-0.203	0.109	0.072	-0.050	0.090	0.071	-0.056
Seed yield/plant	G	-0.019	-0.073	0.083	-0.323	1.190	-0.483	0.233	0.212	-0.020	6.104	-5.647	-0.822	-0.004	0.026	0.458**
	P	0.031	0.026	0.093	0.024	0.508	-0.075	0.038	0.032	-0.022	0.988	-1.150	-0.064	-0.017	0.043	0.454**
Biological yield/ plant	G	-0.034	-0.311	0.042	-0.255	1.224	-0.349	0.132	0.208	0.011	5.721	-6.026	-0.315	0.272	0.010	0.329**
	P	0.067	0.063	0.045	0.019	0.516	-0.047	0.022	0.031	0.012	0.902	-1.259	-0.017	-0.043	0.009	0.319*
Harvest index	G	0.027	0.570	0.150	-0.275	0.386	-0.517	0.326	0.140	-0.087	3.203	-1.212	-1.567	-0.694	0.039	0.488**
	P	-0.067	-0.073	0.155	0.018	0.170	-0.086	0.045	0.023	-0.084	0.519	-0.178	-0.121	0.055	0.072	0.446**
Days to maturity	G	-0.021	-1.497	-0.119	0.057	0.040	0.282	-0.054	0.004	0.111	-0.015	-1.167	0.773	1.407	-0.093	-0.293*
	P	0.014	0.332	-0.067	-0.002	0.086	-0.024	-0.007	-0.011	0.054	0.049	-0.160	0.019	-0.340	-0.051	-0.108
Swelling factor	G	0.034	0.342	-0.080	-0.043	0.126	0.048	-0.005	0.040	-0.025	0.536	-0.208	-0.208	-0.449	0.293	0.401**
	P	-0.060	-0.047	-0.076	0.003	0.076	-0.013	0.001	0.001	-0.031	0.092	-0.025	-0.019	0.038	0.461	0.402**

Residual effect R_g= 0.198 and R_p= 0.257 at genotypic level and phenotypic level, respectively; *,**: Significant at 5% and 1% level of significance, respectively

relative importance of each trait. The results suggested that improvement of husk recovery is directly influenced by seed yield/plant, biological yield/plant, harvest index, spikes/plant, leaf width and swelling factor and selection of these traits might have good impact on husk recovery. Among all these traits seed yield/plant has maximum positive and significant direct effect on husk recovery. Earlier, Qingyu (1992) has also reported highly significant direct effect of seed yield/plant on husk content in sunflower. It is quite evident that the positive direct effect of seed yield/plant on husk recovery was mainly due to spikes/plant. Therefore, seed yield/plant and spikes/plant instead of many selection criteria should firstly be used in selection to increase the husk recovery in isabgol breeding programmes.

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SHORT COMMUNICATION

Suitability of Barley Varieties for Cultivation in Transitional Plain of Luni Basin of Rajasthan

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A total of 11 barley varieties were evaluated under irrigated normal soil and water situation for three years at Agricultural Research Station, Keshwana, Jalore. Sowing was done on November 19th, 29th and 19th in 2009, 2010 and 2011, respectively. Differences among varieties were found statistically significant for grain and biological yield. The maximum grain yield of 62.13 q/ha was provided by RD-2035, followed by RD-2508 and RD-2715 with the grain yield of 59.73 and 59.48 q/ha, respectively. RD-2035 produced maximum biological yield followed by RD-2592, RD-2552 and RD-2660 with 151.03, 144.70 and 144.63 q/ha, respectively. RD-2508 has the maximum test weight of 42.62 g followed by RD-2715 and RD-2552 with 42.25 and 41.42 g, respectively. Therefore, barley varieties RD-2035, RD-2508 and RD-2715 may be cultivated for realising the higher productivity under timely sown conditions of irrigated normal soil and water situation in Transitional Plain of Luni Basin of Rajasthan.

Key Words: Barley, Grain yield, Irrigated situation, Varieties

Introduction

Barley (*Hordeum vulgare* L.) belonging to Family Poaceae, is an important cereal crop of India cultivated widely under cool and dry weather conditions. It is used as food grain, raw material in beverage industries and fodder for animals (Verma *et al*., 2005). Chapattis of mixed flour of barley, wheat and gram are highly palatable and digestible; and beneficial for human health particularly stomach ailment. In the modern time, it is popularly being preferred as medicinal food in urinary as well as diabetes problems (Verma *et al*., 2005). In India, barley productivity witnessed significant increase during last 50 years after the development of high yielding varieties, improved crop management practices, enhanced irrigation facilities, use of fertilizers, bio-regulators and plant protection chemicals, farm machinery and implements, *etc.*

In western Rajasthan, barley is cultivated under three situations *viz*., normal irrigated soil and water, problematic irrigated soil and water, and conserved moisture in low lying areas locally known as'*Sewaj*' cultivation. The high temperature stress coupled with moisture stress during grain filling and development stage is now being faced a common problem in western Rajasthan, which is proving detrimental to the productivity of most of the *rabi* crops. Tingle *et al*. (1970) reported that under high temperature conditions, the fertility of the spikelet declines, and if it coincides with grain development, reduces the length of the grain filling period considerably in wheat (Saini and Dadhwal, 1986), which ultimately results in low yield (Al-Khatib and Paulsen 1984; Ruwali *et al*., 1988; Viswanathan and Khanna-Chopra 2001). Low humidity accompanied by high temperature, causes high evaporation and quick drying of soil (Ruwali and Prasad 1991; Aggarwal and Sinha 1984).

Under such adverse growing conditions, selection of suitable varieties for different situations and their seed availability to farmers attain paramount importance in harnessing the potential yield besides better crop management practices. Barley improvement programme is successfully developing high potential varieties for different agro-ecological situations of India. Besides that State Agricultural Universities (SAUs) are also developing many potential varieties for cultivation of their own states. But despite of the availability of newly developed high potential varieties, many of the old varieties are still occupying large area under cultivation due to poor extension and weak seed production and distribution system. In case of barley these obsolete varieties are characterised by their low yield and disease susceptibility and, therefore, there is an urgent need to

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replace them (Ortiz-Ferrara *et al.*, 2007) with newly developed high potential varieties for better production and profitability, and to maintain varietal diversity for sustainability of the system.

Hence, keeping the current requirement in view, a field trial on evaluation of barley varieties was conducted with the aim to find out high yielding varieties for timely sown conditions of irrigated normal soil and water situation in Transitional Plain of Luni Basin (Zone IIb) of Rajasthan.

Materials and Methods

The experiment has been conducted for three years (2009-10 to 2011-12) at Agricultural Research Station, Keshwana, Jalore. The site is situated at latitude of 25º22'N and longitude of 72º 58'E, elevation 162 msl and has a tropical arid climate with mean annual rainfall of 421 mm. Soil at the site was clay loam slightly saline in reaction (pH 8.7), low in organic carbon (0.23 %) and Fe (1.9 µg/g), high in available P (97 kg/ha) and K (339 kg/ha) and normal in Zn (0.65 µg/g), Cu (0.66 µg/g) and Mn (5 µg/g). The pH and EC of irrigation water was 7.7 and 1.0, respectively.

A total of 11 released and notified varieties were tested in a Randomised Block Design with 3 replications under irrigated situation. Sowing was done on November 19th, 29th and 19th in 2009, 2010 and 2011, respectively accommodating 4 m long 10 rows per plot at 22.50 cm row distance with standard seed rate of 100 kg/ha. A fertilizer dose of 80 kg N, 40 kg P and 30 kg /ha was applied to the crop. A half dose of N and full dose of P and K were applied at the time of sowing, in the form of urea, DAP and MoP. The remaining half dose of the N was top dressed in the form of urea in two splits at the time of first and second irrigation. Foliar spray of zinc sulphate 0.2% at tillering stage, 1% soluble NPK (19:19:19) at flowering stage and thiourea 500 ppm at grain development stage were also applied to the crop for harvesting the higher yield. Total six flood irrigations, each of about 6 cm depth were applied as per the requirement of the crop. Two hand weeding were also carried out at 25 and 45 days after sowing to have the crop free from weeds. Data recorded for biological yield and grain yield for 3 years and test weight in third year only were analysed using standard analysis of variance (ANOVA) technique through Excel software of Microsoft Office.

Results and Discussion

Differences among barley varieties for grain yield were found statistically significant. Variety-wise average grain yield ranged between 47.80 q/ha to 62.13 q/ha with the overall average of 55.29 q/ha. The maximum grain yield of 62.13 q/ha was provided by RD-2035, followed by RD-2508 and RD-2715 with the grain yield of 59.73 and 59.48 q/ha, respectively. The lowest grain yield was provided by variety RD-2668. Kaur *et al.* (2009) and Pal and Kumar (2009) also reported significant differences among barley genotypes evaluated for dual purpose cultivation. Year wise grain yield ranged between 41.12 q/ha to 67.62 q/ha, which may be attributed due to change in the environmental and climatic conditions over the years.

Differences among varieties for biological yield were also found statistically significant. Variety-wise average biological yield ranged between 124.29 q/ha to 156.51 q/ha with the over all average of 135.99 q/ha. The maximum biological yield was provided by RD-2035, followed by RD-2592, RD-2552 and RD-2660 with 151.03, 144.70 and 144.63 q/ha, respectively. The lowest biological yield was provided by variety RD-2508. Year-wise biological yield ranged between 103.33 q/ha to 173.05 q/ha. The difference in the biological yield over the years may be attributed due to change in the environmental and climatic conditions.

One thousand grain weight of barley varieties recorded in third year only ranged between 36.89 to 42.62 g with the overall average of 39.77 g. The maximum test weight was provided by RD-2508, followed by RD-2715 and RD-2552 with 42.25 and 41.42 g, respectively, however, minimum test weight was found in variety RD-2660.

Barley varieties have a wide range of variability in grain yield, biological yield and 1000 grain weight. Grain and biological yield of barley were also varied considerably under different growing seasons and sowing dates. Therefore, most promising and appropriate varieties of barley *viz.,* RD-2035, RD-2508 and RD-2715 should be sown around mid November for realising the higher

Table 1. Grain and biological yield of barley varieties under irrigated situation

Varieties	Grain yield (q/ha)				Biological yield (q/ha)				1000-grain wt. (g)
	2011-12	2010-11	2009-10	Mean	2011-12	2010-11	2009-10	Mean	
RD 2503	64.33	43.78	46.62	51.58	154.10	106.83	112.50	124.48	39.90
RD 2508	66.33	49.54	63.33	59.73	133.37	100.00	139.50	124.29	42.62
RD 2035	69.70	48.09	68.60	62.13	200.17	114.68	154.67	156.51	39.31
RD 2052	62.57	36.60	56.53	51.90	172.47	90.13	125.33	129.31	40.27
RD 2552	70.50	36.35	60.53	55.79	193.17	104.60	136.33	144.70	41.42
RD 2592	70.73	37.93	63.29	57.32	191.20	108.15	153.73	151.03	39.17
RD 2624	64.33	35.40	51.47	50.40	158.67	99.33	123.40	127.13	39.22
RD 2660	71.10	34.55	60.40	55.35	206.13	92.42	135.33	144.63	36.89
RD 2668	66.17	36.97	40.27	47.80	204.63	102.58	103.00	136.74	39.53
RD 2715	73.83	47.87	56.73	59.48	143.17	108.62	133.67	128.49	42.25
PL 751	64.17	45.18	60.73	56.69	146.47	109.33	130.17	128.66	36.92
Mean	67.62	41.12	57.14	55.29	173.05	103.33	131.60	135.99	39.77
SEm±	1.59	1.65	5.46	-	6.07	4.83	9.31	-	-
CD (p=0.05)	4.68	4.81	16.10	-	17.91	14.08	27.48	-	-
CV (%)	4.06	7.12	16.54	-	6.08	8.23	12.26	-	-

yield under irrigated normal soil and water situation in Transitional Plain of Luni Basin of Rajasthan.

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SHORT COMMUNICATION

Varietal Identification of Four Rice Varieties from Chhattisgarh through DUS Characterization

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Rice is an important food crop in India and highest number of rice varieties have been released in India, among crop species, to cater the needs of the farmers and consumers. Assessment of genetic variation is an essential component in genotypes characterization and conservation. Continued usage of morphological data to describe cultivars indicates that these retain popularity in descriptors till date (Pauksens, 1975). Morphological descriptors provide unique identification of cultivated varieties but they not only reflect the genetic constitution of the cultivar but also the environmental interaction within which it is expressed. The basic objective of varietal characterization is to test the occurrence of traits that helps in identifying a particular variety. Keeping this in view, the study was taken up with the objective to determine the relative extent of distinctiveness, uniformity and stability of different morphological DUS descriptors in 4 rice varieties for their protection under the PPV&FR Act, because DUS data have not been available at the time of release.

The experimental material consisted of four rice varieties namely, Karmamahsuri, Danteshwari, Samleshwari and Mahamaya released by Indira Gandhi Vishwavidhyalaya (IGKV), Raipur. The trials were conducted during the two *kharif* seasons of 2011 and 2012 in randomized block design with three replications. Each replication consisted of three rows of 6 m length with 30 cm X 20 cm spacing. The observations were recorded on 30 of the 62 DUS characters at specified stages of crop growth period when characteristics under study had full expression (DRR 2002). Among the 30 morphological characteristics studied, 27 where visually assessed and three were measured. Similarity matrix was generated using the SimQual programme NTSYS-pc software version 2.02 (Rohlf, 1998). The similarity coefficients were used for cluster analysis and dendrogram was constructed by Unweighted Pair-Group Method with Arithmetic Average (UPGMA) (Mathew *et al.*, 2000).

The various morphological traits recorded among rice genotypes are furnished in Table 1. The basal leaf sheath colour for the rice varieties varied from green to light purple in colour. Varieties Karmamahsuri, Danteshwari and Samleshwari had green basal leaf sheath colour, while Mahamaya exhibited as light purple. The intensity of green colour in leaf ranged from medium green to dark green in these varieties. Varieties Danteshwari, Samleshwari and Mahamaya had intensity of colour in leaf as medium green while, it was recorded as dark green in Karmamahsuri.

The anthocyanin colouration of leaf was absent in all the varieties. The pubescence of leaf blade surface was found to be weak in Danteshwari; medium in Samleshwari and it was strong in Karmamahsuri and Mahamaya. Leaf auricles were colourless in three varieties *viz.,* Karmamahsuri, Danteshwari and Samleshwari while, it was purple in Mahamaya. Anthocyanin colouration of collar was found absent in all the genotype except Mahamaya. Colour of ligule also showed variation and found to be white in Karmamahsuri, Danteshwari and Samleshwari while, it was light purple in Mahamaya. The leaf length of blade was noted as short for Danteshwari; medium for Karmamahsuri; long for Samleshwari and Mahamaya. The early observation for attitude of flag leaf revealed erectness in Danteshwari, Samleshwari and Mahamaya whereas, attitude was semi-erect in Karmamahsuri. However, the late observation on flag leaf attitude revealed that Danteshwari, Samleshwari and Mahamaya remained as erect while, Karmamahsuri showed horizontal attitude. The stigma colour was found to be white in three varieties *viz.,* Karmamahsuri, Danteshwari and Samleshwari whereas, it was purple in Mahamaya. The colour of tip of lemma appeared

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Table 1. Morphological characters of rice varieties based on DUS descriptor

S. No.	Character	Varieties			
		Karma-masuri	Dantesh-wari	Samlesh-wari	Maha-maya
1	Basal leaf sheath colour	1	1	1	2
2	Leaf: intensity of green colour	7	5	5	5
3	Leaf: anthocyanin colouration	1	1	1	1
4	Leaf: pubescence of blade surface	7	3	5	7
5	Leaf: auricles	9	9	9	9
6	Leaf: anthocyanin colouration of auricles	1	1	1	3
7	Leaf: collar	9	9	9	9
8	Leaf: anthocyanin colouration of collar	1	1	1	9
9	Leaf: ligule	9	9	9	9
10	Leaf: colour of ligule	1	1	1	2
11	Leaf length of blade	5	3	7	7
12	Leaf: width of blade	5	5	5	5
13	Culm: attitude	3	3	3	3
14	Fag leaf attitude of blade (early observation)	3	1	1	1
15	Lemma: anthocyanin colouration of area below apex	1	1	1	1
16	Spikelet: colour of stigma	1	1	1	5
17	Stem: anthocyanin colouration of nodes	1	1	1	1
18	Stem: anthocyanin colouration of internodes	1	1	1	1
19	Fag leaf attitude of blade (late observation)	5	1	1	1
20	Spikelet: colour of tip of lemma	3	2	2	5
21	Panicle: awns	1	1	1	1
22	Panicle: presence of secondary branching	1	1	1	1
23	Panicle: secondary branching	2	2	2	2
24	Panicle: exsertion	7	7	7	7
25	Panicle: curvature of main axis	7	7	7	7
26	Sterile lemma colour	2	1	1	1
27	Time of maturity (days)	5	3	3	5
28	Grain: weight of 1000 fully developed grains	5	5	5	9
29	Grain: length	3	5	3	3
30	Grain: width	3	3	5	7

yellowish for Danteshwari and Samleshwari; brown for Karmamahsuri; and purple for Mahamaya. Based on days to maturity, the varieties were grouped as early *viz.,* Danteshwari, Samleshwari and Mahamaya and medium *viz.,* Karmamahsuri. Based on 1000 grain weight, Karmamahsuri, Danteshwari and Samleshwari had medium test weight while, Mahamaya had it very high. Based on grain length Karmamahsuri, Samleshwari and Mahamaya had short grain length whereas, Danteshwari had medium length. The grain width was narrow in Karmamahsuri and Danteshwari, whereas, it was medium in Samleshwari and broad in Mahamaya.

Observations for 30 morphological traits taken on ten randomly selected plants in four varieties indicated that 16 traits showed a moderate range of variation *viz.,* Basal leaf sheath colour, leaf: intensity of green colour, Leaf: pubescence of blade surface, Leaf: anthocyanin colouration of auricles, Leaf: anthocyanin colouration of collar, leaf: colour of ligule, leaf: length of blade, flag leaf attitude of blade (early and late observation), spikelet: colour of stigma, spikelet: colour of tip of lemma, sterile lemma colour, time of maturity, grain: weight of 1000 fully developed grains, grain: length, grain: width. Among the traits exhibiting variation, most of the genotypes possessed a particular variant phenotype. Karmamahsuri can be identified by the characters such as intensity of green colour of leaf, pubescence of blade surface, length of leaf blade, flag leaf attitude, colour of tip of lemma, lemma colour, days to maturity and grain width. Like-wise, Danteshwari can be detected by pubescence of blade surface, length of leaf blade, days to maturity and grain length. Whereas characters like pubescence of blade surface, length of leaf blade, and grain width can be used to identify Samleshwari. while, Mahamaya can be distinguished on the basis of basal leaf sheath colour, anthocyanin colouration of auricles, anthocyanin colouration of collar, colour of stigma, colour of tip of lemma, 1000-seed weight and grain width. UPGMA cluster analysis was performed using SM similarity coefficient matrices calculated from morphological data to generate a dendrogram for four varieties (Fig. 1). The varieties were grouped into two major clusters. The similarity coefficient ranged from 0.62 to 0.87. In pair-wise comparison, the maximum similarity was obtained between Danteshwari and Samleshwari with a similarity index of 0.86, whereas Mahamaya showed least similarity with other varieties (similarity index 0.62). Cluster I consisted of variety namely Karmamahsuri,

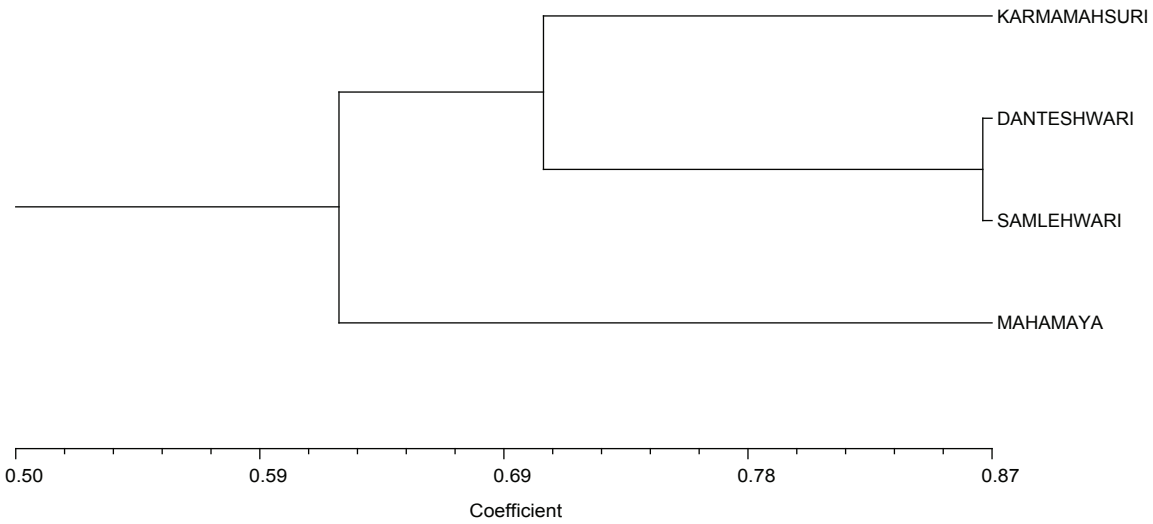

Fig. 1: Dendrogram of rice varieties based on morphological characters

Danteshwari and Samleshwari having 71% similarity whereas, Cluster II consisted of Mahamaya having 62% similarity among them. Cluster I again partitioned into two sub-clusters in which one sub- cluster had Danteshwari and Samleshwari with 87% similarity, whereas another sub- cluster had Karmamahsuri with 71% similarity with Danteshwari and Samleshwari. The basic objective of varietal characterization is to test the occurrence of traits that helps in identifying a particular variety. The characters that are used to distinguish cultivars should have the ability of precise description and recognition and is considered important only when they are not subjected to environmental influences. Thus, the ability to identify and distinguish between varieties is a fundamental component in seed quality programmes. This also benefits the seed production and certification authorities as well as the farmers in ensuring supply and distribution of genetically pure seeds. The morphological dendrogram generated from similarity or genetic distance matrices has provided an overall pattern of variation as well as the degree of relatedness among genotypes. It may be concluded that the morphological DUS descriptors can be effectively used for identification and grouping of varieties. However, morphological descriptors alone may not be sufficient for DUS criteria. Hence, some other markers/ descriptors based on DNA (Simple Sequence Repeat) and protein (SDS-PAGE) markers could be considered for complementing the morphological DUS descriptors.

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SHORT COMMUNICATION

Cabbage: A Rich Natural Supplement of Iodine

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Iodine is one of the most important trace elements in our body and it's deficiency causes a number of dreaded diseases like goiter, mental retardation, hypothyroidism and pregnancy-related problems. Iodine is not synthesized in our body, so it is always recommended to include iodine-rich food in our diet. Cabbage is an important source of iodine. A study was conducted to estimate the iodine concentration in 17 hybrids of cabbage under middle hill conditions of Uttarakhand. Hybrid Varun exhibited highest iodine concentration (7.41µg/100g) followed by CH-2200 (6.41µg/100g). The objective of the present work was to find out iodine-rich hybrids of cabbage, so that they can be used as a supplement of iodine.

Key Words: Cabbage (*Brassica oleracea*), Hybrids, Iodine supplement

Cabbage (*Brassica oleracea* var. *capitata*) is one of the important sources for supplementing iodine in the body (Key *et al*., 1992; Appleby *et al*., 1999). It belongs to cruciferous or mustard family. It is grown for the thickened main bud called head. This vegetable is full of nutrients and is low in calories. It is a rich source of some important elements like calcium, iron, iodine, potassium, sulphur and phosphorus. It is also loaded with a number of vitamins *viz*., A, B_1, B_2, B_6, C, E, K and folic acid. Cabbage is the cheapest and richest source of iodine and thus aids in the proper functioning of brain and nervous system. Iodine is necessary for the synthesis of thyroxin hormone. Goitrogenic compounds found in cabbage can affect the thyroid gland and slow-down hormone production. Fortunately, these goitrogenic compounds in cabbage are destroyed by heat. Cooking the vegetable properly will ensure that they do not affect the functioning of thyroid (Salunkhe and Kadam, 1998).

Owing to the importance of iodine (µg/100g) in human diet and cabbage being one of the important sources, 17 hybrids (Table 1) were selected for iodine estimation using Arsenic-cerium Redox method (Brown and Hutchinson, 1949).The work was carried out at Defence Institute of Bio Energy Research, Field Station, Pithoragarh. The hybrid samples were collected from different public and private seed companies and grown in open field in a randomized block design in three replications in the year 2011-12. The nursery was sown in 30 August, 2011 and seedlings were transplanted on 26 September, 2011. Net plot size was 6 m^2, spaced 50 cm between rows and plants apart. The observations were recorded on various horticultural and quality traits. The marketable heads were selected for iodine estimation on dry weight basis in three replications. Head of each hybrid was cut into small pieces, oven dried at 40°C and then ground to make fine powder. Iodine estimation was based on the principal of quantitative determination of micro amounts of iodine on catalytic reduction of microelements ceric (Ce^{+4}) to cerous (Ce^{+3}) by iodine. A suitable amount of dried sample (usually containing 0.04-0.08 µg of the iodine) was taken in a Pyrex test tube (15 x 125 mm). After digestion, incineration and extraction, the reduction of ceric to cerous is read in a spectrophotometer at 420 nm. Standard solution of KI (Potassium Iodide) containing 0.0-0.16 µg of iodine was run simultaneously. A straight line response is obtained by plotting concentration of iodine in µg against reading on spectrophotometer. Using this standard graph, the value for any sample was read. Data were recorded and analyzed statistically (Gomez and Gomez, 1984).

The iodine content of different cabbage hybrids is presented in Table 1. There were significant differences in the iodine content among the hybrids grown under mid-hill conditions of Uttarakhand Himalayas. The concentration range and mean of 17 samples were 1.60-7.41 and 4.55, respectively. Hybrid Varun exhibited highest iodine content (7.41 µg/100 g) followed by CH-2200 (6.41 µg/100 g) and Green Flash (6.40 µg/100 g). Iodine content of irrigated water and the soil, in which hybrids were planted, was also estimated at 1.23 µg/100 g and 5.59 µg/100 g (mean values), respectively. Iodine concentration

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Table 1. Iodine concentration in cabbage hybrids

Cabbage hybrids	Iodine (µg/100g)
Cabbage hy 1	5.34
Cabbage hy 2	2.73
Cabbage hy 3	4.29
Cabbage hy 4	1.75
Cabbage hy 5	4.51
Cabbage hy 6	4.95
Quisto	4.78
Kranti	3.33
DARL 802	4.00
DARL 801	5.80
CH 21	5.94
Green Flash	6.40
SIR	6.20
CH 2200	6.41
Speed 50	2.91
Krishna	1.60
Varun	7.41
CD @ 1%	1.629
CD @ 5%	1.211
CV%	15.997
SEM	0.420

in water and soil reflects the environmental iodine distribution and is also an important index of natural iodine intake by human beings. Iodine content of the plant is related to it's concentration in the soil as water taken up by plants gets evaporated from the leaves leaving behind iodine in the leaves. Since cabbage consists of leaves, the water lost through transpiration leads to iodine becomimg concentrated in the leaves. The range of iodine content in water, soil and cabbage in hill region was 1.10-1.36 µg/100 ml, 3.46-7.72 µg/100g and 1.59-7.41 µg/100 g respectively.

Food, soil and water are necessary for life and have a profound influence on human beings. Iodine has long been recognized as an essential micronutrient for human and livestock. The most common cause of iodine deficiency is the intake of iodine-deficient food. Besides many iodine supplements available in the market, cabbage can be one of the cheapest and richest source of iodine. The productivity of cabbage is much higher; with a yield potential of 500-600 q/ha especially if it is grown from hybrid seeds. Increased production through use of hybrid seeds can contribute towards global nutritional security.

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SHORT COMMUNICATION

Genetic Variability for Morphological Characters and Glycosides in Stevia *(Stevia rebaudiana* Bertoni)

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Morphological and stevioside parameters in three diverse genotypes (GVS-6, HPSR and MPSR) of *Stevia rebaudiana* were studied under hot and semi- humid climatic conditions of Nagpur, for three years (2008 -2010). The cultivar GVS-6 was identified as most promising for high stevioside content and biomass yield. The variations in morphological parameters of stevia cultivars were significant. Pooled results revealed that cultivar GVS-6 has optimum plant height (36.4 cm) with highest branches (14 number) and leaves (199.9 number), higher total dry biomass yield per plant (126.0 g) and stevioside (49.8%). High biomass production and stevioside content in a variety of stevia is very important for economic valuation in agriculture and medicinal aspects.

Key Words: Glycoside, Morphological characters, *Stevia rebaudiana*, Stevioside

Stevia (*Stevia rebaudiana* Bertoni) 2n = 2x = 22, is a herbaceous perennial belonging to Asteraceae and being a zero calorie sweetener, has many medicinal properties. It is believed to have originated in the high land regions of north-eastern Paraguay (on the Brazilian border) and is widely distributed in USA, Brazil, Japan, China and Korea. Stevia grows in semi-humid and sub-tropical region, like any other vegetative crop. Stevioside, the sweetener, extracted from the plants is 300 times sweeter than sugar and is used as a natural alternative to artificial sweetener (Megeji *et al.,* 2005). In the past, studies on stevia have been confined mainly to the biochemical constituents and very little information is available so far about the extent of variability for various morphological and biochemical traits under semi-arid climate. Hence, the present investigation was undertaken to study the variability for important morphological traits alongwith stevioside content in three diverse genotypes collected from Garshankar, Punjab (GVS-6), Palampur, Himachal Pradesh (HPSR) and Mohankheda, Madhya Pradesh (MPSR).

Above genotypes were established in 30 pots (10 pots of each genotype) in green house of Botany Department, Rashtrasant Tukadoji Maharaj Nagpur University, Nagpur, during September 2007. Three genotypes were replicated 10 times using RBD for statistical analysis to evaluate treatments difference. Observations were recorded for the first cuttings in February of each year for various parameters like vegetative growth, biomass yield and steviol glycoside (stevioside) content. Fertilizer and water management was done as per package of practices. No chemical spray was used on stevia plants. The powder prepared from dried leaves of composite sample of each stevia genotype was subjected to chemical analysis by HPLC method. The Cecil Adept 4201 system was used for the analysis of stevioside content.

Data on morphological parameters, glycoside and stevioside content in stevia, presented in Table 1, is the mean of data for three years. Pooled results revealed that the variation in morphological characters was significant. Maximum plant height (52.8 cm) was observed in variety HPSR followed by MPSR (44.1 cm) and GVS-6 (42.6 cm). Maximum number of branches and leaves per plant (13.3 and 199.6, respectively) were observed in GVS-6 followed by MPSR (7.0 and 156.8, respectively) while HPSR variety showed few branches (5.0) and leaves (114.3) with large leaf (5.7 cm) (Plate 1). Highest dry leaf biomass (96.6 g) was recorded in GVS-6 and lowest (80.5 g) in MPSR while dry stem biomass was maximum (33.5 g) in HPSR (Table 1). Further study revealed that the fresh and dry biomass of stem and leaf were more variable than plant height at first cutting's observation. These findings are in agreement with the findings of Shyu *et al.* (1994) and Chalapathi *et al.* (1998). Total biomass

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Table 1. Morphological characteristics and stevioside of different genotypes of *Stevia rebaudiana*

Characters	GVS-6	HPSR	MPSR	CV	CD at 5%
Plant height (cm)	42.6	52.8	44.0	21.10	7.43
Branches per plant	13.3	5.0	7.0	35.89	2.85
Leaves per plant	199.6	114.3	156.8	26.77	39.40
Days to flowering	65.5	92.9	78.3	4.93	2.16
Leaf length (cm)	3.5	5.7	3.7	2.41	1.60
Dry stem biomass / plant (g)	29.4	33.5	32.0	4.05	3.10
Dry leaf biomass/ plant(g)	96.6	90.4	80.5	4.66	4.91
*Total biomass yield/plant (g)	126.0	123.9	112.5	11.20	9.8
Leaf: Stem ratio	3.3	2.7	2.5	–	–
Total glycoside (mg/100ml)	143.9	238.2	205.5	–	–
Stevioside content (%)	49.8	42.7	45.1		

*Biomass yield: weight of leaves+ stem

yield of stevia (leaf + stem) per plant was highest in GVS-6 (126.0 g) followed by HPSR (123.9 g) and MPSR (112.5 g). Regarding days to flower, HPSR exhibited longer duration (92.9 days) than GVS-6 (65.5 days). More number of leaves and days to flowering are important traits for productivity in stevia. (Sumida, 1980; Shyu *et al.,* 1994). Maximum stevioside content was recorded in GVS-6 (49.8%) followed by MPSR (45.1%) and minimum in HPSR (42.7%). Among the three genotypes of *S. rebaudiana* evaluated in pots, highest concentration of stevioside was in GVS-6. These findings are in accordance with those of Bondarev *et al.* (2003).

The present investigations reveal that GVS-6 (from Punjab collection) is the most suitable variety for semi-arid climate due to high biomass and stevioside content and it would be preferred by the farmers and pharmaceutical industry. Hence, this variety can be utilized in future breeding programme. The demand for stevia leaves has been attracting the attention and interest of farmers who view it as a new opportunity and rich promise for a real agricultural option.

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SHORT COMMUNICATION

Risk Analysis - A Biosecurity Tool to Assess Weed Potential of a Plant

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Seeds and planting materials of different plant species are being imported into India. Many of these have the potential to become agricultural or environmental weeds and this risk needs to be assessed before allowing their entry. Weed risk assessment method was judged on its ability to correctly reject weeds and accept non-weeds. Out of 170 plants tested, a total of 40% plants were classified as serious weeds, 30% as common weeds and remaining 30 % were non weeds. The system is designed to be operated by plant quarantine officers. The weed risk assessment system with explicit scoring of biological, ecological and geographical attributes is a useful tool for detecting potentially invasive weeds in other areas of the world.

Key Words: Plant quarantine, Seeds, Score, Weed, Weed risk assessment

The implementation of New Policy on Seed Development by the Government of India has provided stimulus for the import of seeds of various crops from all over the world. This has increased the risk for the introduction of exotic weeds into India. Weeds have major impacts on economies and natural environments worldwide including India. Many of these weeds have been purposely introduced as new crops or as ornamentals. To counter the threat to agriculture or the environment from new plants, regulatory authorities have a statutory responsibility to ensure that all plants proposed to be imported, which are not already established, be evaluated for their potential to damage the productive capacity or environment of the country. Quarantine in India officially came into operation with the passing of the Destructive Insects and Pests Act (DIP Act) in 1914. Plant Quarantine (Regulation of Import into India) Order 2003, of the Destructive Insects and Pests Act (1914) provides a legislative framework for the application of measures to prevent the introduction or spread of insect-pests and diseases affecting plants. Effective plant quarantine is important for the protection of the biodiversity of the natural environment and agricultural productivity. Infestation of agricultural system has the potential not only to incur costs in controlling pests and losses in production, but also to restrict access to export markets, if the pest has the potential to contaminate the marketable product. There are many approaches to predicting weed potential (Mack, 1996), but there is an urgent need of an objective, credible and publicly acceptable risk assessment system to predict the weediness of the new plant introductions.

An acceptable weed risk assessment system should satisfy a number of requirements. It should be calibrated and validated against a large number of plants already present in the recipient country and representing the full spectrum of plants likely to be encountered as imports into that country. It must discriminate between weeds and non-weeds, such that the majority of weeds are not accepted, non-weeds are not rejected, and the proportion of plants requiring further evaluation is kept to a minimum. As international trade agreements require that prohibited plant should fit in the definition of a quarantine pest before they can be excluded by quarantine regulations (Singh *et al*., 2005), the system must be passed on explicit assumption and scientific principles so that country cannot be accused of applying unjustified non-tariff trade barriers. Ideally the system should be capable of identifying which land use system the plant is likely to invade, to assist in an economic evaluation of its potential impacts. Finally, the system must be cost effective. This Weed Risk Assessment (WRA) system for

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India is designed in consultation with the weed scientists of Australia during the first author's advanced training at the University of Queensland, Brisbane, Australia.

The WRA system is designed to run on Microsoft Excel 2007 and it may be run on a Windows. The basis of the WRA is the answers to 49 questions based on the main attributes and impacts of weeds. These are combined into scoring system which in the absence of any evidence to the contrary, gives an equal weightage to nearly all questions. These cover a range of weedy attributes in order to screen for plants that are likely to become weeds of an environment and /or agriculture. The questions are divided into three sections producing identifiable scores that contribute to the total score. Most questions are answered, as yes, no or don't know.

Biogeography consists the documented distribution, climate preferences, history of cultivation, and weediness of a plant elsewhere in the world, i.e. apart from the proposed recipient country. Weediness elsewhere is a good predictor of a plant becoming a weed in new areas with similar environmental conditions (Forcella and Wood, 1984). The questions concerning the history of cultivation recognizes the important human component of propagule pressure (Williamson and Fitter, 1996), but such data are obviously never available for the proposed new country. The global distribution and climate preferences, where these are available, are used to predict a potential distribution in the recipient country. Undesirable attributes are characteristics such as toxic fruits and unpalatibility, or invasive behaviour, such as a climbing or smothering growth habit, or the ability to survive in dense shade. Biology/ ecology are the attributes that enable a plant to reproduce, spread and persist (Noble, 1989) such as whether the plant is wind dispersed or animal dispersed, and whether the seeds would survive through passage of an animal's gut. Availability of information is often very limited for new species which can restrain the utility of screening systems. To ensure that at least some questions were answered for each section, the WRA system requires the answer to two questions in section A, two in section B and six in section C before it will give an evaluation and recommendation. The recommendation can be compared with the number of questions answered as an indication of its reliability which obviously improves as more questions are answered.

Answers to the questions provide a potential total score ranging from -14 (benign plant) to 29 (maximum weediness) for each plant. The total score is partitioned between answers to questions considered to relate primarily to agriculture, to the environment, or common to both. The total scores are converted to one of the three possible recommendations by two critical score settings. The lower critical scores 0, separates *acceptable* plants from those requiring *evaluation*, and the higher critical score, 6, separates plants requiring *evaluation* from those that should be *rejected*. Evaluation could mean either obtaining more data or re-running the system, or undertaking further investigations such as field trails (Mack, 1996). The model was run to assess the weed potential of plants ranging from beneficial plants to serious weeds.

The answer to most of the questions in WRA is yes (y), no (n) or don't know (leave blank or?). The system translates these responses into a numerical score.

A typical score for a question is Yes=1 point, No= -1 or 0 and don't know/? =0

The questions in section's 2 and 3 (climate & weed elsewhere) of the questionnaire differ from the typical scoring in that they generate a score by a weighting system. The score given for questions 2.01 and 2.02 is used to weight the scores for 'yes' answers in the weed elsewhere questions (3.01 to 3.05). The quality of climate data greatly affects the climate match. A good climate match increases the probability that a weedy species will behave the same way in India as it does overseas. The weediness score also increases if the information used to produce the climate match is not comprehensive, due to the greater uncertainty introduced by this data.

Two other questions do not fit into the standard scoring system:

A score of 'no' for question 3.01, whether a plant has naturalized overseas, is modified by the score to question 2.05, its history of repeated export species with repeated introductions outside of their native range that have not established are a lower risk.

Questions 6.07, the minimum generative time, require the input of a numerical score. This generative time is standardized by the use of correlation factor as shown in Table.

Reproduction	Scores
< 1 to 2 years	1
Between 2 to 4 years	0
Greater than or equal to 4 years	-1

The WRA compares the total score for a species to the critical values to determine the recommendation for the species. The threshold values for the system are shown in following table.

If the plant scores less than 1	Accept the plant
If the plant scores greater than 6	Reject the plant
If the plant scores between 1 to 6	Plant requires further evaluation

The species used for the calibration of the system ranged from severe agricultural and environmental weeds to benign and beneficial plants. The WRA tallies the number of questions answered in each section. The WRA allows for a minimum number of questions in each of its three different categories. The minimum number of questions for each section is: 2 for section A, 2 for section B and 6 for section C. When using the excel spreadsheet if the minimum number of questions is not completed, a message that more information is required is posted by the system. The WRA has some capacity to suggest the type of ecosystem likely to be affected by the plant assessed. The WRA indicates if the plant is more likely to be a specific weed of agriculture or the general environment, once it has assessed the plants potential to become a weed in India. A species may be assessed to be a weed of both categories. The partitioning helps to identify areas most at risk from the characters assessed for the species. The assessment method was tested against 170 plants representing both weeds and useful plants from agriculture and environment. The method was judged on its ability to correctly reject weeds and accept non weeds. A total of 40% plants were classified as serious weeds, 30% as common weeds and remaining 30 % were non weeds (Fig. 1).

The system identifies a wide range of weeds, and does not accept plants known to be major weeds in India. By splitting the total scores the model also allows an estimate of whether the weed is more likely to impact on agricultural or natural environment systems, which may assist regulatory authorities in making a recommendation. These features suggest that the system could be altered and still be expected to produce satisfactory results in other bio-climatic regions of the globe where protocols are lacking (Ruesink *et al.,* 1995). As the system is simple and spreadsheet based it can be used by lay people who wish to import plants and it has an educational role because it shows the effect of individual questions on the total score. The system distinguishes between many useful and non useful plants, but some useful plants can be rejected. This is expected, because planned introductions

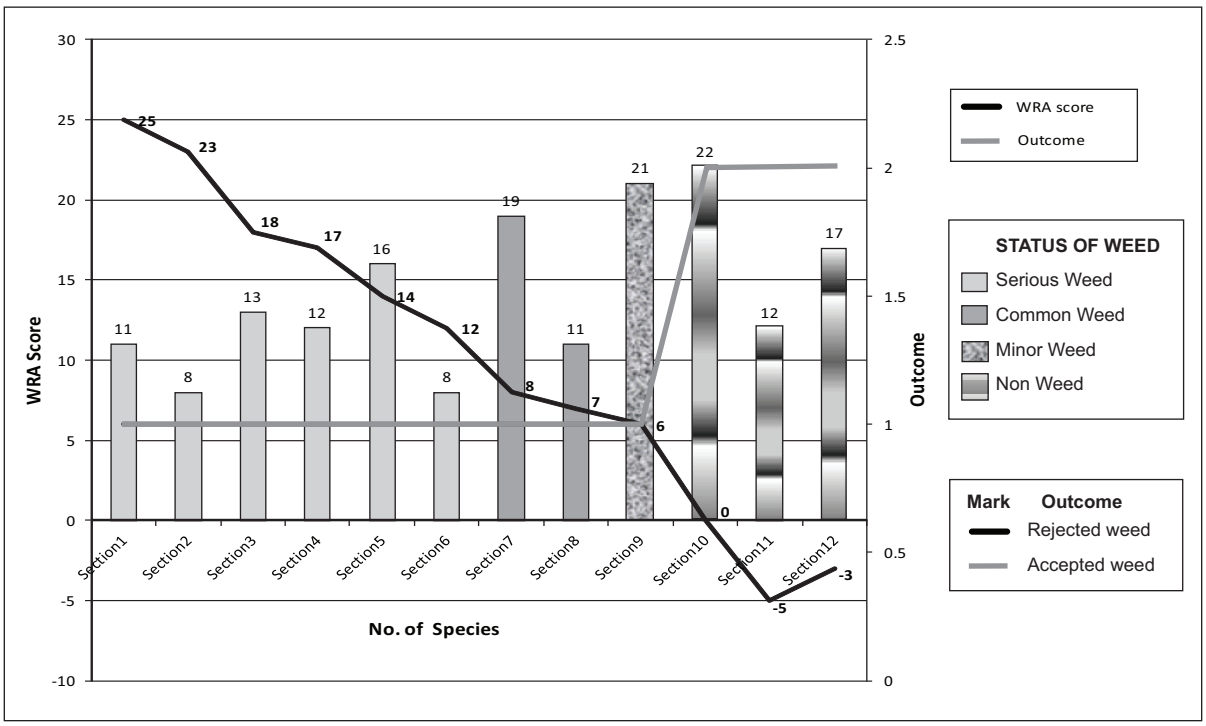

Fig. 1: Weed species assessed through WRA, their score, status and outcome

are chosen for their ability to survive (Ruesink *et al.,* 1995), and the questions asked by the system are based primarily on biological and ecological criteria which identify attributes common to both useful agricultural plants and weeds (Lonsdale, 1994). These may differ only in a small number of characteristics within any single life from (Perrins *et al.,* 1992). Where a plant may have significant economic benefits, a further evaluation of its weediness potential may include experimental studies (Williamson, 1993; Scott and Panetta, 1993). Economic value should be scored in a transparently separate exercise and balanced against weediness in appropriate risk assessment evaluations (Singh *et al*., 2005).

It is concluded that the Weed Risk Assessment System with explicit scoring of biological, ecological and geographical attributes is a useful tool for detecting potentially invasive weeds in other parts of the world and should be used in Indian Plant Quarantine to assess the plants before issue of the Import Permit.

Acknowledgement

The authors are grateful to Dr. KC Bansal, Director and Dr. PC Agarwal, Head, Plant Quarantine Division, National Bureau of Plant Genetic Resources, New Delhi for providing necessary facilities and encouragement.

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SHORT COMMUNICATION

A Note on Crinkle Leaf Virus Disease Resistant Accessions of Mothbean (*Vigna aconitifolia* (jacq.) Marechal)

Om Vir[1], AK Singh[1] and RK Tyagi[2]

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Mothbean (*Vigna aconitifolia* (Jacq.) Marechal) also known as mat bean or Turkish gram belongs to family Fabaceae and sub-family Faboideae. This arid legume, native to India, Pakistan and Myanmar, is an important pulse crop of arid and semi arid regions of India and Pakistan. The plant resembles a small mat and its height is approximately one foot. Its branches are densely mated, grow horizontally and have deeply notched leaflets on long leaf branches. The plant is generally adapted to extremes or uncongenial ecological niches particularly arid regions, receiving fewer rains with erratic distribution. The crop is generally grown in the North-Western deserts of India and Pakistan where droughts are more prevalent. It is extensively grown in Rajasthan as mixed crop with cotton, sorghum, and other pulses. The mothbean is consumed as a rich protein source (22-24 %) by the low income consumers in the rural areas and tribal belts of Rajasthan, Uttar Pradesh, Punjab, Haryana and Madhya Pradesh. It is used in several confectionary items, forming essential components of day to day snacks (Singh *et al*., 2012). Mothbean is a good source of amino acids, particularly lysine and leucine and certain vitamin, like carotene (Swaminathan, 1985). Its green fodder is at par to alfalfa and dry fodder is better than cowpea and clusterbean (Singh *et al*., 2012).

Motbean is a major arid legume and is recognized for its twin tolerance to drought and heat. It is therefore, the ultimate choice of marginal and sub marginal farmers for realization of sustained production under the extreme hostile and harsh climatic conditions. Mothbean is grown in about 12.2 lakhs hectares of area in Rajasthan, however, productivity is very low that varies from 200 to 250 kg/ha (Singh *et al*., 2012). Many constraints are responsible for low productivity including its susceptibility to a number of fungal, bacterial and viral diseases. The most common diseases of mothbean are bacterial leaf blight and leaf spot, seed rot, root rot, seedling blight, fusarium seedling rot, Choanephora pod rot, web blight, Colletotrichum leaf spot and pod infection, Myrothecium leaf spot and pod infection, Alternaria leaf spot, Curvularia leaf spot, powdery mildew, seed microflorra, witchers broom, yellow mosaic virus and leaf crinkle virus (Rathi and Punia, 2002). The crinkle virus, transmitted by white fly is the most dangerous disease and damages crop up to 90% (unpublished data). The initial symptoms of crinkle virus appears three to four weeks after sowing. The growth of plant is stunted and plants look like burnt. Leaflets curl downward with crinkling. At the time of flowering, the peduncles bear a large number of small flower buds. The sepals of the flower of infected plants become thicker and greener than normal and cover half or whole of the bud. This gives a bushy appearance to the inflorescence and pod setting is reduced (Rathi and Punia, 2002).

During *summer* 2012, 44 accessions of mothbean which were collected from different places of India were grown in a randomized complete block design with three replicates at two soil fertility levels manipulated by applying fertilizers in the soil at the time of sowing. The plot size was consisted of three rows of two meter length each. The line to line and plant to plant distances were maintained 45 and 20 cms, respectively. The same experiments were repeated during *kharif* 2012. The data were recorded on morphological traits on five randomly taken plants of middle row of the plot. The mean value of two experiments with three replicates and five plants in each replication of recorded traits are given in Table 1 for both the seasons.

The plants were severely infected by crinkle virus and out of the 44 accessions only two accessions namely IC 39786 and IC 39822 survived and rest

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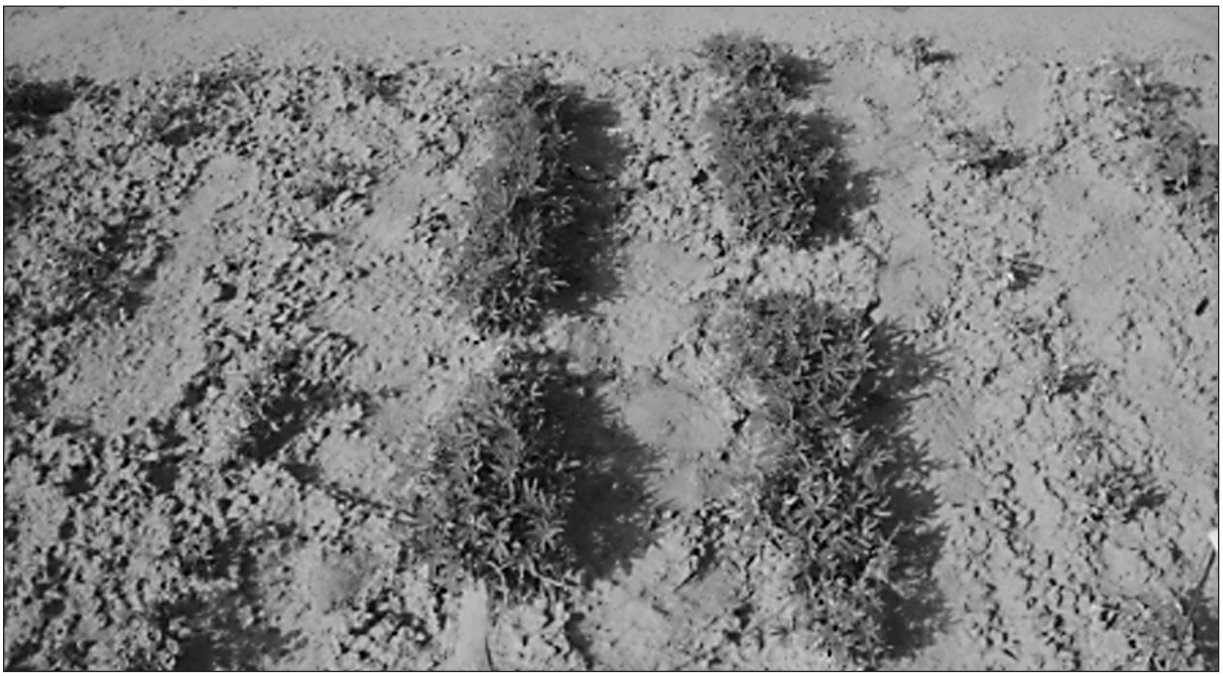

Fig. 1: Crinkle leaf virus disease resistant accession IC 39786. Other accessions seen in the picture were infected up to 90% by this disease

Table 1. Mean value of morphological traits recorded for mothbean accessions IC 39786 and IC 39822.

	Moth bean (IC 39786)		Moth bean (IC 39822)	
Traits	*Summer*	*Kharif*	*Summer*	*Kharif*
Crinkle virus grade	1 (Highly Resistant)	1 (Highly Resistant)	1 (Highly Resistant)	1 (Highly Resistant)
Early plant vigor	Good	Very good	Good	Very Good
Plant growth habit	Spreading	Spreading	Spreading	Spreading
Plant habit	Indeterminate	Indeterminate	Intermediate	Intermediate
Leaf colour	Dark green	Dark green	Green	Green
Leaf pubescence	Moderately pubescent	Moderately -pubescent	Sparsely	Sparsely
Days to 50% flowering	43	47.75	44.2	45.75
Days to maturity	60	65	60	65
Plant height (cm)	25.15	30.43	26.35	30.5
Peduncle length (cm)	3.8	4.27	3.81	4.12
Branches / plant	4.2	8.47	4.56	7.9
Clusters / branch	3.56	11.95	4.02	10.25
Clusters / plant	15.4	75.03	16.2	68.6
Pods / branch	10.6	13.67	11.75	14.75
Pods / plant	38.88	96.87	48.64	103.1
Pod length (cm)	2.55	3.4	2.81	3.52
Seeds / pod	6.0	6.47	4.6	6.3
100 seed wt. (g)	2.53	2.71	2.68	3.01
Seed yield / plant (g)	5.03	12.17	6..89	14.34

of the 42 accessions including checks namely Jadia, Jawal, RMO 40 and FMM-12-6-134 were almost wiped out (80-90% infection) by the crinkle virus (Fig.1). The disease rating was done on 1 to 9 scale being 1- highly resistant, 3- resistant, 5- moderately resistant, 7-susceptible and 9- highly susceptible (Mahajan *et al*., 2000). These two accessions scored 1 whereas other accessions scored 7 or 9. During *kharif* 2012 also these two accessions exhibited the high field resistance to this disease. Thus, mothbean accessions IC 39786 and IC 39822 possess strong genetic resistance scoring to crinkle virus disease, tested at field level. These mothbean accessions IC 39786 and IC 39822 were collected from the villages namely, Paddhar and Vallipur respectively of Vadodra district of Gujarat state on September 12, 1980 by NBPGR. Mothbean breeders may use these two genotypes in their breeding programme to incorporate crinkle leaf virus disease resistance in the high yielding varieties of mothbean.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXVIth meeting held on January 31, 2013 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of 50 germplasm lines out of which information on 19 lines is presented in this issue. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. Vaidehi 95 (MSH- 53) (IC0584260; INGR13032) Dark Brown Linted Introgressed Derivative of Cotton

V Gotmare, P Mohan, G Balasubramani, VN Waghmare, C Rodge, M Katre, BN Tule, PK Chakrabarty and KR Kranthi

Central Institute for Cotton Research, Post Bag No 2, Shankarnagar PO, Nagpur-440010, Maharashtra (E-mail: gotvp2001@yahoo.co.in)

Vaidehi-95 (MSH-53) is a multispecies introgressed reverted tetraploid genotype derived from hexaploid progenies of the cross between *Gossypium hirsutum, G. raimondii, G. barbadense* and *G. thurberi* developed at the Central Institute for Cotton Research (CICR), Nagpur It uniquely possesses dark brown naturally coloured lint. The plant has open canopy and possesses leaves with long pedicel that allow direct penetration of sunlight minimizing bollworm attack. The genotype is also highly tolerant to Jassids by virtue of being a derivative of wild species namely *G. raimondii* and *G. thurberi.* The genotype is homozygous and stable.

The National Gene Bank at CICR possesses colour *G. hirsutum* accessions of various shades like light brown, dark brown and light green. The above colour linted accessions could not be used in breeding programme due to poor fibre quality, colour instability and extremely low yield potential. However, they were preserved as novelty mutant genetic stocks by the breeders in Cotton Gene Bank. The introgressed genotype Vaidehi-95 (MSH-53) overcomes many such limitations and possess durable colour with comparatively better fibre quality traits.

Morpho-agronomic Characteristics

The plant grows to an average height of 113 cm, leaves with admeasuring 5.5- 6.5 x 4 cm, palmate, central lobe much longer, veins covered by trichomes, petiole 3.3-3.9 cm long. Inflorescences axillary, flower solitary, short pedicels, free bracteoles, covering one third of the capsule. Flowers perfect, wide spreading cream coloured petals, calyx undulated, light yellow pollen grains, oblong green bolls, four loculed when open with 9 -11 seeds per capsule and dark brown colour lint and fuzz.

Associated Characters and Cultivated Practices

1.	Yield/plant	113 (g/pl)
2.	Fibre length (2.5% span length)	20.8 mm
3.	Fibre strength (g/tex)	17.2
4.	Uniformity ratio (%)	44
5.	Micronaire value	4.1
6.	GOT	38
7.	Boll numbers per plant	50
8.	Boll weight (gm)	3.42
9.	Highly tolerant to Jassids, Bollworm and Cotton Leaf Curl Virus	

Vaidehi-95 (MSH-53) being a multispecies introgressed derivative can be used in breeding programme for development of dark brown linted promising varieties of *G. hirsutum* and intra- hirsutum colour hybrids. It could be used as a marker trait and has scope for its utility for manufacturing naturally coloured fabrics and would be economically suitable for market/ consumers. Characteristic aesthetic feature of the genotype is that initial light colour of the lint becomes darker with continued exposure to sunlight in the field. Vaidehi – 95 (MSH- 53) was tested for fastness for three years (2008, 2009 and 2010) and that resisted fading of colour during storage.

*Compiled and edited by: Anjali Kak and RK Tyagi, Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

Package of Practices

Deep ploughing of the land once in 2-3 years followed by shallow cultivations every year is recommended. Use of Pre Plant Incorporation of Di-Nitro-Aniline herbicide @ 1 kg Active Ingredient (AI) ha^{-1} can control weeds efficiently. Apply farmyard manure about 5 tonnes ha^{-1}. A basal dose of NPK 30:30:30 and top dressing with 30 kg nitrogen ha^{-1} may be given depending upon the soil fertility. The genotype responds well to higher fertilizer dose. One or two sprays with 2% DAP after flowering will boost the yield.

The seed rate of 16 -20 kg ha^{-1} is sufficient for High Density Planting System in 30 x 15 cm and will vary depending upon spacing. Under irrigated conditions narrow spacing of 90 x 20 cm keeping one plant $hill^{-1}$ may be practiced. In marginal soils, under rainfed conditions, a spacing of 60 x 30 cm will be sufficient. Early sowing is advocated for rainfed crop. Isolation of areas growing colour cotton is advocated to avoid contamination of white linted varieties. The crop matures in 145-150 days.

Vaidehi-95 (MSH-53) is tolerant to sucking pest, the insecticide spray may be given only as and when the pest population exceeds the threshold level. For control of bollworm, need based insecticide sprays may be administered.

2. NISC 40(IC0584261; INGR13033) Jassid Tolerant Compact Plant Type Introgressed Derivative of Cotton

NISC 43(IC0584262; INGR13034) Jassid Tolerant Compact Plant Type Introgressed Derivative of Cotton

NISC 44(IC0584263; INGR13035) Jassid Tolerant Compact Plant Type Introgressed Derivative of Cotton

V Gotmare, P Mohan, G Balasubramani, C Rodge, M Katre, BN Tule, PK Chakrabarty and KR Kranthi
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(E-mail: gotvp2001@yahoo.co.in)

NISC-40 and NISC-43 are introgressed derivatives of wild and cultivated cotton derived from a backcross of *Gossypium hirsutum* and *G. raimondii* to *G. hirsutum* while NISC-44 is a Multi-Species Hybrid (MSH) derivative of G. *hirsutum, G. raimondii*, *G. barbadense* and *G. thurberi*. Each of derivatives is developed from among the reverted tetraploid identified from segregating population of hexaploids of the above crosses. These genotypes are homozygous in nature and are unique for compact plant habit with high level of tolerance against jassids and bollworms. Characteristic features of three introgressed derivatives are elaborated below:

Morpho-Agronomic Characteristics

The plants grows to an average height of 70 – 84 cm (Table 1), leaves admeasuring 5.5 - 6.5 x 4 cm, palmate, central lobe much longer, veins covered by trichomes, petioles 3.0 - 3.5 cm long. Floral characteristics include axillary Inflorescences, solitary flower with short pedicels, free bracteoles, covering one third of the capsule. Flowers normal, wide spreading, cream coloured petals and pollen grains, calyx undulated, oblong shaped green boll and four loculed when open with 8 -10 seeds per capsule and seeds possess white lint and fuzz. The plant type is very compact.

Package of Practices

Deep ploughing of the land once in 2-3 years followed by shallow cultivations every year is recommended. Use of Pre Plant Incorporation (PPI) of Di-Nitro-Aniline herbicide @ 1 kg Active Ingredient (AI) ha^{-1} can control weeds efficiently. Apply farmyard manure about 5 tonnes ha^{-1}. A basal dose of NPK 30:30:30 and top dressing with 30 kg nitrogen ha^{-1} may be given depending upon the soil fertility. The genotype responds well to higher fertilizer dose. One or two sprays of 2% DAP after flowering will boost the yield.

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Vaidehi-95 (MSH-53) is tolerant to sucking pest, the insecticide spray may be given only as and when the pest population exceeds the threshold level. For control of bollworm, need based insecticide sprays may be administered.

2. NISC 40(IC0584261; INGR13033) Jassid Tolerant Compact Plant Type Introgressed Derivative of Cotton

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The seed rate of 16 -20 kg ha^{-1} is sufficient for High Density Planting System in 30 x 15 cm and will vary depending upon spacing. In marginal soils, under rainfed

Table 1: Characteristic Features of NISC- 40, NISC- 43 and NISC 44:

Trait	Genotype		
	NISC- 40	NISC- 43	NISC-44
Yield/plant (g)	63.0	52.0	88.0
Fibre length (2.5% span length)	22.3	23.3	21.7
Fibre strength	17.5	19.3	18.2
Uniformity ratio	49.7	51	50.7
Micronaire value	3.6	3.8	3.2
GOT	40.1	37.5	34.9
Boll numbers per plant	18	20	37
Boll weight (g)	3.1	2.9	3.42
Plant height (cm)	69.9	72.1	84
Highly tolerant to jassids and bollworm			

conditions, a spacing of 60 x 30 cm is sufficient. The plant type being compact in nature; these genotypes are also suitable for High Density Planting System (HDPS) and also for Organic cultivation. Early sowing is advocated for rainfed crop. Isolation distance is advocated to avoid contamination of white linted varieties. The crop matures in 145-150 days.

All the three genotypes namely NISC-40, NISC-43 and NISC-44 are highly tolerant to Jassids and Bollworm. Insecticide spray may be given only as and when the pest population exceeds the threshold level. Need based insecticide sprays may be taken up to control Bollworm attack. Additionally NISC-44 also shows tolerance to drought.

3. P. sq H1; IG08-37 (IC0593641; INGR13036) Interspecific Hybrid between Pearl millet (*Pennisetum glaucum*) and *P. squamulatum* (novel cytotype, 2*n*=56). Obligate Sexual in Reproduction. Chromosome Number, 2*n*=42 (14G+28S), (genomic status *GGSSSS*)

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P. sq H2; IG-08-38 (IC0593642; INGR13037) Interspecific Hybrid between Pearl millet (*Pennisetum glaucum*) and *P. squamulatum* (novel cytotype, 2*n*=56). Obligate Apomictic in Reproduction, Chromosome Number, 2*n*=42 (14G+28S), (genomic status *GGSSSS*)

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Pearl millet (*Pennisetum glaucum* L., Poaceae) is an important crop utilized both for feed and fodder purposes in semi arid tropics. Exotic germplasm in the genus *Pennisetum* comprises of primary, secondary and tertiary gene pools with many species possessing desirable genes for pearl millet improvement such as resistance to diseases, male sterility, improved fodder characteristics and apomixis into pearl millet (Jauhar and Hanna, 1998). *P. squamulatum*, a wild relative of pearl millet, harbours many desirable traits for pearl millet improvement (Hanna

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NISC-40 and NISC-43 are introgressed derivatives of wild and cultivated cotton derived from a backcross of *Gossypium hirsutum* and *G. raimondii* to *G. hirsutum* while NISC-44 is a Multi-Species Hybrid (MSH) derivative of G. *hirsutum, G. raimondii*, *G. barbadense* and *G. thurberi*. Each of derivatives is developed from among the reverted tetraploid identified from segregating population of hexaploids of the above crosses. These genotypes are homozygous in nature and are unique for compact plant habit with high level of tolerance against jassids and bollworms. Characteristic features of three introgressed derivatives are elaborated below:

Morpho-Agronomic Characteristics

The plants grows to an average height of 70 – 84 cm (Table 1), leaves admeasuring 5.5 - 6.5 x 4 cm, palmate, central lobe much longer, veins covered by trichomes, petioles 3.0 - 3.5 cm long. Floral characteristics include axillary Inflorescences, solitary flower with short pedicels, free bracteoles, covering one third of the capsule. Flowers normal, wide spreading, cream coloured petals and pollen grains, calyx undulated, oblong shaped green boll and four loculed when open with 8 -10 seeds per capsule and seeds possess white lint and fuzz. The plant type is very compact.

Package of Practices

Deep ploughing of the land once in 2-3 years followed by shallow cultivations every year is recommended. Use of Pre Plant Incorporation (PPI) of Di-Nitro-Aniline herbicide @ 1 kg Active Ingredient (AI) ha^{-1} can control weeds efficiently. Apply farmyard manure about 5 tonnes ha^{-1}. A basal dose of NPK 30:30:30 and top dressing with 30 kg nitrogen ha^{-1} may be given depending upon the soil fertility. The genotype responds well to higher fertilizer dose. One or two sprays of 2% DAP after flowering will boost the yield.

The seed rate of 16 -20 kg ha^{-1} is sufficient for High Density Planting System in 30 x 15 cm and will vary depending upon spacing. In marginal soils, under rainfed

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Trait	Genotype		
	NISC- 40	NISC- 43	NISC-44
Yield/plant (g)	63.0	52.0	88.0
Fibre length (2.5% span length)	22.3	23.3	21.7
Fibre strength	17.5	19.3	18.2
Uniformity ratio	49.7	51	50.7
Micronaire value	3.6	3.8	3.2
GOT	40.1	37.5	34.9
Boll numbers per plant	18	20	37
Boll weight (g)	3.1	2.9	3.42
Plant height (cm)	69.9	72.1	84
Highly tolerant to jassids and bollworm			

conditions, a spacing of 60 x 30 cm is sufficient. The plant type being compact in nature; these genotypes are also suitable for High Density Planting System (HDPS) and also for Organic cultivation. Early sowing is advocated for rainfed crop. Isolation distance is advocated to avoid contamination of white linted varieties. The crop matures in 145-150 days.

All the three genotypes namely NISC-40, NISC-43 and NISC-44 are highly tolerant to Jassids and Bollworm. Insecticide spray may be given only as and when the pest population exceeds the threshold level. Need based insecticide sprays may be taken up to control Bollworm attack. Additionally NISC-44 also shows tolerance to drought.

3. P. sq H1; IG08-37 (IC0593641; INGR13036) Interspecific Hybrid between Pearl millet (*Pennisetum glaucum*) and *P. squamulatum* (novel cytotype, 2*n*=56). Obligate Sexual in Reproduction. Chromosome Number, 2*n*=42 (14G+28S), (genomic status *GGSSSS*)

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The seed rate of 16 -20 kg ha^{-1} is sufficient for High Density Planting System in 30 x 15 cm and will vary depending upon spacing. Under irrigated conditions narrow spacing of 90 x 20 cm keeping one plant $hill^{-1}$ may be practiced. In marginal soils, under rainfed conditions, a spacing of 60 x 30 cm will be sufficient. Early sowing is advocated for rainfed crop. Isolation of areas growing colour cotton is advocated to avoid contamination of white linted varieties. The crop matures in 145-150 days.

Vaidehi-95 (MSH-53) is tolerant to sucking pest, the insecticide spray may be given only as and when the pest population exceeds the threshold level. For control of bollworm, need based insecticide sprays may be administered.

2. NISC 40(IC0584261; INGR13033) Jassid Tolerant Compact Plant Type Introgressed Derivative of Cotton

NISC 43(IC0584262; INGR13034) Jassid Tolerant Compact Plant Type Introgressed Derivative of Cotton

NISC 44(IC0584263; INGR13035) Jassid Tolerant Compact Plant Type Introgressed Derivative of Cotton

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4. F1GO; IG-08-41 (IC0593643; INGR13038) Diploid Apomeiotic Interspecific Hybrid Between *P. glaucum* and *P. orientale*. Induced Apospory (Apomixes Component). Chromosomes *(GS)*

BC1GO; IG-08-39 (IC0593644; INGR13039) Interspecific Hybrid Derived from *P. glaucum* and *P. orientale* cross (a BIII Hybrid of F1 with *P. glaucum*). Exhibited Inheritable Partitioned Apomixes Components. Chromosomes 2*n*=23 (14G+90, Genomes *GGO*)

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Pearl millet is an important crop both for food and fodder purposes. Genepool of wild *Pennisetum* species offer opportunities to understand genome evolution, domestication, polyploidy effects and apomixis in addition to crop improvement utilizing alien introgressions. We've produced and analyzed interspecific hybrids between two diploid *Pennisetum* species, *viz. P. glaucum* (cultivated pearl millet, 2n=2x=14, *GG*) and its wild relative *P. orientale* (2n=2x=18, *OO*) (Zadoo and Singh, 1986, Kaushal *et al.,* 2010). Pearl millet is sexual in its mode of reproduction, whereas *P. orientale* is known to be sexual at diploid levels while apomictic in naturally occurring higher polyploids.

INGR13038: F_1 Hybrid (F1GO; IG 08-41)

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The F_1 hybrid (*viz.,* F1GO) was backcrossed with *P. glaucum* parent. The BC_1 thus obtained was designated as BC1GO (=IG 08-39) and is characterized by 2n=3x=23 chromosomes (genomic status *GGO*) with 14 chromosomes from *P. glaucum* and 9 chromosomes from *P. orientale*. Meiotic chromosomal analysis alongwith the flow cytometric DNA content measurements confirmed formation of this hybrid (BC1GO) combining unreduced female gamete (*GO*) and reduced male

gamete (*G*). This hybrid is cytologically unique to possess 2n=23 chromosomes with two monoploid genome doses from *P. glaucum* and a monoploid dose from *P. orientale*. The hybrid was facultative apomictic in mode of reproduction, producing 28% aposporous embryo sacs (ES) and 19% sexual ES (Kaushal *et al.,* 2010). Reproductive development in this hybrid is characterized by autonomous endosperm development (proliferation of polar nuclei in absence of pollination) as well as formation of all B_{III} seeds (unreduced egg cell fertilized) upon cross pollination. Independent existence of autonomous endosperm development as well as B_{III} hybridization provides evidence of partitioning of apomixis components for the first time in *Pennisetum*. Partitioned apomixis components were also inherited to subsequent generations. As BC1GO (=IG 08-39) produced only B_{III} seeds, it also represented a clear functional uncoupling of apomeiosis and parthenogenesis (the apomixis components). As this plant is characterized by partitioned apomixis components, showed autonomous endosperm development and produces only B_{III} seeds, it is a potential material for serially raising the ploidy levels as well as to identify genes responsible for apomeiotic (aposporous) ES formation and those involved in B_{III} hybridization events. Furthermore, owing to its capacity to produce B_{III} hybrids, this plant has been utilized to identify differentially expressed genes during apomeiosis. The plant is male sterile, however, is perennial and responds well to multiplication through rooted slips. It is being maintained at NAGS-IGFRI, Jhansi.

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5. GOSh8; IG-08-40 (IC0593645; INGR13040) a First Trispecific Hybrid between *Pennisetum glaucum, P. orientale* and *P. squamulatum*. Chromosomes 2*n*=44 (21G+14S+90, Genomes (*GGGSSO)*)

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4. F1GO; IG-08-41 (IC0593643; INGR13038) Diploid Apomeiotic Interspecific Hybrid Between *P. glaucum* and *P. orientale*. Induced Apospory (Apomixes Component). Chromosomes *(GS)*

BC1GO; IG-08-39 (IC0593644; INGR13039) Interspecific Hybrid Derived from *P. glaucum* and *P. orientale* cross (a BIII Hybrid of F1 with *P. glaucum*). Exhibited Inheritable Partitioned Apomixes Components. Chromosomes 2*n*=23 (14G+90, Genomes *GGO*)

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6. DGS-22 (IC0590889; INGR13041) a High Fruit Producing Madhunashini (*Gymnema sylvestre*)

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7. DMAPR AP3; NRC AP3 (IC0593956; INGR13042) a Kalmegh (*Andrographis paniculata*) Germplasm with Narrow Leaf Very High Andrographoloide (2.97%)

Geetha KA, S Maiti, Narendra Gajbhiye, Arun Kumar PH and Anjali Sharma
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8. DMAPR AB1 (IC0283932; INGR13043) is a Aloe (*Aloe bardadensis)* Yellow Flowered Plant Type

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9. NRC CW2 (IC0593954; INGR13044) a Guggal (*Comiphora wrightii*) Male Plant of Divergent/Erect Branch

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11. NKO-68 (IC589087/INGR13046) Oregano (*Origanum vulgare*) for High Percentage of Phenolic Compound Thymol and High Yield of Essential Oil

KS Negi[1], SN Ojha[1], SS Koranga[1], AKS Rawat[2], MM Pandey[2]and Archana P Raina[3]
[1]*NBPGR, Regional Station Bhowali- 263132, Niglat, District Nainital, Uttarakhand*
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Oregano (*Origanum vulgare* L.) is an important member of mint family, Lamiaceae. The genus *Origanum* comprises about 39 species, most of which are indigenous to the Mediterranean region and distributed all over Europe, West and Central Asia upto Taiwan. In India the herb is found in the temperate Himalayas from Kashmir to Sikkim between 1000- 3600 m asl. It is widely distributed in open forest, open scrub of hilly districts of Kumaun and Garhwal region of Uttarakhand and Himachal Pradesh. It is known locally as Van tulsi, Sathra, Vishnu Priya, Jakhmbuti and Baslo ghas etc. *Origanum vulgare L.* commonly known as 'Oregano' in the most of European countries and in India it is known as 'Himalayan Marjoram'.

During the project period (April, 2008- June, 2012) entitled "Studies on relationship between ecogeography of the chemotypic variation of nine important but highly threatened medicinal plant species and prospects of their cultivation" financed by NAIP-IV, a total of 34 accessions of oregano was collected from North-West Himalaya, Central Himalayan Region and North- East Hills of India and identified a superior chemotype i.e., Thymol rich and high yielding essential oil. The Oregano germplasm (NKO-68/ IC 589087) was collected and identified from on way to Vashudhara fall from Sh. Badarinath shrine, District- Chamoli, Uttarakhand. It was successfully raised and thrives well with luxuriant growth in Field Gene Bank/ Herbal Garden, NBPGR, R/S Bhowali, Nainital, Uttarakhand. High Thymol content (85.87%) was observed from essential oil isolated from aerial part and high yield of essential oil (2.07%) was reported during flowering stage (Anonymous, 2010; Negi, *et al*., 2011).

Morpho-agronomic Characteristics

It is aromatic, branched, perennial, 30-60 cm. high. Leaves are dark green, broadly ovate; and ; stem light green, pubescent, soft woody; bracts purple and flowers pale- pink colour, flowers are in terminal corymbose cyme, The herb contains a high yield of essential oil (2.07%) and rich phenolic compound – Thymol (85.87%) –Table 1 and 2.

Table 1. Comparative analysis of thymol and percentage of essential oil in 30 accession of *Origanum vulgare*

S. No.	Collector number	IC No.	Essential oil (%)	Thymol (%)
1	NMB- 2955	IC566859	0.5	1.51
2	***NKO-09 (Local check)**	**IC573209**	**0.17**	**16.78**
3	NMVM KO 14	IC573213	0.86	1.52
4	NKO- 15	IC573214	1.06	3.95
5	NKO- 16	IC573215	0.7	32.16
6	NKO- 17	IC573216	1.43	53.5
7	NKO- 18	IC573217	1.41	37.34
8	NKO- 19	IC573218	1.2	26.31
9	NKO- 20	IC573219	2	28.26
10	NKO- 21	IC573220	0.22	5.99
11	****NKO- 25**	**IC573224**	**0.4**	**0.42**
12	NKO- 26	IC573225	0.4	4.86
13	NKO-30	IC573229	0.88	30.74
14	NKO- 45	IC574508	0.4	7.12
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18	NKO-57	IC574519	1.31	42.68
19	NKO- 58	IC574520	1.7	45.61
20	NMJO-2983	IC582500	0.67	2.74
21	NMJO-2993	IC582510	0.48	29.42
22	NMJO- 3004	IC582521	0.9	45.19
23	NMO 3015	IC582532	0.44	3.06
24	NMO- 3019	IC582536	0.6	2.17
25	MMBO-3040	IC589077	0.57	12.9
26	MMBO-3055	IC589079	1.41	21.38
27	NKO-64	IC589084	0.29	6.02
28	NKO-65	IC589085	0.98	81.45
29	****NKO-68**	**IC589087**	**2.07**	**85.87**
30	NKO-72	IC589090	0.32	9.02
Range of variation			**0.17-2.07**	**0.42-85.87**
Average			**0.89**	**24.36**

*NKO-09/ IC573209 Local check
**NKO- 25/ IC573224 Lowest percentage of thymol
***NKO-68/ IC589087 Thymol rich and high essential oil yield genotype

Table 2. Percentage of essential oil and thymol in aerial parts of different *Origanum vulgare* L. strains

Items	*Origanum vulgare* (NKO-68/IC589087)	*O. vulgare* (Kumaon Himalya) Verma *et al.* (2010)	*O. vulgare* (Jageshwar, Almora, UK) Raina A *et al.* (2010)	Origanum species (Greek) Wogiatzi, (2009)	*O. vulgare* Lithuania, Mockute *et al.* (2004)	*O. vulgare* ssp. *vulgare* (Vilnius district-Lithuania) Mockute *et al.* (2001)	*O. vulgare* ssp. *vulgare* (Italy) Melegari *et al.* (1995)
Essential oil extracted from aerial parts (dried) (%)	**2.07**	0.25-1.30	0.14-0.37	0.3-0.4	NR	*NR	*NR
Thymol (%)	**85.87**	0.37-0.70	33.92	57.2	0.0-3.2	0.1-0.5	39.3

*NR – Not Reported

Associated Characters and Cultivated Practices

The herb occurs abundantly under pine forest, near scrub forest, open scrubs and near agricultural land in the sub-tropical, temperate and alpine Himalayan region at an elevation of 1100- 3600 m asl. Oregano was propagated by seeds, stem cuttings and sprouted root divisions successfully. The herbage was harvested after rainy season and dried in shade for its natural green colour and fragrance. A total of 6-8 q/ha dried aerial parts obtained. The market price of dry herbage is Rs. 200/- to 250/- per kg. Total return from dried herbage is Rs. 1.0- to 1.2 lakh annually.

It has various ethno botanical notes and much popular in traditional medicinal systems for the treatment of cold, cough, fever, cuts in heal, diarrhoea, ear ache, flavoring agent, healing wounds, insect repellent, inflammation, local beverage, herbal tea, aesthetic purpose and skin diseases.

The present genetic stock of *Origanum vulgare L.* germplasm **NKO-68/ IC589087** showed Thymol rich and high yield of essential oil as compared to other accessions including local check collected from Central Himalayan region (Table 1 and 2).

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12. DWS-6 (IC0590838; INGR13047) a New Plant Type of Ashwagandha (*Withania somnifera*) which is a Unique and Distinct than Normal Erect Type

P Manivel, NA Gajbhiye and S Maiti

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components, specially the interaction between genes for apomeiosis (from BC1GO parent) and parthenogenesis (from GSH2 parent). One of these GOS tri-species hybrids, *viz*. GOSh8 (=accession IG 08-40) (Kaushal *et al*. 2010) showed better tillering and vigour than other siblings, and is proposed for registration. The hybrid is male sterile, however, could be easily multiplied by rooted slips. It is being maintained at NAGS-Forage Crops at IGFRI Jhansi.

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6. DGS-22 (IC0590889; INGR13041) a High Fruit Producing Madhunashini (*Gymnema sylvestre*)

P Manivel, Saravanan Raju, Sandip Kumar L Patel and S Maiti
Directorate of Medicinal & Aromatic Plants Research, Boriavi, Anand-387 310, Gujarat
(E-mail: manivelp@yahoo.com)

7. DMAPR AP3; NRC AP3 (IC0593956; INGR13042) a Kalmegh (*Andrographis paniculata*) Germplasm with Narrow Leaf Very High Andrographoloide (2.97%)

Geetha KA, S Maiti, Narendra Gajbhiye, Arun Kumar PH and Anjali Sharma
Directorate of Medicinal & Aromatic Plants Research, Boriavi, Anand-387 310, Gujarat
(E-mail: geethaka99@yahoo.com)

8. DMAPR AB1 (IC0283932; INGR13043) is a Aloe (*Aloe bardadensis)* Yellow Flowered Plant Type

Geetha KA, S Maiti, Narendra Gajbhiye and Sanghamitra Saman
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9. NRC CW2 (IC0593954; INGR13044) a Guggal (*Comiphora wrightii*) Male Plant of Divergent/Erect Branch

10. NRC CW1 (IC0593955; INGR13045) is a Weeping Branch Type Female Plant of Guggal (*Comiphora wrightii*)

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11. NKO-68 (IC589087/INGR13046) Oregano (*Origanum vulgare*) for High Percentage of Phenolic Compound Thymol and High Yield of Essential Oil

KS Negi[1], SN Ojha[1], SS Koranga[1], AKS Rawat[2], MM Pandey[2]and Archana P Raina[3]
[1]*NBPGR, Regional Station Bhowali- 263132, Niglat, District Nainital, Uttarakhand*
[2]*National Botanical Research Institute (CSIR), Lucknow-226001, Uttar Pradesh*
[3]*NBPGR, Pusa Campus, New Delhi-110012*
(E-mail: officerinchargebhowali@yahoo.com)

Oregano (*Origanum vulgare* L.) is an important member of mint family, Lamiaceae. The genus *Origanum* comprises about 39 species, most of which are indigenous to the Mediterranean region and distributed all over Europe, West and Central Asia upto Taiwan. In India the herb is found in the temperate Himalayas from Kashmir to Sikkim between 1000- 3600 m asl. It is widely distributed in open forest, open scrub of hilly districts of Kumaun and Garhwal region of Uttarakhand and Himachal Pradesh. It is known locally as Van tulsi, Sathra, Vishnu Priya, Jakhmbuti and Baslo ghas etc. *Origanum vulgare L.* commonly known as 'Oregano' in the most of European countries and in India it is known as 'Himalayan Marjoram'.

During the project period (April, 2008- June, 2012) entitled "Studies on relationship between ecogeography of the chemotypic variation of nine important but highly threatened medicinal plant species and prospects of their cultivation" financed by NAIP-IV, a total of 34 accessions of oregano was collected from North-West Himalaya, Central Himalayan Region and North- East Hills of India and identified a superior chemotype i.e., Thymol rich and high yielding essential oil. The Oregano germplasm (NKO-68/ IC 589087) was collected and identified from on way to Vashudhara fall from Sh. Badarinath shrine, District- Chamoli, Uttarakhand. It was successfully raised and thrives well with luxuriant growth in Field Gene Bank/ Herbal Garden, NBPGR, R/S Bhowali, Nainital, Uttarakhand. High Thymol content (85.87%) was observed from essential oil isolated from aerial part and high yield of essential oil (2.07%) was reported during flowering stage (Anonymous, 2010; Negi, *et al*., 2011).

Morpho-agronomic Characteristics

It is aromatic, branched, perennial, 30-60 cm. high. Leaves are dark green, broadly ovate; and ; stem light green, pubescent, soft woody; bracts purple and flowers pale- pink colour, flowers are in terminal corymbose cyme, The herb contains a high yield of essential oil (2.07%) and rich phenolic compound – Thymol (85.87%) –Table 1 and 2.

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29	****NKO-68**	**IC589087**	**2.07**	**85.87**
30	NKO-72	IC589090	0.32	9.02
Range of variation			**0.17-2.07**	**0.42-85.87**
Average			**0.89**	**24.36**

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Associated Characters and Cultivated Practices

The herb occurs abundantly under pine forest, near scrub forest, open scrubs and near agricultural land in the sub-tropical, temperate and alpine Himalayan region at an elevation of 1100- 3600 m asl. Oregano was propagated by seeds, stem cuttings and sprouted root divisions successfully. The herbage was harvested after rainy season and dried in shade for its natural green colour and fragrance. A total of 6-8 q/ha dried aerial parts obtained. The market price of dry herbage is Rs. 200/- to 250/- per kg. Total return from dried herbage is Rs. 1.0- to 1.2 lakh annually.

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21	NMJO-2993	IC582510	0.48	29.42
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27	NKO-64	IC589084	0.29	6.02
28	NKO-65	IC589085	0.98	81.45
29	****NKO-68**	**IC589087**	**2.07**	**85.87**
30	NKO-72	IC589090	0.32	9.02
Range of variation			**0.17-2.07**	**0.42-85.87**
Average			**0.89**	**24.36**

*NKO-09/ IC573209 Local check
**NKO- 25/ IC573224 Lowest percentage of thymol
***NKO-68/ IC589087 Thymol rich and high essential oil yield genotype

Table 2. Percentage of essential oil and thymol in aerial parts of different *Origanum vulgare* L. strains

Items	*Origanum vulgare* (NKO-68/IC589087)	*O. vulgare* (Kumaon Himalya) Verma *et al.* (2010)	*O. vulgare* (Jageshwar, Almora, UK) Raina A *et al.* (2010)	Origanum species (Greek) Wogiatzi, (2009)	*O. vulgare* Lithuania, Mockute *et al.* (2004)	*O. vulgare* ssp. *vulgare* (Vilnius district-Lithuania) Mockute *et al.* (2001)	*O. vulgare* ssp. *vulgare* (Italy) Melegari *et al.* (1995)
Essential oil extracted from aerial parts (dried) (%)	**2.07**	0.25-1.30	0.14-0.37	0.3-0.4	NR	*NR	*NR
Thymol (%)	**85.87**	0.37-0.70	33.92	57.2	0.0-3.2	0.1-0.5	39.3

*NR – Not Reported

Associated Characters and Cultivated Practices

The herb occurs abundantly under pine forest, near scrub forest, open scrubs and near agricultural land in the sub-tropical, temperate and alpine Himalayan region at an elevation of 1100- 3600 m asl. Oregano was propagated by seeds, stem cuttings and sprouted root divisions successfully. The herbage was harvested after rainy season and dried in shade for its natural green colour and fragrance. A total of 6-8 q/ha dried aerial parts obtained. The market price of dry herbage is Rs. 200/- to 250/- per kg. Total return from dried herbage is Rs. 1.0- to 1.2 lakh annually.

It has various ethno botanical notes and much popular in traditional medicinal systems for the treatment of cold, cough, fever, cuts in heal, diarrhoea, ear ache, flavoring agent, healing wounds, insect repellent, inflammation, local beverage, herbal tea, aesthetic purpose and skin diseases.

The present genetic stock of *Origanum vulgare L.* germplasm **NKO-68/ IC589087** showed Thymol rich and high yield of essential oil as compared to other accessions including local check collected from Central Himalayan region (Table 1 and 2).

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12. DWS-6 (IC0590838; INGR13047) a New Plant Type of Ashwagandha (*Withania somnifera*) which is a Unique and Distinct than Normal Erect Type

P Manivel, NA Gajbhiye and S Maiti

Directorate of Medicinal & Aromatic Plants Research, Boriavi, Anand-387 310, Gujarat
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components, specially the interaction between genes for apomeiosis (from BC1GO parent) and parthenogenesis (from GSH2 parent). One of these GOS tri-species hybrids, *viz*. GOSh8 (=accession IG 08-40) (Kaushal *et al*. 2010) showed better tillering and vigour than other siblings, and is proposed for registration. The hybrid is male sterile, however, could be easily multiplied by rooted slips. It is being maintained at NAGS-Forage Crops at IGFRI Jhansi.

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6. DGS-22 (IC0590889; INGR13041) a High Fruit Producing Madhunashini (*Gymnema sylvestre*)

P Manivel, Saravanan Raju, Sandip Kumar L Patel and S Maiti
Directorate of Medicinal & Aromatic Plants Research, Boriavi, Anand-387 310, Gujarat
(E-mail: manivelp@yahoo.com)

7. DMAPR AP3; NRC AP3 (IC0593956; INGR13042) a Kalmegh (*Andrographis paniculata*) Germplasm with Narrow Leaf Very High Andrographoloide (2.97%)

Geetha KA, S Maiti, Narendra Gajbhiye, Arun Kumar PH and Anjali Sharma
Directorate of Medicinal & Aromatic Plants Research, Boriavi, Anand-387 310, Gujarat
(E-mail: geethaka99@yahoo.com)

8. DMAPR AB1 (IC0283932; INGR13043) is a Aloe (*Aloe bardadensis)* Yellow Flowered Plant Type

Geetha KA, S Maiti, Narendra Gajbhiye and Sanghamitra Saman
Directorate of Medicinal & Aromatic Plants Research, Boriavi, Anand-387 310, Gujarat
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9. NRC CW2 (IC0593954; INGR13044) a Guggal (*Comiphora wrightii*) Male Plant of Divergent/Erect Branch

10. NRC CW1 (IC0593955; INGR13045) is a Weeping Branch Type Female Plant of Guggal (*Comiphora wrightii*)

Geetha KA, S Maiti, Narendra Gajbhiye, AK Bishoyi and Anjali Sharma
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11. NKO-68 (IC589087/INGR13046) Oregano (*Origanum vulgare*) for High Percentage of Phenolic Compound Thymol and High Yield of Essential Oil

KS Negi[1], SN Ojha[1], SS Koranga[1], AKS Rawat[2], MM Pandey[2]and Archana P Raina[3]
[1]*NBPGR, Regional Station Bhowali- 263132, Niglat, District Nainital, Uttarakhand*
[2]*National Botanical Research Institute (CSIR), Lucknow-226001, Uttar Pradesh*
[3]*NBPGR, Pusa Campus, New Delhi-110012*
(E-mail: officerinchargebhowali@yahoo.com)

Oregano (*Origanum vulgare* L.) is an important member of mint family, Lamiaceae. The genus *Origanum* comprises about 39 species, most of which are indigenous to the Mediterranean region and distributed all over Europe, West and Central Asia upto Taiwan. In India the herb is found in the temperate Himalayas from Kashmir to Sikkim between 1000- 3600 m asl. It is widely distributed in open forest, open scrub of hilly districts of Kumaun and Garhwal region of Uttarakhand and Himachal Pradesh. It is known locally as Van tulsi, Sathra, Vishnu Priya, Jakhmbuti and Baslo ghas etc. *Origanum vulgare L.* commonly known as 'Oregano' in the most of European countries and in India it is known as 'Himalayan Marjoram'.

During the project period (April, 2008- June, 2012) entitled "Studies on relationship between ecogeography of the chemotypic variation of nine important but highly threatened medicinal plant species and prospects of their cultivation" financed by NAIP-IV, a total of 34 accessions of oregano was collected from North-West Himalaya, Central Himalayan Region and North- East Hills of India and identified a superior chemotype i.e., Thymol rich and high yielding essential oil. The Oregano germplasm (NKO-68/ IC 589087) was collected and identified from on way to Vashudhara fall from Sh. Badarinath shrine, District- Chamoli, Uttarakhand. It was successfully raised and thrives well with luxuriant growth in Field Gene Bank/ Herbal Garden, NBPGR, R/S Bhowali, Nainital, Uttarakhand. High Thymol content (85.87%) was observed from essential oil isolated from aerial part and high yield of essential oil (2.07%) was reported during flowering stage (Anonymous, 2010; Negi, *et al*., 2011).

Morpho-agronomic Characteristics

It is aromatic, branched, perennial, 30-60 cm. high. Leaves are dark green, broadly ovate; and ; stem light green, pubescent, soft woody; bracts purple and flowers pale- pink colour, flowers are in terminal corymbose cyme, The herb contains a high yield of essential oil (2.07%) and rich phenolic compound – Thymol (85.87%) –Table 1 and 2.

Table 1. Comparative analysis of thymol and percentage of essential oil in 30 accession of *Origanum vulgare*

S. No.	Collector number	IC No.	Essential oil (%)	Thymol (%)
1	NMB- 2955	IC566859	0.5	1.51
2	***NKO-09 (Local check)**	**IC573209**	**0.17**	**16.78**
3	NMVM KO 14	IC573213	0.86	1.52
4	NKO- 15	IC573214	1.06	3.95
5	NKO- 16	IC573215	0.7	32.16
6	NKO- 17	IC573216	1.43	53.5
7	NKO- 18	IC573217	1.41	37.34
8	NKO- 19	IC573218	1.2	26.31
9	NKO- 20	IC573219	2	28.26
10	NKO- 21	IC573220	0.22	5.99
11	****NKO- 25**	**IC573224**	**0.4**	**0.42**
12	NKO- 26	IC573225	0.4	4.86
13	NKO-30	IC573229	0.88	30.74
14	NKO- 45	IC574508	0.4	7.12
15	NKO- 49	IC574512	0.48	2.51
16	NKO- 50	IC574513	1.5	38.92
17	NKO- 56	IC574518	1.25	51.45
18	NKO-57	IC574519	1.31	42.68
19	NKO- 58	IC574520	1.7	45.61
20	NMJO-2983	IC582500	0.67	2.74
21	NMJO-2993	IC582510	0.48	29.42
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29	****NKO-68**	**IC589087**	**2.07**	**85.87**
30	NKO-72	IC589090	0.32	9.02
Range of variation			**0.17-2.07**	**0.42-85.87**
Average			**0.89**	**24.36**

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Table 2. Percentage of essential oil and thymol in aerial parts of different *Origanum vulgare* L. strains

Items	*Origanum vulgare* (NKO-68/IC589087)	*O. vulgare* (Kumaon Himalya) Verma *et al.* (2010)	*O. vulgare* (Jageshwar, Almora, UK) Raina A *et al.* (2010)	Origanum species (Greek) Wogiatzi, (2009)	*O. vulgare* Lithuania, Mockute *et al.* (2004)	*O. vulgare* ssp. *vulgare* (Vilnius district-Lithuania) Mockute *et al.* (2001)	*O. vulgare* ssp. *vulgare* (Italy) Melegari *et al.* (1995)
Essential oil extracted from aerial parts (dried) (%)	**2.07**	0.25-1.30	0.14-0.37	0.3-0.4	NR	*NR	*NR
Thymol (%)	**85.87**	0.37-0.70	33.92	57.2	0.0-3.2	0.1-0.5	39.3

*NR – Not Reported

Associated Characters and Cultivated Practices

The herb occurs abundantly under pine forest, near scrub forest, open scrubs and near agricultural land in the sub-tropical, temperate and alpine Himalayan region at an elevation of 1100- 3600 m asl. Oregano was propagated by seeds, stem cuttings and sprouted root divisions successfully. The herbage was harvested after rainy season and dried in shade for its natural green colour and fragrance. A total of 6-8 q/ha dried aerial parts obtained. The market price of dry herbage is Rs. 200/- to 250/- per kg. Total return from dried herbage is Rs. 1.0- to 1.2 lakh annually.

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Range of variation			**0.17-2.07**	**0.42-85.87**
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Table 2. Percentage of essential oil and thymol in aerial parts of different *Origanum vulgare* L. strains

Items	*Origanum vulgare* (NKO-68/IC589087)	*O. vulgare* (Kumaon Himalya) Verma *et al.* (2010)	*O. vulgare* (Jageshwar, Almora, UK) Raina A *et al.* (2010)	Origanum species (Greek) Wogiatzi, (2009)	*O. vulgare* Lithuania, Mockute *et al.* (2004)	*O. vulgare* ssp. *vulgare* (Vilnius district-Lithuania) Mockute *et al.* (2001)	*O. vulgare* ssp. *vulgare* (Italy) Melegari *et al.* (1995)
Essential oil extracted from aerial parts (dried) (%)	**2.07**	0.25-1.30	0.14-0.37	0.3-0.4	NR	*NR	*NR
Thymol (%)	**85.87**	0.37-0.70	33.92	57.2	0.0-3.2	0.1-0.5	39.3

*NR – Not Reported

Associated Characters and Cultivated Practices

The herb occurs abundantly under pine forest, near scrub forest, open scrubs and near agricultural land in the sub-tropical, temperate and alpine Himalayan region at an elevation of 1100- 3600 m asl. Oregano was propagated by seeds, stem cuttings and sprouted root divisions successfully. The herbage was harvested after rainy season and dried in shade for its natural green colour and fragrance. A total of 6-8 q/ha dried aerial parts obtained. The market price of dry herbage is Rs. 200/- to 250/- per kg. Total return from dried herbage is Rs. 1.0- to 1.2 lakh annually.

It has various ethno botanical notes and much popular in traditional medicinal systems for the treatment of cold, cough, fever, cuts in heal, diarrhoea, ear ache, flavoring agent, healing wounds, insect repellent, inflammation, local beverage, herbal tea, aesthetic purpose and skin diseases.

The present genetic stock of *Origanum vulgare L.* germplasm **NKO-68/ IC589087** showed Thymol rich and high yield of essential oil as compared to other accessions including local check collected from Central Himalayan region (Table 1 and 2).

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12. DWS-6 (IC0590838; INGR13047) a New Plant Type of Ashwagandha (*Withania somnifera*) which is a Unique and Distinct than Normal Erect Type

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11. NKO-68 (IC589087/INGR13046) Oregano (*Origanum vulgare*) for High Percentage of Phenolic Compound Thymol and High Yield of Essential Oil

KS Negi[1], SN Ojha[1], SS Koranga[1], AKS Rawat[2], MM Pandey[2]and Archana P Raina[3]
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Oregano (*Origanum vulgare* L.) is an important member of mint family, Lamiaceae. The genus *Origanum* comprises about 39 species, most of which are indigenous to the Mediterranean region and distributed all over Europe, West and Central Asia upto Taiwan. In India the herb is found in the temperate Himalayas from Kashmir to Sikkim between 1000- 3600 m asl. It is widely distributed in open forest, open scrub of hilly districts of Kumaun and Garhwal region of Uttarakhand and Himachal Pradesh. It is known locally as Van tulsi, Sathra, Vishnu Priya, Jakhmbuti and Baslo ghas etc. *Origanum vulgare L.* commonly known as 'Oregano' in the most of European countries and in India it is known as 'Himalayan Marjoram'.

During the project period (April, 2008- June, 2012) entitled "Studies on relationship between ecogeography of the chemotypic variation of nine important but highly threatened medicinal plant species and prospects of their cultivation" financed by NAIP-IV, a total of 34 accessions of oregano was collected from North-West Himalaya, Central Himalayan Region and North- East Hills of India and identified a superior chemotype i.e., Thymol rich and high yielding essential oil. The Oregano germplasm (NKO-68/ IC 589087) was collected and identified from on way to Vashudhara fall from Sh. Badarinath shrine, District- Chamoli, Uttarakhand. It was successfully raised and thrives well with luxuriant growth in Field Gene Bank/ Herbal Garden, NBPGR, R/S Bhowali, Nainital, Uttarakhand. High Thymol content (85.87%) was observed from essential oil isolated from aerial part and high yield of essential oil (2.07%) was reported during flowering stage (Anonymous, 2010; Negi, *et al*., 2011).

Morpho-agronomic Characteristics

It is aromatic, branched, perennial, 30-60 cm. high. Leaves are dark green, broadly ovate; and ; stem light green, pubescent, soft woody; bracts purple and flowers pale- pink colour, flowers are in terminal corymbose cyme, The herb contains a high yield of essential oil (2.07%) and rich phenolic compound – Thymol (85.87%) –Table 1 and 2.

Table 1. Comparative analysis of thymol and percentage of essential oil in 30 accession of *Origanum vulgare*

S. No.	Collector number	IC No.	Essential oil (%)	Thymol (%)
1	NMB- 2955	IC566859	0.5	1.51
2	***NKO-09 (Local check)**	**IC573209**	**0.17**	**16.78**
3	NMVM KO 14	IC573213	0.86	1.52
4	NKO- 15	IC573214	1.06	3.95
5	NKO- 16	IC573215	0.7	32.16
6	NKO- 17	IC573216	1.43	53.5
7	NKO- 18	IC573217	1.41	37.34
8	NKO- 19	IC573218	1.2	26.31
9	NKO- 20	IC573219	2	28.26
10	NKO- 21	IC573220	0.22	5.99
11	****NKO- 25**	**IC573224**	**0.4**	**0.42**
12	NKO- 26	IC573225	0.4	4.86
13	NKO-30	IC573229	0.88	30.74
14	NKO- 45	IC574508	0.4	7.12
15	NKO- 49	IC574512	0.48	2.51
16	NKO- 50	IC574513	1.5	38.92
17	NKO- 56	IC574518	1.25	51.45
18	NKO-57	IC574519	1.31	42.68
19	NKO- 58	IC574520	1.7	45.61
20	NMJO-2983	IC582500	0.67	2.74
21	NMJO-2993	IC582510	0.48	29.42
22	NMJO- 3004	IC582521	0.9	45.19
23	NMO 3015	IC582532	0.44	3.06
24	NMO- 3019	IC582536	0.6	2.17
25	MMBO-3040	IC589077	0.57	12.9
26	MMBO-3055	IC589079	1.41	21.38
27	NKO-64	IC589084	0.29	6.02
28	NKO-65	IC589085	0.98	81.45
29	****NKO-68**	**IC589087**	**2.07**	**85.87**
30	NKO-72	IC589090	0.32	9.02
Range of variation			**0.17-2.07**	**0.42-85.87**
Average			**0.89**	**24.36**

*NKO-09/ IC573209 Local check
**NKO- 25/ IC573224 Lowest percentage of thymol
***NKO-68/ IC589087 Thymol rich and high essential oil yield genotype

Table 2. Percentage of essential oil and thymol in aerial parts of different *Origanum vulgare* L. strains

Items	*Origanum vulgare* (NKO-68/IC589087)	*O. vulgare* (Kumaon Himalya) Verma *et al.* (2010)	*O. vulgare* (Jageshwar, Almora, UK) Raina A *et al.* (2010)	Origanum species (Greek) Wogiatzi, (2009)	*O. vulgare* Lithuania, Mockute *et al.* (2004)	*O. vulgare* ssp. *vulgare* (Vilnius district-Lithuania) Mockute *et al.* (2001)	*O. vulgare* ssp. *vulgare* (Italy) Melegari *et al.* (1995)
Essential oil extracted from aerial parts (dried) (%)	**2.07**	0.25-1.30	0.14-0.37	0.3-0.4	NR	*NR	*NR
Thymol (%)	**85.87**	0.37-0.70	33.92	57.2	0.0-3.2	0.1-0.5	39.3

*NR – Not Reported

Associated Characters and Cultivated Practices

The herb occurs abundantly under pine forest, near scrub forest, open scrubs and near agricultural land in the sub-tropical, temperate and alpine Himalayan region at an elevation of 1100- 3600 m asl. Oregano was propagated by seeds, stem cuttings and sprouted root divisions successfully. The herbage was harvested after rainy season and dried in shade for its natural green colour and fragrance. A total of 6-8 q/ha dried aerial parts obtained. The market price of dry herbage is Rs. 200/- to 250/- per kg. Total return from dried herbage is Rs. 1.0- to 1.2 lakh annually.

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The present genetic stock of *Origanum vulgare L.* germplasm **NKO-68/ IC589087** showed Thymol rich and high yield of essential oil as compared to other accessions including local check collected from Central Himalayan region (Table 1 and 2).

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13. SS1735-02 (IC0594469; INGR13048) a Hexaploid Wild Potato Clone (*Solanum demissum*) with High Resistance against Late Blight and Low Cold Induced Sweetening even after 6 Months of Cold Storage (2-4ºC)

Vinay Bhardwaj[1], SK Luthra[2], Dalamu[1], Bir Pal Singh[1], Vinod Kumar[3], Dinesh Kumar[4] and Sanjeev Sharma[1]

[1]*Central Potato Research Institute, Shimla-171001, Himachal Pradesh*
[2]*Central Potato Research Institute Campus, Modipuram-250110, Uttar Pradesh*
[3]*Central Potato Research Station, Kufri-171001, Himachal Pradesh*
[4]*Directorate of Wheat Research, Karnal-132001, Haryana*
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The genetic stock, 'SS 1735-02' is an elite clone of wild potato species *Solanum demissum* (2n=6x; 4 EBN) possessing a unique set of quantitative traits i.e. very high resistance against late blight and low cold induced sweetening even after 6 months' cold storage. True Potato Seed (TPS) of *Solanum demissum* accession GLKS-269 was introduced from Institute of Plant Genetics and Crop Plant Research (GLKS), Gross Luessewitz, Germany during the year 2000. Further conversion into tuber form and selections were undertaken at Central Potato Research Institute, Shimla and SS 1735-02 is one of the superior clone selected from GLKS-269.

Late blight caused by *Phytophthora infestans* is the most important biotic stress of potato worldwide causing more than USD 13 million losses annually in the developing countries alone. The most effective and environmentally safe means to defeat *P. infestans* is by incorporation of resistance genes from new sources of wild potato species. Processed potatoes are one of the most important value-added commodities. Low reducing sugars (<100mg/100 g fresh tuber weight) and high dry matter (>20%) are basic requirements for processing tubers into chips/ French fries. Harvested tubers are cold stored (at 2-4ºC) for year round availability of potatoes for table/ processing purposes. The long term cold storage results in excessive accumulation of reducing sugars imparting sweetening known as 'cold induced sweetening'. In cultivated potato, there is little variability for reducing sugar content after cold storage and few genotypes are suitable for cold chipping (Bhardwaj *et al*, 2011). SS 1735-02 maintains low reducing sugar (glucose < 50mg/ 100 Fwt.) and superior chip colour compared to processing varieties Atlantic, Kufri Chipsona-1 and Kufri Chipsona-3 even after 6 months of cold storage and without reconditioning (Luthra *et al*, 2009). Besides, this genotype is highly resistant (lesion area < 1.0 cm^2) in laboratory as well as under natural epiphytotic conditions against complex races of *P. infestans* (Gopal *et al*., 2008). This elite wild potato clone has short plant height, open canopy with red-brown stem, blue violet flowers, moderate flowering and high pollen fertility. The genotype possesses acceptable tuber traits with purple, smooth skin, oblong tubers with shallow eyes.

This genetic stock holds promise to exploit the resistance genes to low cold induced sweetening and late blight resistance in cultivated potato by hybridization through bridge species like *S. phureja* and thus will be helpful in strengthening the breeding programme for developing cultivars possessing both the quantitative traits.

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Luthra SK, J Gopal, D Kumar, BP Singh and SK Pandey (2009) *Solanum* wild and cultivated species as source of resistance to cold induced sweetening. *Potato J.* **36**: 115-120.

13. SS1735-02 (IC0594469; INGR13048) a Hexaploid Wild Potato Clone (*Solanum demissum*) with High Resistance against Late Blight and Low Cold Induced Sweetening even after 6 Months of Cold Storage (2-4ºC)

Vinay Bhardwaj[1], SK Luthra[2], Dalamu[1], Bir Pal Singh[1], Vinod Kumar[3], Dinesh Kumar[4] and Sanjeev Sharma[1]

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14. MP/97-921(IC0594469; INGR13048) an Elite Potato (*Solanum tuberosum* ssp. *tuberosum*) Germplasm with Superior Processing Traits and High Resistance to Late Blight and Potato Virus-Y

SV Singh[1], Vinay Bhardwaj[2], P Manivel[3], Dinesh Kumar[4], Bir Pal Singh[2], VK Gupta[1] and SK Kaushik[1]
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[2]*Central Potato Research Institute, Shimla-171001, Himachal Pradesh*
[3]*Directorate of Medicinal and Aromatic Plants, Boriavi, Anand-378310, Gujarat*
[4]*Directorate of Wheat Research, Karnal-132001, Haryana*
(E mail: vinaycpri@gmail.com)

MP/97-921 is a potato (*Solanum tuberosum* ssp. *tuberosum*) hybrid developed from cross between MP/92-154 X MP/91-65 following the recurrent breeding selection method at Central Potato Research Institute, Shimla, Himachal Pradesh. This hybrid has high dry matter content, acceptable chip colour (score < 2), low reducing sugars & sucrose, maintains acceptable sugar level for six months storage at 10-12° C with CIPC treatment, acceptable amino acid and phenol content (Table 1.) with high resistance to late blight (Thakur *et al*., 2007) and potato virus Y (Fig.1).

The plant is tall with semi-compact canopy, stem thin, predominantly green with red-brown pigment lightly scattered throughout, wings highly developed and straight. The leaves are intermediate, leaflet narrow and rachis and midrib pigmentation absent. White coloured flowers with moderate flowering. Tubers are round-oval, white to creamy skin, eyes shallow, flesh cream pale yellow. Hybrid is medium maturing and yields 37.7 t/ha with 70-75 % processing grade (>45 mm dia.) tubers in plains and 23.5 t/ha and 71-76% processing grade in hills (Singh *et al.,* 2005). Considering its best performance

Table 1: Processing qualities of advanced hybrid MP/97-921 at Modipuram

Hybrid/Variety	Dry matter (%)	Chip colour score*	Reducing sugars**	Sucrose**	Total free amino acids **	Phenols**
MP/97-921	23.31	1.81	33.21	161.91	808.94	15.66
Kufri Chipsona-1	21.28	1.13	25.66	176.35	926.91	15.26
Atlantic	20.97	2.02	38.44	177.10	852.84	15.65

* = 1 to 9 scale (1 = lightest and 9 = darkest); ** mg/100 g fresh weight

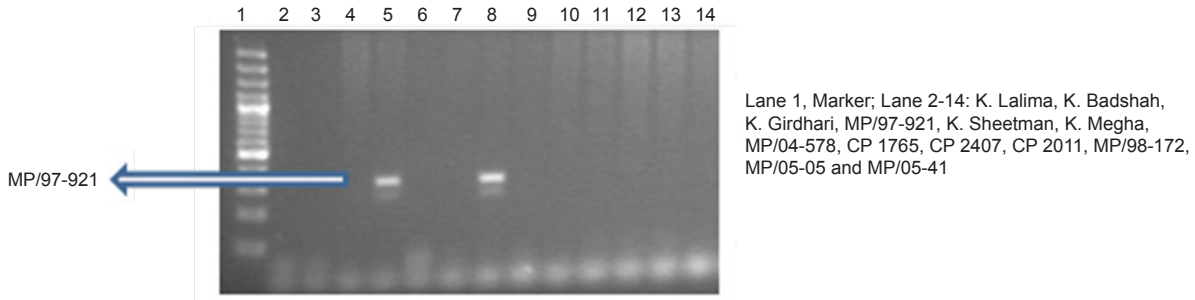

Fig. 1: Presence of Ryadg gene imparting extreme resistance to PVY

for different quality parameters as well as resistance against late blight and potato virus Y this hybrid can be used as a suitable parent for developing superior potato varieties for processing and resistance breeding.

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15. SBIEC11004 (IC0594464; INGR13050) a Sugarcane *Erianthus* Clone with High fiber content: 30.21%

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SBIEC 11004 was developed from cross between IK 76-92 (*Erianthus arundinaceus*) and 98 N1 1405 (interspecific hybrid involving *Saccharum officinarum* and *Saccharum spontaneum*) for introgressing high fibre content from the parent IK 76-92. The clone was selected through hybridization and clonal selection method at Sugarcane Breeding Institute, Coimbatore. INGR 13050 is one of the potential high fibre energy cane with the highest cane fibre content of 30.21 % which is more than 120 % higher than the commercial sugarcane varieties presently cultivated. It also recorded high harvestable biomass/year of 193.83 t/ha and 75.94 t/ha of dry matter production/year (Govindaraj, 2011). The clone is a high yielding, fast growing, high tillering and thick cylindrical canes without wax coating and amenable for multiple ratooning. Bud is small and pentagonal in shape. Leaf sheath is green with smooth hairs and dewlap is absent. Under the abiotic stress conditions also it can perform well.

Sugar factories with cogeneration facility require more and continuous supply of bagasse to generate electricity through out the year. Present day cultivars have 13-15 % fibre content and available for crushing for about 200 days per year. The clone can be utilized for the establishment of energy plantations for supply of biomass. This is also a potential alternate raw materials to wood pulp in the paper industries.

Table: Performance of SBIEC 11001 for energy cane traits

Clone	Harvestable biomass t/ha	Fibre (% cane)	Juice brix (%)	Dry matter (%)	Dry matter yield (t/ha)
SBIEC 11004	193.83	30.21	7.80	39.18	75.94
IA 1167	208.95	22.56	16.88	35.53	74.25
SBIEC 11005	181.79	25.55	16.60	39.88	72.50
SBIEC 11006	197.22	25.77	11.00	35.24	69.50
IA 3135	160.49	23.48	17.51	37.88	60.80
SBIEC 11007	191.05	25.91	8.09	29.38	56.13
ISH 100	145.24	16.44	18.21	23.34	33.90

Reference

P Govindaraj (2011) Annual Report. Sugarcane Breeding Institute pp 28.

ERRATUM: In Indian Journal of Plant Genetic Resources: 26(2) 2013 on page 190, the title no. 24 should be read as WF Sarson of yellow Sarson (*Brasica rapa* var. Yellow Sarson) instead of WF Yellow Sarson an Indian Mustard (*Brasica rapa*).

for different quality parameters as well as resistance against late blight and potato virus Y this hybrid can be used as a suitable parent for developing superior potato varieties for processing and resistance breeding.

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15. SBIEC11004 (IC0594464; INGR13050) a Sugarcane *Erianthus* Clone with High fiber content: 30.21%

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SBIEC 11004 was developed from cross between IK 76-92 (*Erianthus arundinaceus*) and 98 N1 1405 (interspecific hybrid involving *Saccharum officinarum* and *Saccharum spontaneum*) for introgressing high fibre content from the parent IK 76-92. The clone was selected through hybridization and clonal selection method at Sugarcane Breeding Institute, Coimbatore. INGR 13050 is one of the potential high fibre energy cane with the highest cane fibre content of 30.21 % which is more than 120 % higher than the commercial sugarcane varieties presently cultivated. It also recorded high harvestable biomass/year of 193.83 t/ha and 75.94 t/ha of dry matter production/year (Govindaraj, 2011). The clone is a high yielding, fast growing, high tillering and thick cylindrical canes without wax coating and amenable for multiple ratooning. Bud is small and pentagonal in shape. Leaf sheath is green with smooth hairs and dewlap is absent. Under the abiotic stress conditions also it can perform well.

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