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Collecting Crop Genetic Resources from Mon, A Remote District of Nagaland

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An exploration for agri-horticultural crops from Mon district of Nagaland has resulted in the collection of 138 accessions representing rich variability in major field crops such as rice, maize and foxtail millet, besides first time collection of local germplasm of chenopod and prosomillet in this state. Drastic reduction in cultivation of Job's tears, a native crop of North-eastern Hill region, was observed. Diversity in exotic vegetables–*Abelmoschus caillei*, *Capsicum chinense* and *C. frutescens*, *Solanum aethiopicum* and *S. macrocarpon* along with important crops *viz*. okra, chilli and brinjal was also noted. Brief information on the salient collections, cultivation practices, local type preferences, folk use and conservation strategies are also highlighted.

Key Words: Collection, *Konyak*, Mon district, Nagaland, Plant genetic resources

Introduction

Mon district is located in North-East Nagaland, bordered by Sibsagar district of Assam in the North, Tuensang district of Nagaland in the South, Myanmar in the East, Longleng district of Nagaland in the West and in the North-East lies the Longding district of Arunachal Pradesh. The Naga tribe *Konyak* predominates in this district, and are challenged by inhospitable mountainous terrain, poor communication and transport facilities. Almost all the cultivated areas are under *jhum*; of these, about 70% area belong to cereals (Department of Planning and Coordination, 2011). This district is known for rich diversity in rice, maize, millets, chilli, cucurbits, etc. and the inhabitants of this district have a rich tradition of biodiversity conservation strategies (Godbole, 2000). This area has not been extensively explored and a very meagre collection exists in the National Genebank (NGB) of NBPGR, New Delhi from this district. Thus a special exploration trip was undertaken for collecting germplasm of different agri-horticultural crops, especially those that can be conserved through seeds.

Materials and Methods

Exploration was undertaken in five (out of six) blocks of Mon district *viz*. Chen, Mon, Phomching, Tizit and Wakching for ten days during November 2013, lying between latitude 26° 30' to 26° 53' N and longitude 94° 51' to 95° 13' E with altitude ranging from 174 to 1,626 m. Climate of the upper region is sub-temperate, while the middle region is warmer and the lower region is sub tropical. Temperature varies from 16 to 31° C in summer (March-September), 4 to 24° C in winter (October to February) while average rainfall is about 200-300 cm and average relative humidity is 76%. Soil is mostly lateritic while red soils occur in the plains bordering Assam. Besides *jhum* cultivation, handicraft, hunting and collection of minor forest products are other important occupations. Staple food of these people includes rice, taro, pork, etc.

The collection sites were identified based on published information on environmental variation, diversity and distribution of target crops, coupled with interaction with the officials of Krishi Vigyan Kendra (KVK) and agricultural departments at the district/sub-divisional level. Visit to local markets (within the broader collection sites) helped to further narrow down, sometimes to the particular farmer(s) within the site. In general, efforts were made to collect the desired germplasm from field (farmer's field/home garden). Where the crop had already been harvested, collections were made from the threshing yards/farm store. In general, random sampling was followed for field collection and farm-stored germplasm whereas small samples were bulked in case of wild species. Passport data for each collected sample were recorded as per standard format (Moss and Guarino, 1995). A semi-structured questionnaire was used to record the characteristics/cultivation practices (method of cultivation, sowing and harvesting time, frequency/ extent of cultivation, specific use, and important grain characteristics, etc.) of collected local types through

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direct observation or questioning the family members or more often by a combination of both after necessary triangulation. Each collection was assigned a unique collector number. Most of the collected materials are conserved in NGB, and under characterization.

Results and Discussion

A total of 138 accessions belonging to 42 taxa were collected from 34 sites in the district (Table 1 and 2; Fig. 1).

Cereals, Millets and Pseudocereals

Usually seeds are sown during end of February to first week of March and harvested during June-July for millets, July-August for maize, August end to September first week for rice. Upland direct seeded rice (in *jhum* lands) is the most common rice cultivation system in the areas surveyed. Popcorn type maize is grown at lower altitudes up to 1,200 m while the larger-grained types are generally at higher altitudes that are unsuitable for rice cultivation. Millets are generally grown as mixed crops with chenopod, perilla and soybean. In cooler areas lying in eastern and southern regions, chenopod is cultivated.

Rice forms the single most common crop and rich diversity covering 35 local types were collected (Table 2 and Fig. 2). Data from questionnaire revealed that two-thirds of local types belong to the less-sticky type which is preferred for daily consumption. Sticky types of rice are special utility ones used in preparation of homemade biscuits and rice beer, and in ceremonies, festivals, etc. They, in general, are poor yielders, and hence farmers grow these in less quantity (Nakro, 2011). *Gam* (KP/SC-1538) is a popular sticky type with scented-grains and early maturity. *Tahnyu* (KP/SC-1449) is a speciality less sticky type exclusively given to children in Ngangching area. Another scented upland type *Thaling* (KP/SC-1537), confined to the areas bordering Myanmar (Longwa and Phomching), takes nearly nine months to harvest, but is popular owing to its good taste. Both scented and non-scented types are found in both sticky and less-sticky categories. White sterile lemma colour, a very rare character, was recorded in three accessions (KP/SC-1504, KP/SC-1564 and KP/SC-1582).

The maize germplasm collected during the exploration belongs to flint (77%), dent and popcorn types (Table 2 and Fig. 3). Mature kernels are roasted and pounded in traditional wooden mortar and pestle; the fine powder is either used for preparing soup/ porridge or as an alternative to milk powder for preparing tea; the coarse granules are either cooked and eaten as rice or used as pig feed. Different varieties are grown for specific purpose – immature grain (*Shiyam*; KP/SC-1453), mature grains (for food use in winter), popcorn (puffed kernel) and for pig feed. *Thoagong* (KP/SC-1477), however, is one common flint-type grown for multiple use.

Millets contribute the main food until the harvest of rice. Foxtail millet grains are easy to cook and cooked either alone or with rice; also used in the preparation of biscuits and as a substrate for making local beer. *Kho* (KP/SC-1532), a local type in Longwa area, is preferred to rice due to superior taste. Local type *Keisa* (KP/SC-1579), confined to Yannyu area of Tizit block, has a distinctive panicle shape like a cat's foot (four well-developed lobes at the distal end). Prosomillet, a first time collection from Nagaland, is another crop under occasional cultivation in this area since long. Its grains are cooked like rice (after pounding) and were once used as a substrate for beer.

Job's tears was once a common staple crop, but now is not preferred in the entire tract owing to long duration, difficult cultivation methods and availability of alternative crops. At present in Chenwetnyu village, only 2-3 families out of 450 continued to cultivate this crop (an elliptic-oval grain type) whereas almost 40 years back every household used to cultivate it.

Two types of *Chenopodium album* are cultivated, *Yaolu* (also known as *Waothroi*), a short type (1.2-1.5 m) with small pink-tinged leaves, maturing early (i.e. June, nearly 120 days) and grains used in biscuit preparation; *Yaoha* (also known as *Aphom*) is a common tall type (3-4 m) with big green leaves and huge inflorescence, maturing late, (i.e. November-December, nearly 280 days) and grains used to prepare tasty gruel. In either case, young leaves are plucked for vegetable use till flowering, and later left undisturbed for their mature grains (used as pseudocereal). It was collected for the first time from Nagaland, though Hore (2007) reported the cultivation of tall type as pseudocereal in other districts of Nagaland–Phek and Tuensang. Unlike in the Himalaya, *Amaranthus caudatus* L. is grown here more as an ornamental than pseudocereal.

Table 1. Crop genetic resources collected from Mon district, Nagaland

S.No.	Crop group/Species	Common name	Local name	Accessions (No.)
Cereals (51)				
1.	*Coix lacryma-jobi* L.	Job's tears	Nyekok	1
2.	*Oryza sativa* L.	Rice	Ong, Dhan	37
3.	*Zea mays* L.	Maize	Shoavang, Shongta, Wongli, Phom	13
Millets (17)				
4.	*Panicum miliaceum* L.	Proso millet	La	4
5.	*Setaria italica* (L.) P Beauv.	Foxtail millet	Shee	12
6.	*Sorghum bicolor* (L.) Moench	Sorghum	Manlom	1
Pseudocereals (6)				
7.	*Chenopodium album* L.	Chenopod	Aphom, Waothroi	6
Pulses (6)				
8.	*Cajanus cajan* (L.) Millsp.	Pigeon pea	Mansha	1
9.	*Mucuna pruriens* (L.) DC. var. *utilis* (Wall. ex Wight) Baker ex Burck	Velvet bean	Peo	1
10.	*Vigna umbellata* (Thunb.) Ohwi & H Ohashi	Ricebean	Naga dal	4
Oilseeds (11)				
11.	*Glycine max* (L.) Merr.	Soybean	Longphe	6
12.	*Perilla frutescens* (L.) Britton	Perilla	Num	5
Fibres (3)				
13.	*Gossypium barbadense* L.	Sea Island cotton	Pai, Laken	3
Vegetables (35)				
14.	*Abelmoschus caillei* (A Chev.) JMC Stevels	West African okra		1
15.	*Abelmoschus esculentus* (L.) Moench	Okra	Bhendi	1
16.	*Allium chinense* G Don	Chinese onion	Temam	1
17.	*Allium sativum* L.	Garlic	Luson	1
18.	*Amaranthus blitum* L.	Purple amaranth	Chekoi, Phowang	1
19.	*Benincasa hispida* (Thunb.) Cogn.	Ash gourd	Waolo	1
20.	*Brassica juncea* (L.) Czern. var. *integrifolia* (Stokes) Sinskaya	Leafy mustard	Layeepatta	1
21.	*Canavalia gladiata* (Jacq.) DC.	Sword bean	Powo	1
22.	*Capsicum annuum* L.	Chilli	Maktikülow, Muktek	3
23.	*Capsicum chinense* Jacq.	King chilli	Rajamircha	1
24.	*Capsicum frutescens* L.	Bird's-eye chilli	Maktek	2
25.	*Cucumis sativus* L.	Cucumber	Maiko	1
26.	*Cucurbita moschata* (Duchesne ex Lam.) Duchesne ex Poir.	Pumpkin	Kamkai, Khailo	5
27.	*Lablab purpureus* (L.) Sweet	Lablab	Yonghe	2
28.	*Lagenaria siceraria* (Molina) Standl.	Bottle gourd	Vim	1
29.	*Luffa acutangula* (L.) Roxb.	Ridge gourd	Naovün	1
30.	*Luffa aegyptiaca* Mill.	Sponge gourd	Nauoah	1
31.	*Solanum aethiopicum* L.	Scarlet eggplant	Chamka	2
32.	*Solanum macrocarpon* L.	African eggplant	Chamkei	1
33.	*Solanum melongena* L.	Eggplant	Anthao	2
34.	*Vigna unguiculata* (L.) Walp.	Cowpea	Linglo	5
Crop Wild Relatives (9)				
35.	*Abelmoschus manihot* (L.) Medik. subsp. *tetraphyllus* (Hornem.) Borss.Waalk. var. *pungens* (Roxb.) Hochr.			1
36.	*Solanum viarum* Dunal	Tropical soda-apple		1
37.	*Solanum violaceum* Ortega		Khasa, Koikha	1
38.	*Trichosanthes bracteata* (Lam.) Voigt			2
39.	*Trichosanthes cordata* Roxb.		Nagpotak	1
40.	*Trichosanthes lepiniana* (Naud.) Cogn.			1
41.	*Vigna pilosa* (Willd.) Baker		Henyaam	1
42.	*Vigna sublobata* (Roxb.) Babu & SK Sharma			1
Total				138

Table 2. Local types of major crops collected from Mon district, Nagaland

S.No.	Crop	Local types
1.	Rice	***Sticky***: Gam*[a], Khamgong*, Kezak, Nyakha, Phuha, Shüovem, Tahmei, Yam, Yamshang*; ***Less sticky***: Chah[b], Chahkat[b], Chahpang[b], Chungchak, Dhaoha*, Gamgan, Hahpang, Kongkosh#, Laihee (=Shachu)#, Menjyu, Phesha*, Shahshu*, Shago*[a], Sheleai, Taha*, Tahnyu*, Taheang, Tahtak (=Pantah)*, Thosa*[a], Thrahsu*, Tishah#, Wongshu, Yemtong **(*stickiness not recorded*: Paajah, Tahzyah, Thaling*[b])**
2.	Maize	***Dent type***: Wangshang; ***Flint type***: Khuzyak, Kongliak, Neihelo, Paochao, Thoagong, Shenei, Shiyam; ***Popcorn type***: Phuhwonglick, Yongleng
3.	Foxtail millet	Hanei, Kawkha, Keisa, Kho, Konyu, Junsee, Seebhuk, Seeha, Seeong, Shanei, Shetak, Shi
4.	Prosomillet	Jeha, Jela, Lah, Thela
5.	Soybean	Ekhalonghi, Longphe, Pheo, Sheyonghe
6.	Cowpea	Kowlinglo, Linglo, Phealo, Tohlinglo, Wethrui

*scented; [a]early maturing; [b]late maturing; #wetland cultivation

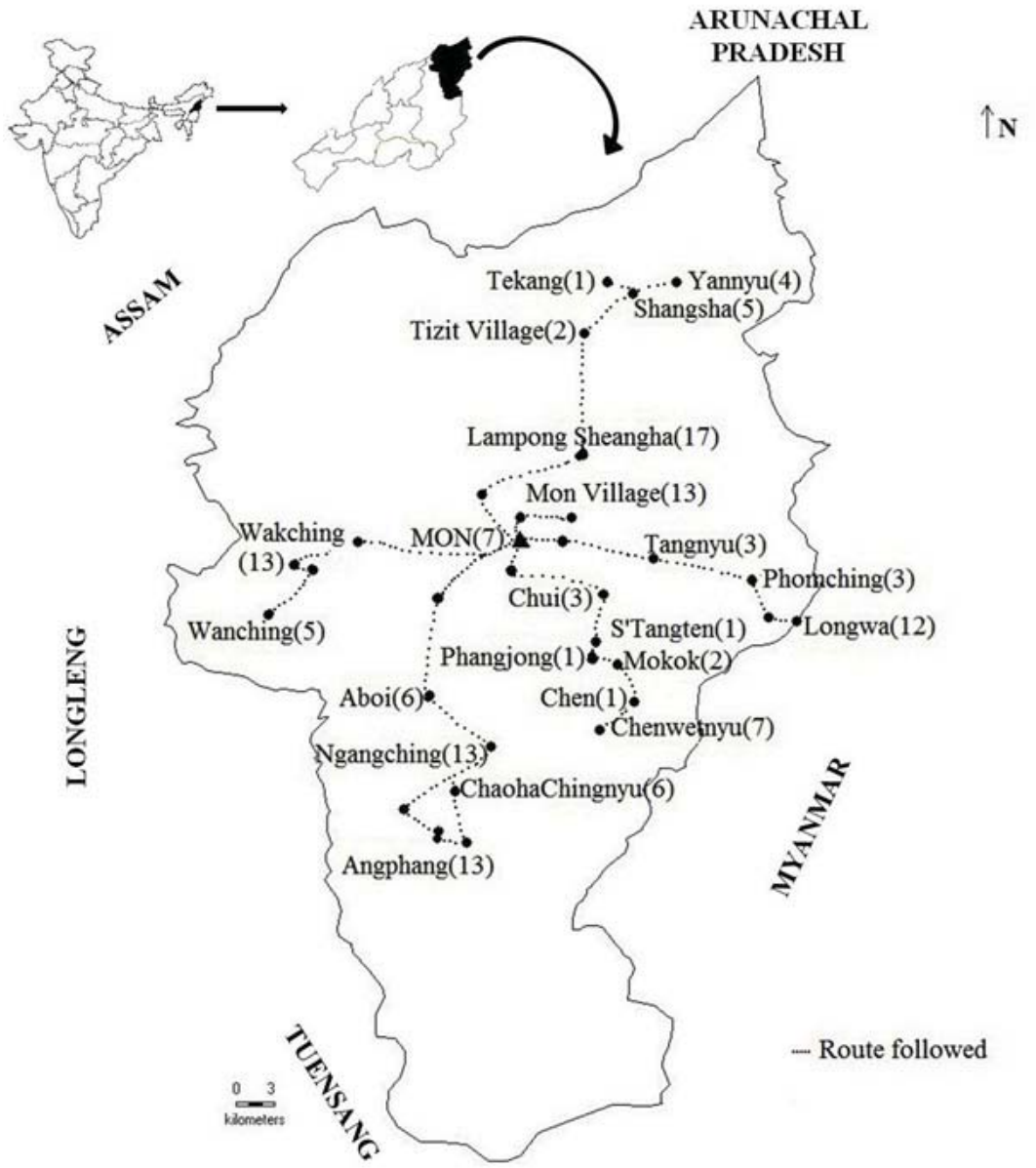

Fig. 1. Sites of germplasm collection in Mon district, Nagaland (numbers in parenthesis are collected accessions)

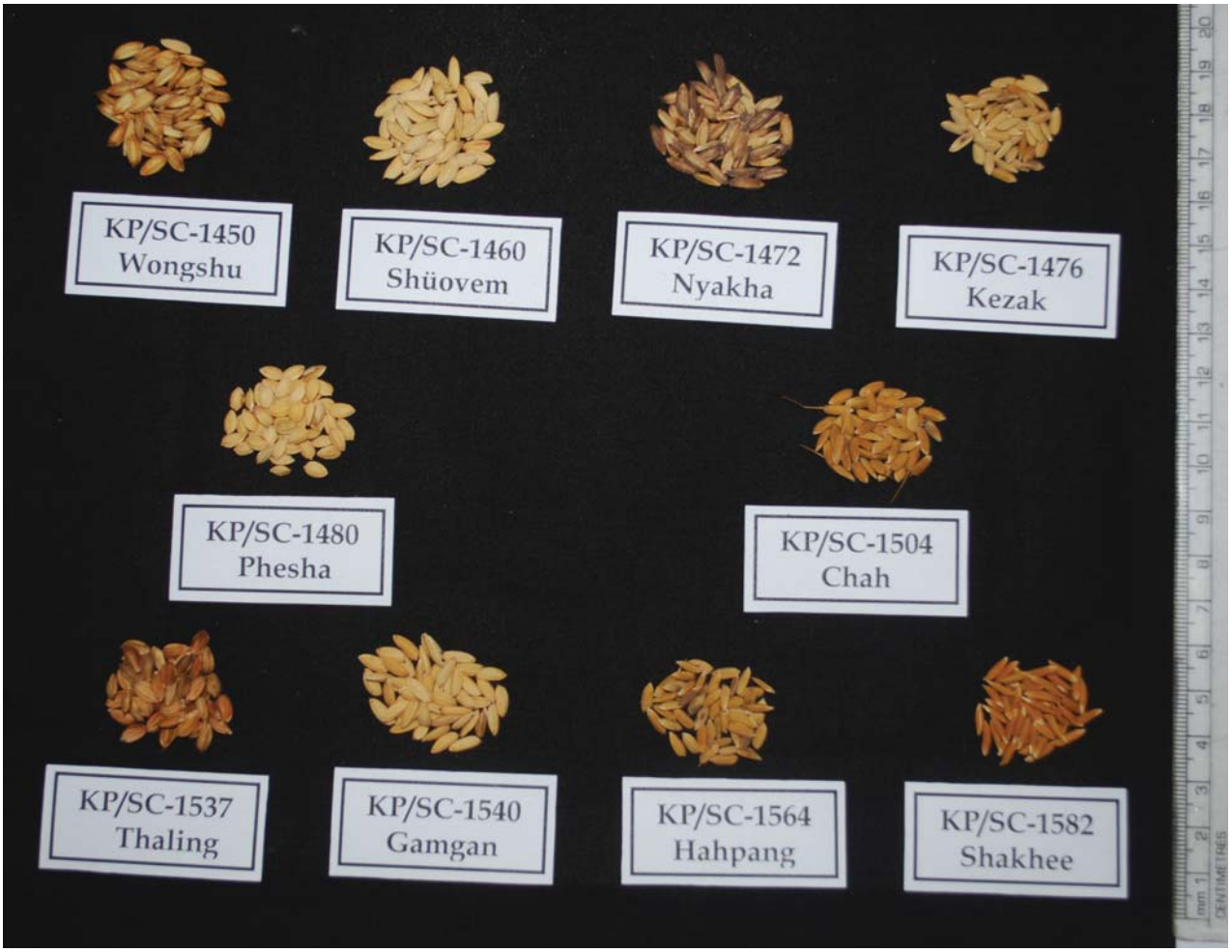

Fig. 2. Diverse local types of rice germplasm

Grain Legumes, Vegetables and Others

Ricebean exhibited variability in grain colour. Annual type red gram (having red coloured standard petal) is cultivated as pulse in the plain areas of Tizit block, while perennial type is cultivated in hilly areas at homestead level and preferred for immature pod as vegetable (rather than as pulse). Most vegetables are cultivated in specialized patches in *jhum* lands as mono-crops or in home gardens or near huts, while beans and cucurbits are grown along the fringes. Diversity in cowpea is rich and invariably for use as vegetable, especially for preparation of soup. *Abelmoschus caillei* is more commonly cultivated compared to *A. esculentus*. Three *Capsicum* species *viz*. *C. annuum*, *C. frutescens* and *C. chinense* and three *Solanum* species *viz*. *S. aethiopicum*, *S. melongena* and *S. macrocarpon* are in cultivation as vegetables in the explored areas and exhibited moderate variability. In *Solanum aethiopicum*, apart from the *Gilo* cultivar group, *Kumba* group (which is *S. integrifolium* Poir. of Arora and Hardas, 1977) was collected. Apart from use of fruits, flowering twigs of *S. macrocarpon* are also sold in markets as edible greens.

Interestingly, a white seeded type of *Perilla frutescens* apart from variability in seed size was collected. Soybean is commonly grown for its fermented product (*akhuni*) for consumption. The milk extracted from its beans is used for treating stomach disorders. *Gossypium barbadense* was occasionally found in cultivation at homestead level.

Traditional Agricultural Practices

Konyak Nagas avert the risk of crop failure by planting several economic species (in home gardens) and diverse varieties of crops (in *jhum* lands). This ensures yield in the long term, maximum returns with low levels of

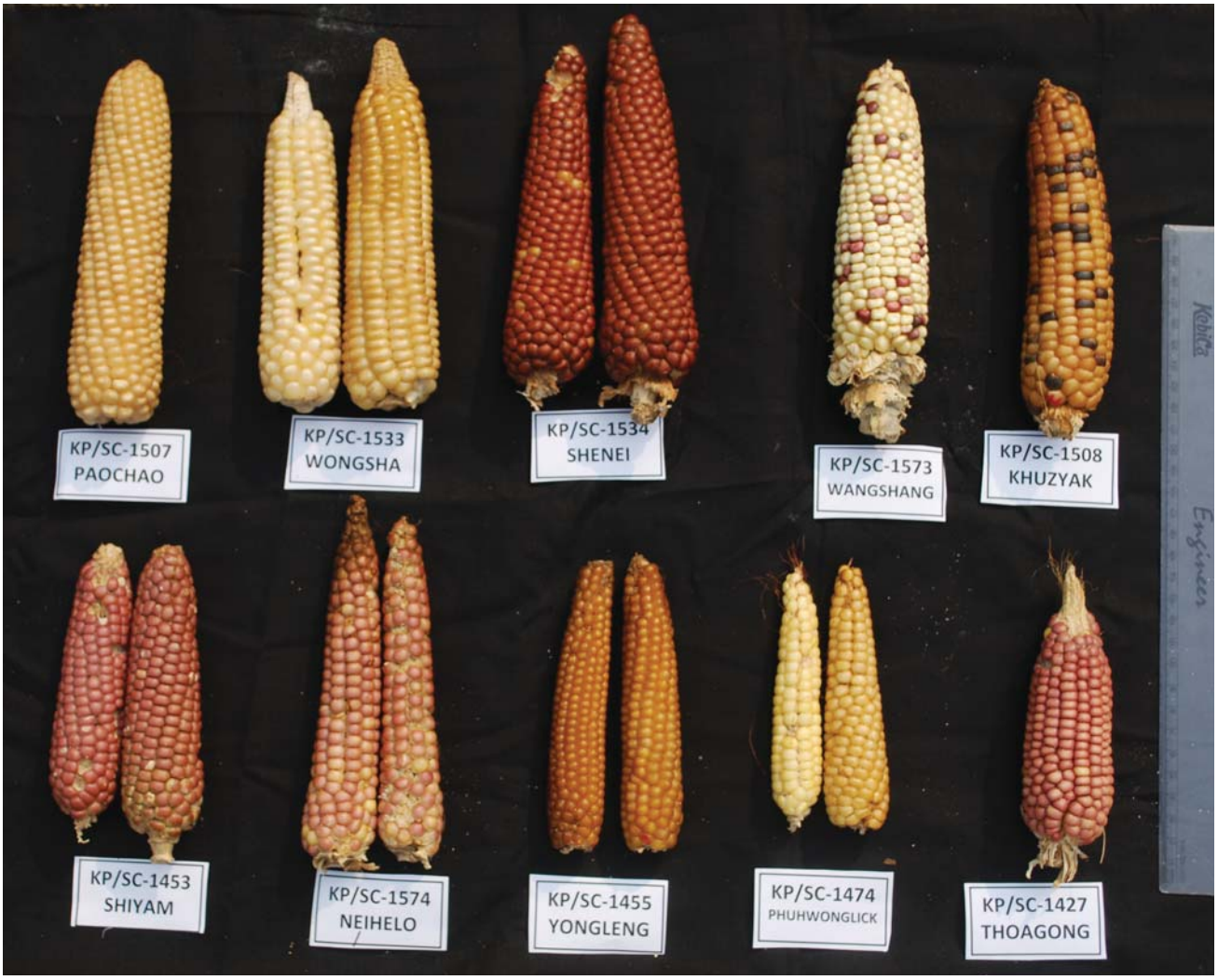

Fig. 3. Variability in cob characteristics of maize germplasm

technology and limited resources and promotes diverse options in diet (Harwood, 1979). Some observations worthy of highlighting are as follows:

- *Konyaks* prefer local varieties to improved ones, select elite material to suit their needs and maintain pure varieties. Two such recently selected rice varieties are *Tahtak* (KP/SC-1471; from an indigenous material) at Wanching village for delicious taste and late harvest (October) and *Shakhee* (KP/SC-1582; from an introduced material) in Tizit area for slender, highly scented grain and early harvest (3 months). Their preference for local varieties was also reported by Godbole and Sarnaik (2009). In maize, local types are maintained pure; in a few cases only, small proportion of dissimilar coloured kernels is observed.
- Women play a major role in conservation of local seed material. They take part in all farm related works including carrying farm products, and wild harvest of fruits, vegetables, etc. to nearby market. Panicles of foxtail millet, ears of maize and bulbs of alliums, dried fruits of brinjal (often longitudinally cut into four splits), chilli and cucurbits are safely kept for next year's sowing by hanging them on the rafter inside the home near smoke kiln to ward off pests. Home gardens are mostly managed by women folk. More than 120 species of plants are reported in *Konyak* home gardens (Zaren, 1999) and a market survey of Mon town indicated that out of 68 plant products recorded, 40 were harvested from home gardens (Godbole, 1998). Some notable wild plants commonly observed in home gardens

are *Clerodendrum colebrookianum* Walp. (leafy vegetable), *Crotalaria tetragona* Roxb. ex Andrews (edible flower buds and flowers), *Gynura cusimbua* (D. Don) S.Moore (leafy vegetable), *Hodgsonia heteroclita* (Roxb.) Hook.f. & Thomson (oil-rich seed kernels) and *Solanum violaceum* (young fruits as vegetable).

- Like other areas in the Northeastern Hill region, many crops native to Africa/ South America, are adapted to the local conditions in Mon district, and contributing to agricultural diversity through supplementing/ substituting native crops. Examples include *Abelmoschus caillei*, *Capsicum chinense*, *Cucurbita ficifolia* Bouché, *Cyclanthera pedata* (L.) Schrad., *Cyphomandra betacea* (Cav.) Sendtn., *Eryngium foetidum* L., *Gossypium barbadense*, *Passiflora edulis* Sims, *Sechium edule* (Jacq.) Sw., *Solanum aethiopicum* and *S. macrocarpon*. The role of Christian missionaries in their introduction/ popularization in these regions cannot be ruled out, as also opined by Arora and Singh (1973).

With the shortening of *jhum* cycle (to 6-7 years), climate change and imposition of high yielding varieties in recent years, collection activity is of paramount importance in this region. However, tribal people's preference for indigenous germplasm over improved varieties is a ray of hope for *in-situ* conservation activities. Considerable diversity in rice, maize and foxtail millet and chenopod was collected for the first time. Eastern and southern parts of the district, which were explored during the later phase of the trip, are in fact richer in crop biodiversity as evident from equal or higher diversity in germplasm collections from these parts as compared to northern and western parts. Future explorations need to be undertaken in remaining diversity rich pockets like Hunza, Longchang, Longshen, Mopong, Monyakshu, Naginimora, Tobu and Zangkham areas of Mon district, preferably in August-September and end of January. Yanger (1999) mentioned that Nagas cultivate about 360 different varieties of rice; our collection from a single tribe itself accounts for nearly 10% of it. Matching of names of local types indicated that about 95% of collected ones were not represented in NGB. People in this region expressed the need for cold-tolerant rice germplasm suited for higher hills so as to extend the area under this staple crop, which warrants the need for detailed characterization of the collected germplasm. Considering the enormous number of wild edible plants utilized by this tribal people, proper documentation and studies pertaining to nutritive value, method of utilization and identification of elite types would be beneficial for the sustainable growth of this native community.

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Molecular Genetic Diversity Analysis of Commercial Mango (*Mangifera indica* L.) Cultivars Employed as Parents in Hybrid Development in India

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Mango hybridization programmes use commercial cultivars as parents. Twenty three such popular cultivars of mango belonging to different regions of India were analyzed by employing multi-locus marker techniques to measure the genetic diversity existing among them. Twelve unanchored ISSR primers (114 markers) and 15 AFLP primer-pair combinations (1,073 markers) revealed average gene diversity over loci to be 0.231 and 0.257 respectively. Mango cultivars from southern India were found to be significantly different ($p<0.001$). In order to decipher how these markers are inherited, three popular hybrids 'Amrapali', 'Mallika' and 'Ratna' were compared with their parents for band sharing information. Number of ISSR markers shared between pairs of parents and their hybrid was nearly 20% more than that of AFLP markers, endorsing the conserved nature of ISSR profiles. Our observations on (i) genetic relatedness among popular cultivars and (ii) band sharing pattern among parents and hybrids have implications on mango germplasm collection and breeding activities.

Key Words: AFLP, Band sharing, Diversity analysis, ISSR, Mango hybrids

Introduction

Mango *(Mangifera indica* L.) is the most important fruit of tropics and nearly all the world's monoembryonic cultivars have Indian pedigree (Mukherjee, 1953). Most of the present day popular mango cultivars in India have originated as chance seedlings that were maintained through vegetative propagation (Mukherjee, 1972). In addition to thousands of cultivars developed as chance seedlings, India has produced many commercially successful hybrid mango cultivars. However, despite the wide range of available genetic variation and ease with which the selected hybrid can be vegetatively propagated, very few parents have generally been employed in mango hybridization efforts in India. For instance, Indian Agricultural Research Institute (IARI), New Delhi and Central Institute of Sub-tropical Horticulture (CISH), Lucknow often use 'Dashehari' or 'Amrapali'; Indian Institute of Horticultural Research (IIHR), Bangalore and Fruit Research Station, Vengurla choose 'Alphonso'; and IARI, New Delhi and Fruit Research Station, Sangareddy employ 'Neelum' as parents.

Because few genotypes have been employed as parents (based, mostly on fruit traits and adaptation), extensive knowledge of genetic base of such cultivars turns out to be a prerequisite for developing sustainable breeding and systematic conservation strategies. Consequently, it becomes indispensable to plan, explore, assemble, establish and characterize large number of individual genotypes bearing the name of these cultivars, in order to conserve and exploit maximum allelic variability available within elite cultivars. Nevertheless, cultivation of different cultivars under the same name together with existence of many synonyms for popular cultivars e.g. 'Langra' (12), 'Dashehari' (5), 'Bangalora' (10), 'Alphonso' (8) can render germplasm utilization complicated (Pandey, 1984). Under such circumstances, unambiguous identification and meticulous diversity analysis can save a lot of investment in terms of time, effort and cost.

Traditionally, genetic characterization in mango has been carried out by means of morphological characters (IPGRI, 2006; PPVFRA, 2008). However, influence of environmental and developmental factors, existence of limited variation and subjective nature of evaluation of these traits have often posed problems (Adato *et al.*, 1995). Since 1990's various types of DNA markers have been employed to complement the characterization procedure including RAPD (Schnell *et al.*, 1995), ISSR (Eiadthong *et al.*, 1999), AFLP (Kashkush *et al.*, 2001), cpSSR (Xin-Hua *et al.*, 2007), SSR (Ravishankar *et al.*,

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2011), SCOT (Luo *et al.*, 2010), CAPS (Shudo *et al.*, 2013) and SNP (Kuhn, 2014). The markers have been used extensively to characterize germplasm accessions of mango in the USA (Schnell *et al.*, 1995), India (Karihaloo *et al.*, 2003, Ravishankar *et al.*, 2011), Iran (Shamili *et al.*, 2012), Australia (Dillon *et al.*, 2013), China (Gao *et al.*, 2013), *etc.*, with various objectives and varying degrees of success and utility. An overview of use of different marker techniques in mango genetic analysis showed that all the markers were good enough, when used suitably, for diversity analysis in an outcrossing tree species like mango.

From the available information in mango, the genetics of inheritance of various horticultural characters appears to be unclear. However, such information along with scorable markers is extremely useful in understanding the genetic relatedness between the putative parents to decide which parental types ought to be used in hybridization programmes. For instance, leaf flavor for fruit flavour, higher phloem: xylem ratio, higher phenolics in the apical bud and low stomatal density for dwarfness etc. have been identified as valuable morphological markers. Use of molecular marker profiles as a complementary approach was shown to enhance the effectiveness of pre-selection (Krishna and Singh, 2007). Comparison of morphological and physiological traits between hybrids and parents would only present part of a picture. Molecular marker analysis is expected to provide a genome wide comparison both in expressed and unexpressed regions. Srivastava *et al*. (2007) and Hemanthkumar and Vasanthaiah (2009) reported clustering of cultivars on the basis of common parentage whereas Srivastava *et al*. (2004) actually attempted to identify genetic relatedness between hybrids and parents on the basis of various multi-locus markers. However, these attempts reduced the band sharing into similarity coefficients and comparisons were generally based on the clustering pattern alone and stopped short of actually analyzing band sharing patterns. Band sharing studies can provide vital cues to the breeders about parents, hybrids and selection process. For instance, in an experimental cross it was demonstrated that 85% of the AFLP markers exhibited Mendelian segregation and 15% showed distorted segregation (Kashkush *et al.*, 2001). Therefore, it would be interesting to know band-sharing pattern between the marker profiles of commercially successful Indian mango hybrids and their parents.

Among various DNA markers used in mango genetic studies, SSRs have been established as superior because of their co-dominance and reproducibility. SSRs are particularly employed in DNA fingerprinting, marker associated selection studies involving homozygous parents, and population genetics. However, SSRs with a maximum of two alleles per diploid genome are less suitable for band sharing studies in tree species where parents and offspring are highly heterozygous. Conversely, in multi-locus marker techniques a single assay can hit multiple locations on the genome to provide a possibility of greater genome coverage. PCR-based markers inter simple sequence repeats (ISSR) and amplified fragment length polymorphism (AFLP) do not need any prior information about the target genome sequences, generate large number of amplicons and are adequately reproducible.

We selected a set of popular mango cultivars employed as parents in hybridization programmes and representing different geographical regions of India, for the present study. The objectives were: (1) to assess genetic diversity among the elite cultivars based on ISSR and AFLP profiles and (3) to study band sharing pattern in mango hybrid cultivars and their parents.

Materials and Methods

Plant Material and DNA Extraction

The study was carried out in 23 selected commercial cultivars of mango (Table 1). These included 16 monoembryonic cultivars, three polyembryonic cultivars and four hybrid cultivars. Flushing tender leaves from single trees of each cultivar were used for DNA isolation by cTAB method with minor modifications established in our laboratory (Archak *et al*., 2003). DNA was treated with RNase and purified by repeated ethanol precipitation. Quantification was carried out by fluorometry.

Marker Analysis

Twelve primers pre-selected for clarity, scorability and reproducibility of banding pattern were employed for ISSR analysis (Table 2). Fifteen fluorescently-labelled primer combinations were employed for the generation of AFLP markers (Table 3). Amplification and documentation of ISSR and AFLP markers were carried out as per established procedures (Archak *et al.*, 2003). Amplicons were scored as discrete variables, using 1 to indicate presence and 0 for absence. Variant status of the amplicon in even one of the cultivars was counted as polymorphic. A binary matrix was created by scoring bands in case of ISSR and peaks in case of AFLP. Resolving power of a primer/ primer combination

Table 1. Mango cultivars profiled in the study

Cultivars	Region of origin/ pedigree	Source#
'Alphonso'	Maharastra	FHT
'Amrapali'	Dashehari × Neelum	FHT
'Bangalora'	Karnataka, Tamil Nadu	FHT
'Bhadauran'	Uttar Pradesh	FHT
'Bombay Green'	Uttar Pradesh	FHT
'Chandrakaran*'	Kerala	RARS
'Chausa'	Uttar Pradesh	FHT
'Dashehari'	Uttar Pradesh	FHT
'Fazli'	Bihar	FHT
'Husnara'	Bihar	FHT
'Jamadar'	Gujarat	FHT
'Kurukkan*'	Kerala	FHT
'Lal Sundari'	Andhra Pradesh	FHT
'Langra'	Uttar Pradesh	FHT
'Mallika'	Neelum × Dashehari	FHT
MCDH-1	North East India	Goa
'Neelum'	Tamil Nadu	FHT
'Olour*'	Tamil Nadu	RARS
'Rajapuri'	Gujarat	FHT
'Rataul'	Uttar Pradesh	FHT
'Ratna'	Neelum × Alphonso	FHT
'Vanaraj'	Gujarat	FHT
'Zardalu'	West Bengal	FHT

* Polyembryonic cultivar
FHT= Division of Fruit and Horticultural Technology, Indian Agricultural Research Institute, New Delhi; RARS= Regional Agricultural Research Station, Kerala Agriculture University, Ambalavayal, Kerala; Goa= ICAR Research complex, Goa.

was calculated as the sum of band informativeness of all the markers generated by that primer. Genetic diversity was estimated by computing average gene diversity over loci (Nei, 1973). Partitioning of variance between different mango growing regions was carried out by AMOVA version 1.55 (Excoffier, 1992; Huff *et al*., 1993). Band sharing pattern of AFLP and resultant average taxonomic distance based on two-dimensional cluster were determined using JMP version 10 (SAS Institute, 2012).

Results

Marker Profiles

Twelve oligonucleotide primers produced a total of 140 ISSR markers amplifying on an average 94.9 bands per cultivar (Table 2). 81.4% of the amplicons were polymorphic. Primers $(GAAGTGGG)_2$, $(AT)_5$ $(GT)_5$, $(TA)_5$ $(GT)_5$ and $(AGG)_6$ generated only polymorphic markers, whereas more than half the markers produced by $(ACTG)_4$ were monomorphic. Fifteen primer-pair combinations generated 1228 AFLP peaks with an average of 651.7 amplicons per cultivar (Table 3). 87.4% AFLP markers were polymorphic. All the three *Mse*I-CAG combinations (J, K and L) produced only polymorphic markers.

Both ISSR and AFLP markers could clearly distinguish all the cultivars. Oligonucleotide primers displayed an average resolving power of 4.87 against 28.84 of AFLP primers (Table 2 and Table 3). This was reflected in the inability of individual ISSR primers to distinguish each cultivar whereas each AFLP primer could do so independently. Four cultivar specific ISSR markers, two for 'Lal Sundari' [$(GATA)_4$-650, $(GACAC)_4$-250] and one each for 'Rataul' [$(GACAC)_4$-1500] and 'Chandrakaran' [$(GATA)_4$-600] were obtained. Cultivar specific AFLP markers could be identified for each cultivar except for 'Dashehari'. Remarkably, 14 cultivar specific markers were identified for 'Amrapali'. AFLP primer pair *Mse*I CAC+*Eco* RI ACA (code M) generated as many as 14 cultivar specific markers.

Diversity Estimates and AMOVA

Genetic diversity of 23 mango cultivars was estimated as average gene diversity over loci. The values of overall diversity were 0.257 and 0.231 for AFLP and ISSR respectively. Distribution of the diversity was estimated by grouping cultivars of chance origin (i.e. excluding hybrids) based on geographic differentiation. The regions were – *northern* ('Bhadauran', 'Bombay Green', 'Chausa', 'Dashehari', 'Langra' and 'Rataul'), *southern* ('Bangalora', 'Chandrakaran', 'Kurukkan', 'Lal Sundari', 'Neelum' and 'Olour'), *eastern* ('Fazli', 'Husnara', MCDH-1 and 'Zardalu') and *western* ('Alphonso', 'Jamadar', 'Rajapuri' and 'Vanaraj'). Cultivars were compared, region wise, for polymorphism of markers and average gene diversity over loci (Table 4). The estimates revealed maximum diversity in the southern cultivars. AMOVA revealed that, 96.3% of the total ISSR marker diversity was attributed to within region and 3.7% to between regions, whereas AFLP markers displayed a higher between regions distribution at 7.8% (Table 5). Southern Indian cultivars were significantly different from northern and eastern Indian cultivars ($p<0.001$) as deduced by both ISSR and AFLP markers.

Table 2. Primers used for ISSR analysis

Sequence	Annealing temperature (°C)	Total bands	Polymorphism (%)	Resolving power
$(GATA)_4$	43	9	77.78	2.43
$(ACTG)_4$	45	14	42.86	1.65
$(GACA)_4$	45	17	94.12	7.74
$(GAAGTGGG)_2$	50	14	100	7.43
$(GGAT)_4$	45	7	57.14	2.58
$(AT)_5$ $(GT)_5$	52	8	100	4.52
$(TA)_5$ $(GT)_5$	52	11	100	6.76
$(GACAC)_5$	61	9	77.78	3.27
$(GTG)_6$	57	15	80	7.09
$(AGG)_6$	57	10	100	4.16
$(GTG)_4$	36	12	66.67	4.43
$(TCC)_5$	52	14	78.57	6.33
		140*	81.43**	4.87**

* Total across primers
** Mean values across primers

Table 3. Primer combinations used for AFLP analysis

Primer combination	Code	Total Bands	Polymorphism (%)	Resolving power
*Mse*I CAT+*Eco* RI ACA	A	119	87.39	42.84
*Mse*I CAT+*Eco* RI AAG	B	112	86.61	45.00
*Mse*I CAT+*Eco* RI AGC	C	60	95.00	25.30
*Mse*I CTT+*Eco* RI ACA	D	103	88.35	40.92
*Mse*I CTT+*Eco* RI AGG	E	81	77.78	29.23
*Mse*I CTT+*Eco* RI AAC	F	58	87.93	23.64
*Mse*I CTG+*Eco* RI ACA	G	113	83.19	38.57
*Mse*I CTG+*Eco* RI AGG	H	104	90.38	38.48
*Mse*I CTG+*Eco* RI AAC	I	57	73.68	16.73
*Mse*I CAG+*Eco* RI ACA	J	98	100.00	44.72
*Mse*I CAG+*Eco* RI AAG	K	43	100.00	21.59
*Mse*I CAG+*Eco* RI AGC	L	61	100.00	23.79
*Mse*I CAC+*Eco* RI ACA	M	69	84.06	18.87
*Mse*I CAC+*Eco* RI AAG	N	90	78.89	29.86
*Mse*I CAC+*Eco* RI AGC	O	60	81.67	21.93
		1228*	87.38**	28.84**

* Total across primers
** Mean values across primers

In addition, AFLP could discern between other regions as well. However, differences between east and north Indian cultivars were found to be non-significant.

Band Sharing

The six cultivars (three hybrids and their parents) analyzed, exhibited a total of 125 ISSR bands

Table 4. Comparison between different groups of mango cultivars

Group	AFLP				ISSR			
	North	South	East	West	North	South	East	West
Total number of markers	953	977	941	998	127	129	128	117
Per cent polymorphism	62.75	72.36	57.70	64.93	48.03	70.54	41.41	53.85
Average gene diversity over loci	0.235	0.271	0.238	0.266	0.187	0.268	0.175	0.226

Table 5. Analysis of molecular variance (AMOVA)

Source of variation	df	Percentage of variance	p value (1000 permutations)
AFLP			
Among regions	4	7.80	<0.001
Among cultivars within regions	18	92.20	<0.001
ISSR			
Among regions	4	3.71	<0.001
Among cultivars within regions	18	96.29	<0.001

(44% polymorphic) and 1022 AFLP bands (72.1% polymorphic). The average number of bands per genotype was more than 190 (69.5% polymorphic), which is by far the maximum compared to any of the previous reports on mango genetic analyses. Markers observed in the profiles of hybrid cultivars were shared either with only male parent (*male parent specific*) or female parent (*female parent specific*) or were common among parents and the hybrid (*shared*). Markers which could not be attributed to either of the parents were termed as *novel*. Mean number of ISSR markers shared by hybrids with both the parents were largely equal (~10%) whereas on an average hybrids shared greater number (17.9%) of AFLP markers with female parents (Table 6). ISSR profiles of 'Amrapali' and 'Mallika', the products of reciprocal crosses, revealed that 'Dashehari' contributed significantly higher number of markers to both the hybrids irrespective of whether it was male or female parent. 'Ratna' shared higher percentage (~24%) of AFLP markers with 'Neelum' (female parent) but most remarkably, 'Amrapali' exhibited more than 20% AFLP bands that could not be assigned to either of the parents (Table 6).

Overall pairwise similarity among parents and hybrids was higher using ISSR markers (0.898), compared to AFLP (0.770). Based on AFLP, 'Amrapali' was equidistant from parents (0.275). Furthermore, assembly of banding pattern in the form of a 2D cluster (Fig. 1) illustrated that 'Amrapali' carries distinctive AFLP pattern in relation to all other genotypes particularly, its parents.

Discussion

Breeding in mango has been bringing together desirable characters from two established cultivars. Estimating the diversity existing among 23 leading cultivars therefore assumes practical significance. To ensure our estimates based on dominant markers reflect the actual state, more than thousand markers were employed of which recessive markers ("0" score) were of greater proportion.

Genetic Diversity and Distribution

Genetic diversity in 23 mango cultivars expressed as average gene diversity over loci was moderate; the

Table 6. Marker assignment* in mango hybrid cultivars

	Total markers	Female parent specific	Male parent specific	Shared	Novel
AFLP					
'Amrapali'	742	11.7	13.7	54.0	20.5
'Mallika'	612	17.8	12.6	67.3	2.3
'Ratna'	683	24.3	13.5	55.2	7.0
Mean	679	17.9	13.3	58.8	9.9
ISSR					
'Amrapali'	99	11.1	5.1	80.8	3.0
'Mallika'	109	8.3	12.8	76.1	2.8
'Ratna'	104	12.5	12.5	73.1	1.9
Mean	104	10.6	10.1	76.7	2.6

*Expressed as per cent of total markers

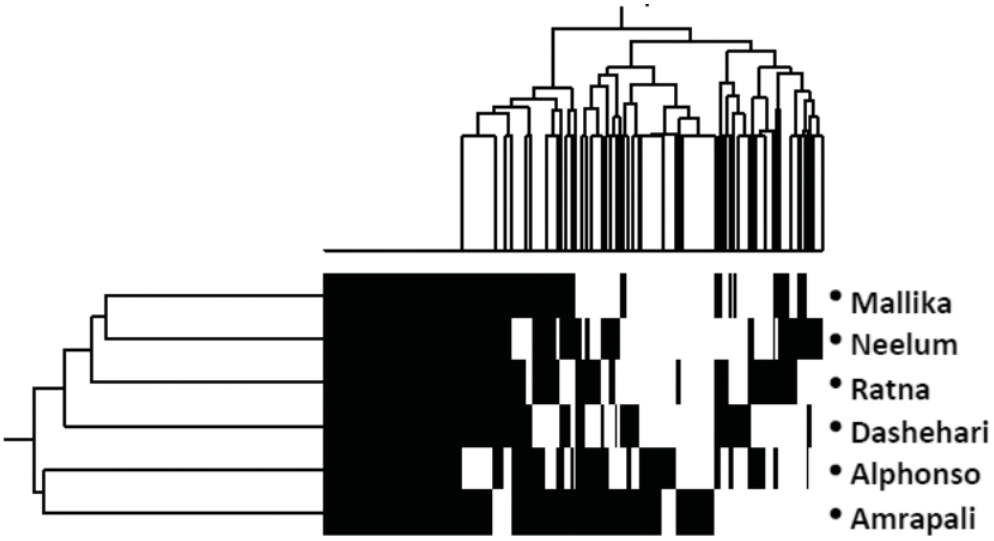

Fig. 1. Two-dimensional dendrogram of mango parents ('Dashehari', 'Neelum' and 'Alphonso') and hybrids ('Amrapali', 'Mallika' and 'Ratna') derived from 1022 AFLP markers. The OTUs are clustered horizontally and markers are grouped vertically. The binary data are represented as band profiles. Black band represents "1" and white represents "0". Note the remarkably distinct pattern of 'Amrapali'.

values were 0.257 and 0.231 based on AFLP and ISSR respectively. These values are indicative of the extent of diversity represented in the elite commercial cultivars and do not represent the overall diversity present in Indian mango germplasm. It is pertinent here for mango breeders to note that combinatorial breeding may be bringing preferred traits together but at the cost of overall genetic base (Iyer and Degani, 1997).

Mango cultivars have been selected and cultivated in different regions of India based on taste and adaptation. Cultivars could be early and late bearers, mono and polyembryonic, regular and alternate bearers, dessert type and pickling type etc. Among different mango growing regions, southern cultivars were significantly different from cultivars from northern and eastern regions as deduced by both ISSR and AFLP markers (Table 4). Moreover, majority of the molecular variation from both AFLP and ISSR data was found within rather than between regions (Table 5), which is consistent with the general trend in other out crossing species (Huff *et al.*, 1993; Nesbitt *et al.*, 1995; Hwang *et al.*, 2001). Cultivars belonging to diverse regions differ largely in their adaptability as some of them are proven ecotypes. When cultivars from one region are grown at other region, they vary in bearing characteristics, fruit quality and time of flowering. Superior chance seedlings selected as cultivars led to fixation of very high degree of heterozygosity, leading to high within-region variation.

There was no apparent clustering of 23 cultivars based on either geographical location or embryo type. Lopez-Valenzula *et al.* (1997) have reported such grouping by analyzing 15 cultivars from 4 different countries. In the present experiment, plant material belonged to different areas within India. Therefore, absence of groupings in relation to geographical location may be indicative of the *continuum of variability* existing among Indian cultivars (Mukherjee, 1972; Majumdar and Sharma, 1985). Our analysis did not cluster polyembryonic cultivars together as reported by Iyer and Degani (1997) but in contrast to observations of Ravishankar *et al.* (2004).

Band Sharing and Selection of Parents

The study was carried out in three hybrid cultivars of mango and their parents. 'Mallika' ('Neelum' × 'Dashehari') and 'Amrapali' ('Dashehari' × 'Neelum') are the two most successful regular-bearing hybrids developed by IARI, New Delhi in 1972 (Singh *et al.*, 1972). 'Mallika' has high total soluble solids content, a higher percentage of pulp, fibreless flesh and a fruit size of about 300g. 'Amrapali' is precocious, distinctly dwarf, fruit with excellent quality and very rich in vitamin A. 'Ratna' ('Neelum' × 'Alphonso') was developed in 1981 at Regional Fruit Research Station, Vengurla, Maharashtra (Salvi and Gunjate, 1989). 'Ratna' has a larger fruit size, fruit quality similar to 'Alphonso' and is free of spongy tissue.

The band sharing results of the present experiment need to be considered in the light of following facts: (i) In mango hybridization, unlike field crops, neither the parents are homozygous nor is the progeny heterozygous for all loci, and (ii) Both ISSR and AFLP are multi-locus markers, hence, apparent band sharing may be due to identity by descent or to identity by state. Therefore, the observations presented and the inferences drawn here are best taken as additional information for mango breeders and not as inheritance studies *per se*. Detailed inheritance studies require (i) pre-screening of the primers to minimize background variation, highlighting only the true differences in the inheritance pattern and (ii) both useful and discarded individuals of the hybrid progeny.

Genetic recombination events occur during the gamete formation in the parents. This may lead to changes in the primer binding sites as well as restriction sites resulting in the loss of bands or occurrence of *de novo* amplicons. Nevertheless, such events are not very common and therefore novel bands occur in negligible number. However, since AFLP and ISSR techniques generate dominant and multi-locus markers, we end up scoring variant alleles as novel bands. Based on our own studies in mango and cashew (unpublished), novel AFLP and ISSR bands may range up to 3-5% of the total number of bands. Conserved nature of ISSR markers was evident because: (i) average number of ISSR markers shared between parents and their hybrid (~77%) was nearly 20% more than those observed in case of AFLP (~59%); (ii) compared to AFLP (~10%), very few novel bands were produced by ISSR (average number of novel bands 2.6%).

Higher number of 'Neelum' specific AFLP markers observed in 'Ratna' supports the observation of fewer 'Alphonso'-like fruit and other morphological characters in 'Ratna', which necessitated backcrossing of 'Ratna' with 'Alphonso' (Salvi and Gunjate, 1989). Occurrence of 20.5% of novel AFLP bands in 'Amrapali' could not be explained on the basis of recombination events alone in the origin of the cultivar. 'Mallika' and 'Amrapali' were developed and released by Indian Agricultural Research Institute, New Delhi (Singh *et al.*, 1972). Between 1961 and 1980, 1200 hybrids were raised at IARI of which 710 had 'Neelum' as a parent. Dwarfness, regularity of bearing, and better fruit quality were the traits for which selection was carried out. There were only two successful lines with excellent fruit quality and regularity of bearing, which were subsequently released as 'Mallika' and 'Amrapali'. 'Mallika' showed vigorous habit but 'Amrapali' was the only hybrid line that had distinct dwarf stature (Sharma and Majumdar, 1989). Our observation of higher novel AFLP bands in 'Amrapali' may not be just circumstantial, but might provide clues to the marked morphological differences exhibited by the hybrid. Since 'Amrapali' has been used as a parent (mostly as a female parent) in many of the crosses dwarfness, regularity of bearing and fruit quality (Pinto and Byrne, 1993), detailed molecular analysis may pave way for marker assisted selection of the progeny. Advanced genomic tools can help scan large genome regions to provide find out if there is any correlation between observation of higher novel AFLP bands and typical morphology of 'Amrapali'.

Mango breeding remains to be a slow process without novel strategies incorporated in the programmes. As a result, conservation programmes of mango genetic resources have not translated anything into germplasm utilization. The PGR efforts in mango need to grow beyond clonal orchards and seek to characterize and conserve products of crossing programmes. Without DNA markers, screening large number of trees at younger stage is impossible. An accurate view of inheritance of DNA markers in mango can be obtained with mapped markers distributed across linkage groups. Our investigation is a preliminary attempt in demonstrating the usefulness of DNA marker inheritance study in mango.

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Screening of Groundnut (*Arachis hypogaea* L.) Mini Core Collection against Late Leaf Spot Disease Caused by *Phaeoisariopsis personata* (Berk & M.A Curtis van Arx)

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Groundnut is considered as a "poor man's almond" possessing nutritional and medicinal properties constituting 44-50% edible oil, dietary protein (25-33%) and carbohydrates (20%). Diseases like early and late leaf spot caused by *Cercospora arachidicola* and *Phaeoisariopsis personata* and rust (*Puccinia arachidis*) are causing yield loss upto 70% resulting in a lower productivity of the crop. Germplasm collection is a reservoir of genetic variability comprising of promising genes for various characters that can be incorporated in the breeding programme to develop and broaden the genetic base of cultivars. Thus the investigation was carried out to screen the mini core collection comprising of 188 accessions representing *fastigiata* (33), *vulgaris* (71), *peruviana* (2), *aequatoriana* (1), *hypogaea* runner (33) and *hypogaea* bunch (48) and identify the genotypes resistant to late leaf spot. The experiment was conducted in a Simple Lattice Design (15 × 15) in two replications during *kharif* 2011 at UAS, Bangalore. The cultivar TMV-2 highly susceptible to late leaf spot was used as a spreader row for natural disease incidence. Phenotypic screening was done using modified nine point scale. The genotypes such as ICG 5286, ICG 2773, ICG 111426, ICG 2857 and ICG 6022 recorded as resistant to late leaf spot can be used as a donor of disease resistance in breeding of disease resistant cultivars. SSR marker GM 1009 was validated through single marker analysis.

Key Words: Groundnut, mini core, late leaf spot, modified 9 point scale, germplasm

Introduction

Groundnut (*Arachis hypogaea* L.) is an important crop both in subsistence and commercial agriculture in arid and semi-arid regions of the world. Groundnut kernels are rich source of edible oil (44-50%), dietary protein (25-33%) and carbohydrates (20%). Diseases like early leaf spot and late leaf spot caused by *Cercospora arachidicola* and *Phaeoisariopsis personata* and rust (*Puccinia arachidis*) are causing yield losses up to 70% (Grichar *et al.,* 1998; McDonald *et al.,* 1985; Miller *et al.,* 1990) resulting in a lower productivity of the crop. Among different approaches of disease management, growing resistant variety is the best environment friendly means of reducing yield losses from the diseases (Gibbons, 1980 and Subrahmanyam *et al.,* 1995). Therefore, it is important to identify sources of resistance that can be used in breeding programme to evolve resistant varieties.

Plant genetic resources are essential components to meet future food security needs of the world. Germplasm collection is a reservoir of genetic variability comprising of promising genes for various characters that can be incorporated in the breeding programme to develop and broaden the genetic base of cultivars. Screening for resistance to leaf spots and rust has been intensively carried out by many workers and a number of sources of resistance have been reported in both cultivated groundnut and wild *Arachis* species. The objective of the study was to screen the mini core collection of groundnut (*Arachis hypogaea* L.) for late leaf spot disease and identify the accessions resistant to late leaf spot disease under field conditions.

Materials and Methods

The field experiment was undertaken at University of Agricultural Sciences, Bengaluru during *kharif* 2011 favourable for natural spread of late leaf spot disease. The experimental site was located at an altitude of 899 m above Mean Sea Level and at 13.00^{o}N latitude and 77.35^{o} E longitude.

The experiment was conducted in *kharif* 2011 on 1st June 2011 in Simple Lattice (15 × 15) design with two replications. The cultivar TMV 2 was used as susceptible check and spreader row for natural late leaf spot disease incidence and its spread. The experimental material comprised of 225 genotypes which includes 188 accessions of groundnut mini core set procured from ICRISAT, Patancheru, Hyderabad, representing different

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species of *Arachis* such as *fastigiata* (33), *vulgaris* (71), *peruviana* (2), *aequatoriana* (1), *hypogaea* runner (33) and *hypogaea* bunch (48) and other advanced breeding lines. These genotypes are listed in Table 1.

Each genotype was grown with a spacing of 40 cm between rows and 15 cm between plant to plant within the rows. After every six rows of different genotypes, a row of TMV 2 and two border rows of TMV 2 around the experimental plot was grown for uniform natural dispersal of pathogen spores. All the 225 genotypes were evaluated for late leaf spot disease incidence through visual screening method (Fig. 1) and modified nine point scale (Table 2) given by Subbarao *et al.* in 1990 (0: no disease severity and 9: 81-100% disease severity). The visual scores (1-9) and the extent of leaf area destroyed (0-100%) are linearly related. The field disease scores are mainly based on the extent of leaf area damage. The scores were converted into Percentage Disease Index (PDI) using the following formula:

$$\text{PDI (\%)} = \frac{\text{Sum of individual ratings}}{\text{Number of observations assessed}} \times \frac{100}{\text{Maximum disease rating}}$$

Phenotypic screening of all the 225 genotypes was done at five different intervals of time starting from 30% disease incidence to 100% *i.e.,* at 70 days after sowing (DAS), 80DAS, 90DAS, 100DAS and 110DAS. Five plants in each genotype were randomly selected for scoring and were tagged for easy identification during each scoring. Two replication data was pooled and the genotypes are categorised into different disease reaction groups based on the disease severity such as resistant, moderately resistant, susceptible, moderately susceptible and highly susceptible.

SSR marker GM 1009 identified to be linked to late leaf spot resistance (Sujay *et al*. 2011) was validated in different resistance and susceptible genotypic backgrounds. CTAB method of DNA extraction (Saghai-Maroof *et al.* 1984) was carried out during the study. DNA was quantified by loading the samples on 0.8% agarose gel containing 0.5 µl/10 ml Ethidium bromide (10mg/ml). The diluted DNA samples with the standard λ DNA molecular weight markers (5 ng/µl and 10 ng/µl) were loaded on 0.8% agarose gel and runned in 0.5X TBE (Tris borate EDTA) buffer at a constant voltage (80 V) for 20 min. The images of gels were documented under UV illumination using Uvi Tech gel documentation system (DOL-008.XD, England).

Polymerase Chain Reactions (PCR) were performed by using a Touch-Down PCR. DNA amplification was performed in 10 µl reaction mixture using Gene Amp® PCR system 9700. Before loading PCR products in the polyacrylamide gel electrophoresis (PAGE), amplification was checked on 1.2% agarose gel. For the separation of DNA fragments, non-denaturing PAGE was used.

Results and Discussion

All the 225 genotypes have shown different disease reaction to late leaf spot (Table 3). None of them are devoid of disease incidence. Among them few genotypes were resistant *viz.,* ICGV 91177 (2.3), ICGV 86699 (2.5), GBFD5272 (2.5), GPBD-4 (3.1), ICGV 86590 (3.1) and IGCV 99005 (3.6). The mini core comprised of accessions moderately resistant to late leaf spot such as ICG 5286 (4.1), ICG 2773 (4.3) ICG 11426 (4.3), M-282 (4.4), ICG 2857 (4.5), ICG 6022 (4.5), ICG 6766 (4.7), ICG 532 (4.8), ICG 2772 (4.8), ICG 5745 (4.9) and ICG 14475 (4.9). Several sources of resistance to late leaf spot and rust have been reported in *A. hypogaea* (Waliyar *et al.,* 1993; Anderson *et al.,* 1993; Mehan *et al.,* 1996; Singh *et al.,* 1997; Dwivedi *et al*., 2002).

The accessions identified as resistant to late leaf spot can be used as parents in hybridization programme to transfer the resistant gene to the agronomically superior cultivated genotypes to develop a variety resistant to late leaf spot. The core and mini core collections of various crops were evaluated to identify trait-specific diverse parents at ICRISAT. Due to the reduced size, the core and the mini core sets have been evaluated and characterized precisely and useful trait-specific accessions have been identified for use in breeding programme to develop varieties with a broad genetic base. Although there is an increase in the number of germplasm accessions in genebanks, there is no corresponding increase in their use by the crop improvement scientists, indicating that the collections were not being used to their full potential. Thus, a very large gap exists between availability and actual utilization of the material. Hence there is a need to utilize the germplasm in crop improvement programmes to till the genes for various traits including disease resistance.

Confirmation of Reaction to Late Leaf Spot and Validation of Markers

The SSR marker GM 1009 which was detected by Sujay *et al*. (2011) through comprehensive quantitative trait loci (QTL) analysis was tightly linked to late leaf spot resistance. The banding profile of selected genotypes were in confirmation of resistance *i.e.,* at 411bp length there

Table 1. List of mini core set of groundnut (*Arachis hypogaea* L.)

S.No	ICG No.	Origin	Species	Subspecies	Botanical type
1	36	India	*hypogaea*	*fastigiata*	VUL
2	76	India	*hypogaea*	*hypogaea*	HYR
3	81	Unknown	*hypogaea*	*fastigiata*	VUL
4	111	Unknown	*hypogaea*	*hypogaea*	HYB
5	115	India	*hypogaea*	*fastigiata*	FST
6	118	India	*hypogaea*	*vulgaris*	VUL
7	163	Unknown	*hypogaea*	*hypogaea*	HYR
8	188	India	*hypogaea*	*hypogaea*	HYB
9	297	UAS	*hypogaea*	*fastigiata*	FST
10	332	Brazil	*hypogaea*	*fastigiata*	FST
11	334	China	*hypogaea*	*fastigiata*	VUL
12	397	UAS	*hypogaea*	*fastigiata*	VUL
13	434	UAS	*hypogaea*	*fastigiata*	VUL
14	442	UAS	*hypogaea*	*fastigiata*	VUL
15	513	India	*hypogaea*	*hypogaea*	HYB
16	532	Unknown	*hypogaea*	*hypogaea*	HYB
17	721	UAS	*hypogaea*	*hypogaea*	HYB
18	862	India	*hypogaea*	*hypogaea*	HYR
19	875	India	*hypogaea*	*hypogaea*	HYR
20	928	Unknown	*hypogaea*	*hypogaea*	HYR
21	1137	India	*hypogaea*	*fastigiata*	VUL
22	1142	Benin	*hypogaea*	*fastigiata*	FST
23	1274	Indonesia	*hypogaea*	*fastigiata*	FST
24	1399	Malawi	*hypogaea*	*fastigiata*	FST
25	1415	Senegal	*hypogaea*	*fastigiata*	FST
26	1519	India	*hypogaea*	*fastigiata*	VUL
27	1668	UAS	*hypogaea*	*hypogaea*	HYB
28	1711	Bolivia	*hypogaea*	*fastigiata*	VUL
29	1973	India	*hypogaea*	*fastigiata*	VUL
30	2019	India	*hypogaea*	*fastigiata*	VUL
31	2106	India	*hypogaea*	*fastigiata*	VUL
32	2381	Brazil	*hypogaea*	*hypogaea*	HYR
33	2511	India	*hypogaea*	*hypogaea*	HYR
34	2772	Nigeria	*hypogaea*	*hypogaea*	HYB
35	2773	Tanzania	*hypogaea*	*hypogaea*	HYR
36	2777	India	*hypogaea*	*hypogaea*	HYR
37	2827	Argentina	*hypogaea*	*hypogaea*	HYR
38	2925	India	*hypogaea*	*hypogaea*	HYR
39	3027	India	*hypogaea*	*hypogaea*	HYB
40	3053	India	*hypogaea*	*hypogaea*	HYB
41	3102	India	*hypogaea*	*fastigiata*	
42	3240	Uganda	*hypogaea*	*fastigiata*	VUL
43	3343	India	*hypogaea*	*fastigiata*	VUL
44	3421	India	*hypogaea*	*fastigiata*	VUL
45	3584	India	*hypogaea*	*fastigiata*	VUL
46	3673	Korea	*hypogaea*	*fastigiata*	
47	3681	USA	*hypogaea*	*fastigiata*	FST
48	3746	Argentina	*hypogaea*	*fastigiata*	VUL
49	3775	Brazil	*hypogaea*	*fastigiata*	
50	3992	India	*hypogaea*	*hypogaea*	HYR
51	4156	Unknown	*hypogaea*	*hypogaea*	HYR
52	4343	India	*hypogaea*	*hypogaea*	HYR
53	4389	India	*hypogaea*	*hypogaea*	HYR
54	4412	USA	*hypogaea*	*hypogaea*	HYR
55	4527	Uganda	*hypogaea*	*hypogaea*	HYB
56	4538	India	*hypogaea*	*hypogaea*	HYB
57	4543	Unknown	*hypogaea*	*vulgaris*	VUL
58	4598	India	*hypogaea*	*hypogaea*	HYB
59	4670	Sudan	*hypogaea*	*fastigiata*	FST
60	4684	USA	*hypogaea*	*fastigiata*	VUL
61	4729	China	*hypogaea*	*fastigiata*	VUL
62	4746	Isreal	*hypogaea*		HYB
63	4750	Paraguay	*hypogaea*	*fastigiata*	VUL
64	4911	Malawi	*hypogaea*	*fastigiata*	VUL
65	4955	India	*hypogaea*	*fastigiata*	VUL
66	4998	China	*hypogaea*	*hypogaea*	HYR
67	5016	USA	*hypogaea*		
68	5051	USA	*hypogaea*		
69	5195	Sudan	*hypogaea*	*fastigiata*	VUL
70	5221	Argentina	*hypogaea*	*fastigiata*	FST
71	5236	Chile	*hypogaea*	*fastigiata*	VUL
72	5286	Zambia	*hypogaea*	*hypogaea*	HYB
73	5327	USA	*hypogaea*	*hypogaea*	HYB
74	5475	Kenya	*hypogaea*	*fastigiata*	FST
75	5494	Malaysia	*hypogaea*	*vulgaris*	VUL
76	5609	Sri Lanka	*hypogaea*	*fastigiata*	FST
77	5662	China	*hypogaea*	*hypogaea*	HYB
78	5663	China	*hypogaea*	*hypogaea*	HYB
79	5745	Puerto Rico	*hypogaea*	*hypogaea*	HYB
80	5779	India	*hypogaea*	*fastigiata*	VUL
81	5827	USA	*hypogaea*	*hypogaea*	HYR
82	5891	India	*hypogaea*	*hypogaea*	HYB
83	6022	Sudan	*hypogaea*	*fastigiata*	FST
84	6057	USA	*hypogaea*	*hypogaea*	HYB
85	6201	Cuba	*hypogaea*	*fastigiata*	FST
86	6263	Burkina Faso	*hypogaea*	*fastigiata*	VUL
87	6375	Unknown	*hypogaea*	*fastigiata*	VUL
88	6402	Unknown	*hypogaea*	*hypogaea*	HYB
89	6407	Zimbabwe	*hypogaea*	*fastigiata*	VUL
90	6646	Unknown	*hypogaea*	*fastigiata*	FST
91	6654	Unknown	*hypogaea*	*fastigiata*	VUL
92	6667	USA	*hypogaea*	*hypogaea*	HYB
93	6703	Paraguay	*hypogaea*	*hypogaea*	VUL
94	6766	USA	*hypogaea*	*hypogaea*	HYB
95	6813	Senegal	*hypogaea*	*hypogaea*	HYR
96	6888	Brazil	*hypogaea*	*fastigiata*	VUL

HYB: *Hypogaea* bunch; HYR: *Hypogaea* runner; VUL: *Vulgaris;* FST: *Fastigiata*

HYB: *Hypogaea* bunch; HYR: *Hypogaea* runner; VUL: *Vulgaris;* FST: *Fastigiata*

Table 1. Contd.

S.No	ICG No.	Origin	Species	Subspecies	Botanical type
97	6892	USA	*hypogaea*	*hypogaea*	HYB
98	6913	USA	*hypogaea*	*hypogaea*	HYB
99	6993	Brazil	*hypogaea*	*hypogaea*	HYR
100	7000	USA	*hypogaea*	*hypogaea*	HYR
101	7153	India	*hypogaea*	*hypogaea*	HYR
102	7181	India	*hypogaea*	*fastigiata*	FST
103	7190	Brazil	*hypogaea*	*vulgaris*	VUL
104	7243	USA	*hypogaea*	*hypogaea*	HYR
105	7906	Zimbabwe	*hypogaea*	*vulgaris*	VUL
106	7963	USA	*hypogaea*	*hypogaea*	VUL
107	7969	Zimbabwe	*hypogaea*	*vulgaris*	VUL
108	8083	Russia & CISs	*hypogaea*	*vulgaris*	VUL
109	8106	Peru	*hypogaea*	*fastigiata*	FST
110	8285	USA	*hypogaea*	*hypogaea*	HYB
111	8490	Somalia	*hypogaea*	*hypogaea*	HYR
112	8517	Bolivia	*hypogaea*	*fastigiata*	FST
113	8567	Uruguay	*hypogaea*	*vulgaris*	VUL
114	8760	Zambia	*hypogaea*	*hypogaea*	HYR
115	9037	Cote d'Ivoire	*hypogaea*	*hypogaea*	HYR
116	9157	Puerto Rico	*hypogaea*	*vulgaris*	VUL
117	9249	Mauritius	*hypogaea*	*vulgaris*	
118	9315	USA	*hypogaea*	*fastigiata*	FST
119	9418	Martinique	*hypogaea*	*vulgaris*	VUL
120	9507	Philippines	*hypogaea*	*vulgaris*	VUL
121	9666	India	*hypogaea*	*hypogaea*	HYB
122	9777	Mozambique	*hypogaea*	*hypogaea*	HYB
123	9809	Mozambique	*hypogaea*	*vulgaris*	VUL
124	9842	Tanzania	*hypogaea*	*hypogaea*	HYB
125	9905	Zambia	*hypogaea*	*hypogaea*	HYR
126	9961	Unknown	*hypogaea*	*hypogaea*	HYB
127	10036	Peru	*hypogaea*	*peruviana*	FST
128	10092	Zimbabwe	*hypogaea*	*fastigiata*	
129	10185	USA	*hypogaea*	*hypogaea*	HYB
130	10384	Nigeria	*hypogaea*	*vulgaris*	VUL
131	10474	Cuba	*hypogaea*	*fastigiata*	FST
132	10479	Uruguay	*hypogaea*	*hypogaea*	
133	10554	Argentina	*hypogaea*	*fastigiata*	FST
134	10566	Congo	*hypogaea*	*fastigiata*	FST
135	10890	Peru	*hypogaea*	*fastigiata*	FST
136	11088	Peru	*hypogaea*	*peruviana*	FST
137	11109	Taiwan	*hypogaea*	*hypogaea*	HYR
138	11144	Argentina	*hypogaea*	*fastigiata*	FST
139	11219	Mexico	*hypogaea*	*hypogaea*	HYR
140	11249	Tanzania	*hypogaea*	*vulgaris*	VUL
141	11322	India	*hypogaea*	*hypogaea*	HYB
142	11426	India	*hypogaea*	*hypogaea*	HYB
143	11457	India	*hypogaea*	*hypogaea*	HYR
144	11515	China	*hypogaea*	*vulgaris*	VUL
145	11651	China	*hypogaea*	*vulgaris*	VUL
146	11687	India	*hypogaea*	*vulgaris*	VUL
147	11855	Korea	*hypogaea*	*hypogaea*	HYB
148	11862	Korea	*hypogaea*		HYB
149	12000	Mali	*hypogaea*	*hypogaea*	HYB
150	12189	Isreal	*hypogaea*	*vulgaris*	VUL
151	12276	Bolivia	*hypogaea*	*hypogaea*	HYB
152	12370	India	*hypogaea*	*hypogaea*	HYR
153	12625	Ecuador	*hypogaea*	*aeguatoriana*	FST
154	12672	Bolivia	*hypogaea*	*hypogaea*	HYB
155	12682	India	*hypogaea*	*vulgaris*	VUL
156	12697	India	*hypogaea*	*vulgaris*	VUL
157	12879	Myanmar	*hypogaea*	*vulgaris*	VUL
158	12921	Zimbabwe	*hypogaea*	*vulgaris*	VUL
159	12988	India	*hypogaea*	*vulgaris*	VUL
160	13099	Unknown	*hypogaea*	*hypogaea*	HYR
161	13491	Central Afr. Rep	*hypogaea*	*vulgaris*	VUL
162	13603	Indonasia	*hypogaea*	*vulgaris*	VUL
163	13723	Niger	*hypogaea*	*hypogaea*	HYR
164	13787	Niger	*hypogaea*	*hypogaea*	HYB
165	13856	Uganda	*hypogaea*	*fastigiata*	FST
166	13858	Uganda	*hypogaea*	*fastigiata*	FST
167	13982	USA	*hypogaea*	*hypogaea*	VUL
168	14008	Central Afr. Rep	*hypogaea*	*hypogaea*	HYB
169	14106	Zaire	*hypogaea*	*fastigiata*	FST
170	14118	Zaire	*hypogaea*	*vulgaris*	VUL
171	14127	Zaire	*hypogaea*	*fastigiata*	VUL
172	14466	Nigeria	*hypogaea*	*hypogaea*	HYB
173	14475	Nigeria	*hypogaea*	*hypogaea*	HYB
174	14482	Nigeria	*hypogaea*	*hypogaea*	HYB
175	14523	Unknown	*hypogaea*		
176	14630	Brazil	*hypogaea*	*fastigiata*	FST
177	14705	Cameroon	*hypogaea*	*hypogaea*	HYB
178	14710	Cameroon	*hypogaea*	*fastigiata*	FST
179	14985	Unknown	*hypogaea*	*vulgaris*	VUL
180	15042	Unknown	*hypogaea*	*fastigiata*	FST
181	15190	Costa Rica	*hypogaea*	*hypogaea*	HYB
182	15287	Brazil	*hypogaea*	*fastigiata*	HYB
183	15309	Brazil	*hypogaea*	*fastigiata*	FST
184	15419	Ecuador	*hypogaea*	*fastigiata*	FST
	Controls				
1	156	India			
2	2738	India			
3	13941	ICRISAT			
4	13942	ICRISAT			

HYB: *Hypogaea* bunch; HYR: *Hypogaea* runner; VUL: *Vulgaris;* FST: *Fastigiata*

HYB: *Hypogaea* bunch; **HYR**: *Hypogaea* runner; **VUL**: *Vulgaris;* **FST**: *Fastigiata*

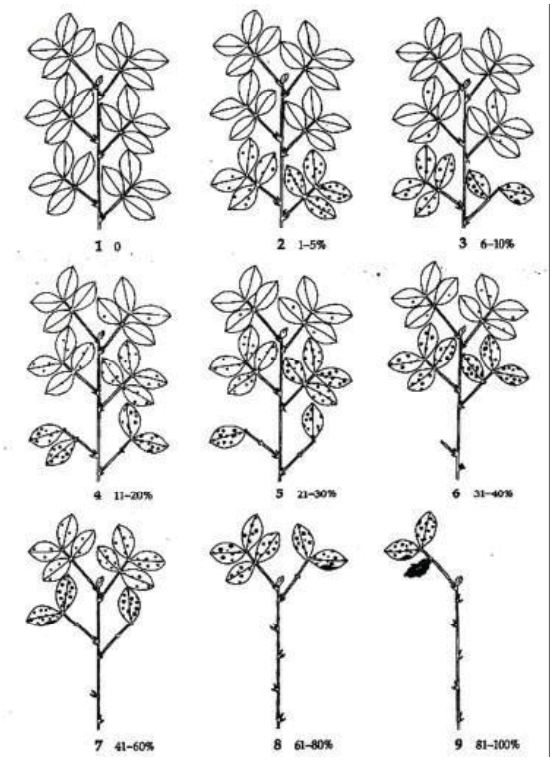

Fig. 1. Diagram showing leaf symptoms used for scoring late leaf spot disease resistance (Subbarao *et al.*, 1990)

Table 2. Modified 9-point scale used for field-screening of groundnut genotypes for late leaf spot disease resistance (Subbarao *et al.*, 1990)

Disease score	Description	Disease severity (%)
1	No disease	0
2	Lesions present largely on lower leaves; no defoliation	1-5
3	Lesions present largely on lower leaves, very few on middle leaves; defoliation of some leaf lets evident on lower leaves	6-10
4	Lesions present on lower and middle leaves but severe on lower leaves; defoliation of some leaf lets evident on lower leaves	11-20
5	Lesions present on lower and middle leaves, over 50 % of defoliation of lower leaves	21-30
6	Severe; eosins on lower and middle leaves; lesions present but less severe on top leaves; extensive defoliation of lower leaves; some defoliation on middle leaves	31-40
7	Lesions on all leaves but less severe on top leaves; defoliation of all lower and middle leaves	41-60
8	Defoliation of all lower and middle leaves; severe lesions on top leaves evident.	61-80
9	Almost all leaves defoliated, leaving bare stem; some leaflets may remain, but show severe leaf spot	81-100

was presence of band in case of resistant genotypes and absent in case of susceptible genotypes (Fig. 2).

Clear and unambiguous bands were scored for their presence or absence with the score 1 indicating their presence and 0 indicating their absence of band on the gel at 411bp. The data matrix of binary codes thus obtained was subjected to further analysis. The genotypic and phenotypic data obtained from set of individuals were subjected to single marker analysis (Table 4) using one

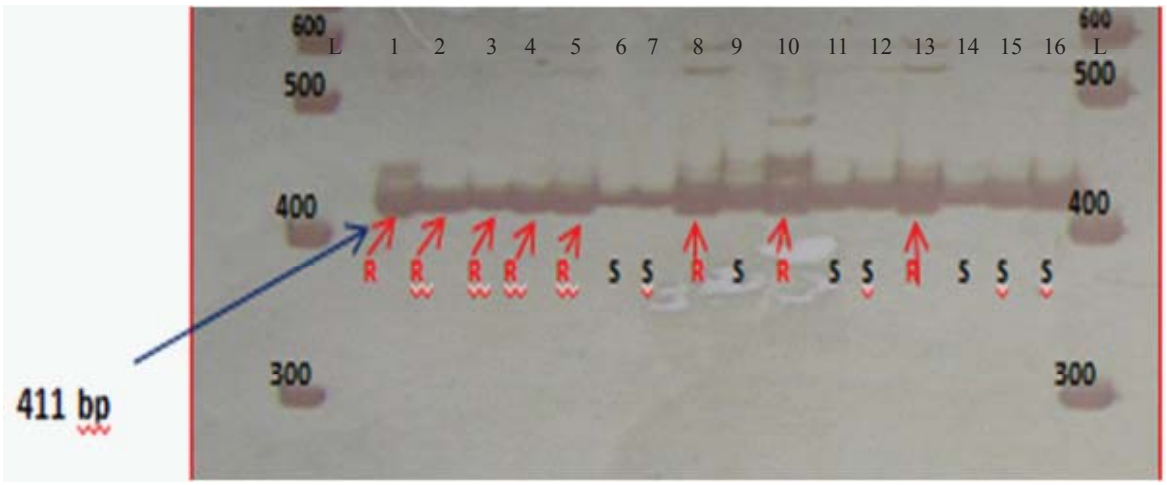

Fig. 2. Banding profile of 16 genotypes for marker GM 1009. DNA fragments were separated on 6% non-denaturing poly acrylamide gel electrophoresis (PAGE). The left side arrow shows the resistant band at 411bp. Resistance genotypes are marked as (R) and susceptible genotypes are marked as (S). Lane L, 100bp DNA ladder, lane 1-5, 8, 10 and 13, ICGV 86699, GPBD 4, ICG 2857, ICG 2773, ICG 5286, ICG 5745, M-282 and ICG 11426 respectively. Lane 6, 7, 9, 11, 12, 14 and 15, ICGV 99003, ICG 3027, GKVK 13, ICGV 99004, ICGV 93021, ICG 13099 and ICG 10036, respectively.

Table 3. Reactions of genotypes to late leaf spot during *kharif* 2011

Disease reaction	Resistant (0-3.5)*		Moderately Resistant (3.6-4.9)*	
No. of genotypes	7		18	
	Genotypes/Lines	Score	Genotypes/Lines	Score
	ICGV 91177	2.3	GPBD 5	4.0
	ICGV 86699	2.5	ICGV 99003	4.0
	GBFD5272	2.5	ICG 5286	4.1
	GPBD-4	3.1	GKVK-13	4.2
	ICGV 86590	3.1	ICG 2773	4.3
	IGCV 99005	3.6	ICG 11426	4.3
			M-282	4.4
			ICGV 87165	4.4
			ICG 2857	4.5
			ICG 6022	4.5
			ICG 6766	4.7
			ICG 532	4.8
			ICG 2772	4.8
			ICG 5745	4.9
			ICG 14475	4.9

*Disease score

Disease reaction	Moderately Susceptible (5.0-6.5)*							
No. of genotypes	88							
	Genotypes/Lines	Score	Genotypes/Lines	Score	Genotypes/Lines	Score	Genotypes/Lines	Score
	1	2	1	2	1	2	1	2
	ICGV 99004	5.0	ICG 1973	5.5	ICG 7000	5.9	ICG 6813	6.2
	ICG 4412	5.0	ICG 4389	5.5	ICG 9961	5.9	ICG 11109	6.2
	ICG 3027	5.0	ICG 6913	5.5	JL-24	5.9	GKVK17	6.2
	ICG 2925	5.0	ICG 11088	5.5	ICG 163	6.0	ICG 14710	6.3
	1	2	1	2	1	2	1	2
	ICG 5663	5.0	ICG 9666	5.5	ICG 5016	6.0	ICG 188	6.3
	ICG 9037	5.0	ICG 12276	5.5	ICG 4343	6.0	ICG 6057	6.3
	ICG 14466	5.0	ICG 156	5.6	ICG 4156	6.0	ICG 11862	6.3
	ICGV 93021	5.0	ICG 2511	5.6	ICG 7963	6.0	ICG 6892	6.3
	ICG 2381	5.1	ICG 5662	5.6	ICG 8490	6.0	ICG 9777	6.3
	ICG 4527	5.1	ICG 11457	5.6	ICG 8285	6.0	ICG 8106	6.3
	ICG 14008	5.1	ICG 11515	5.6	ICG 13942	6.0	ICG 334	6.4
	ICG 4538	5.2	ICG 12000	5.6	GKVK 8b	6.0	ICG 12625	6.4
	ICG 14482	5.2	ICG 13099	5.6	NCAC 17090	6.0	ICG 13941	6.4
	ICG 4746	5.2	ICG B 37C	5.6	ICG 15190	6.0	GKVK 12	6.4
	ICG 5827	5.2	ICG 6993	5.7	ICG 721	6.1	ICG 76	6.5
	ICG 12672	5.2	ICGV 87264	5.7	ICG 2777	6.1	ICG 10036	6.5
	VL-1	5.2	ICG 875	5.8	ICG 10479	6.1		
	ICG 5051	5.3	ICG 5327	5.8	ICG 13787	6.1		
	ICG 5891	5.3	ICG 8760	5.8	GKVK 4	6.1		
	ICG 9842	5.3	ICG 14705	5.8	ICG 9905	6.2		
	ICG 513	5.4	R 8801	5.8	ICG 14630	6.2		
	ICG 6667	5.4	ICG 4955	5.9	ICG 15419	6.2		
	ICG 14523	5.4	ICG 4598	5.9	ICG 862	6.2		
	ICG 928	5.5	ICG 3053	5.9	ICG 5475	6.2		

*Disease score

Contd.

Disease reaction Susceptible (6.6-7.5)*					Highly susceptible (7.6- 9.0)*					
No. of genotypes 88					81					
	Genotypes	Score	Genotypes	Score	Genotypes	Score	Genotypes	Score	Genotypes	Score
	ICG 1668	6.6	ICG 11651	7.0	ICG 4911	7.6	ICG 3102	8.0	ICG 8567	8.3
	ICG 6646	6.6	ICG 8517	7.0	ICG 11322	7.6	ICG 2019	8.0	TMV 2	8.3
	ICG 11855	6.6	ICG 13713	7.1	ICG 11144	7.6	ICG 5609	8.0	ICG 36	8.4
	ICG 13982	6.6	GKVK 2	7.1	ICG 10474	7.6	ICG 9809	8.0	ICG 5221	8.4
	ICG 115	6.7	ICG 81	7.2	ICG 9507	7.6	ICG 9315	8.0	ICG 7190	8.4
	ICG 6402	6.7	ICG 1415	7.2	ICG 9157	7.6	ICG 14127	8.0	ICG 4750	8.4
	ICG 7969	6.7	ICG 2738	7.2	ICG 3775	7.7	ICG 4684	8.1	ICG 6407	8.4
	ICG 10185	6.7	ICG 6263	7.2	ICG 3673	7.7	ICG 6375	8.1	ICG 7181	8.4
	ICGV86155	6.7	ICG 13603	7.2	ICG 6703	7.7	ICG 10556	8.1	ICG 10890	8.4
	ICG 297	6.8	ICG 13856	7.2	ICG 397	7.8	ICG 12879	8.1	ICG 10384	8.5
	ICG 3992	6.8	ICG 1274	7.3	ICG 6888	7.8	ICG 6654	8.2	ICG 10092	8.5
	NCAC 343	6.8	ICG 9418	7.3	ICG 12189	7.8	ICG 7906	8.2	ICG 5195	8.6
	ICG 7153	6.8	ICG 13491	7.3	ICG 3746	7.8	ICG 11219	8.2	ICG 4729	8.6
	ICG 10554	6.8	GKVK 1	7.3	ICG 5494	7.8	ICG 12988	8.2	ICG 12921	8.6
	GKVK 8a	6.8	ICG 13858	7.3	ICG 9249	7.9	ICG 1519	8.3	ICG 1137	8.7
	ICG 4998	6.9	ICG 15309	7.3	ICG 332	7.9	ICG 2106	8.3	ICG 1711	8.7
	ICG 434	6.9	ICG 3681	7.4	ICG 4670	7.9	ICG 4543	8.3	ICG 3421	8.7
	ICG 14118	6.9	ICG 11687	7.5	ICG 3584	7.9	ICG 3343	8.3	ICG 8083	8.8
	ICG14985	6.9	ICG 12682	7.5	ICG 1142	7.9	ICG 11249	8.3		
	ICG 118	7.0	ICG 106	7.5	ICG 12697	7.9				
	ICG 6201	7.0			ICG 442	8.0				
	ICG 7243	7.0			ICG 1399	8.0				

*Disease score

Table 4. Single marker analysis for validation of SSR marker GM 1009

SSR Marker	Disease	Source of variation	Degrees of freedom	Mean sum of square	Pr > F	R^2
GM 1009	Late leaf spot	Model	1	6.503*	0.0483	0.250506
		Error	14	389		
		corrected total	15			

way regression analysis (Sax, 1923) using Statistical Package for the Social Sciences (SPSS) software. All the marker data and the mean phenotypic traits value of genotypes were used for calculating two marker classes and their variances. The significant threshold for association of marker to the trait was set at P B 0.05 for single marker analysis. The adjusted R2 (phenotypic variance) value was used as per cent of variance explained by the marker on the particular trait of test and used as a measure of the magnitude of association. The MSS was significant for the marker in this study and hence the marker was found to be associated with diseases. The result was in confirmation with Sujay *et al*. (2011).

Thus markers in Marker Assisted Selection (MAS) can offer an effective and efficient breeding tool for detecting, tracking, retaining, combining, and pyramiding disease resistance genes.

Plant genetic resources conserved in the form of germplasm mini core collection preserved the variation in the entire collection of groundnut and the mini core accessions, which only includes 1.29% of the entire collection, represents the total diversity contained in the core collection. This mini core subset drastically reduces the number of entries to be evaluated and provides a working collection of groundnut germplasm that can

be extensively examined for all economically important traits. In this study evaluation of mini core collection helped in identifying the sources of resistance to late leaf spot disease which can be used as a donor of disease resistance in breeding for disease resistant cultivars.

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Clustering Pattern of some Indigenous Rice (*Oryza sativa* L.) Accessions from Chhattisgarh

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The current scenario in the food and agriculture sector marks the sudden increase in concerns towards conservation of genetic biodiversity in rice production. Chhattisgarh state in India is home to a large number of indigenous rice varieties, which may serve a valuable genetic resource for future crop improvement to meet the ever increasing demand for food production. The preliminary characterization of five accessions of clustered spikelet rice germplasm was carried out at IGKV, Raipur during *kharif* 2012 to 2013. The data on qualitative and quantitative descriptors were recorded using standard evaluation system for rice (IRRI, 2002) descriptor for 18 traits. The accessions studied exhibited good variability in both qualitative and quantitative traits. Ama Ruthi showed maximum variation for all the traits *viz.*, basal leaf sheath colour, collar colour, culm interned colour, apiculus colour and high fertility percentage observed in accession Chhind Guchhi (97.24%) followed by Ama Jhopa (97.11%), Nariyal Phool (96.63%), Koudi Dhul (95.51%) and Ama Ruthi (92.18%). So, this study will be useful for breeder and researcher to identify valuable germplasm and their conservation as well as utilization in rice improvement programme.

Key Words: Cluster, Germplasm, Rice accessions, Spikelets

Introduction

Rice is one of the oldest crop domesticated about 10,000 years ago and during this long period, transition from gathering to growing of plants occurred (Choudhury *et al*., 2013). In this process a wide array of crop variability got generated by natural means and through both conscious and unconscious selection. Gradually a new wealth of variability also got generated/adopted and diversified by crop introduction in the exotic environment or through migration of human population. The wealth of land races, which could not even be called varieties and which the farmers grew earlier are gradually disappearing due to fast spread of semi dwarf high yielding rice varieties (Swaminathan, 1984). A collection and study of these has revealed that these exhibit many useful genes and can help in crop improvement programmes (Sahu, 2006). One can thus understand the need for collection and conservation of plant genetic diversity. Its value in the future will be much more than what can be imagined at present considering the diversified crop improvement programmes, technologies and human needs. Considering these facts, a systematic collection of rice germplasm from Madhya Pradesh which included Chhattisgarh was done under leadership of Late Dr RH Richharia during 1972 to 1981. Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) is presently maintaining comparatively quite large number of accessions of rice germplasm (over 22000 nos).

Keeping in view these facts, the present investigation was planned to characterize a set of clustered rice accessions of Chhattisgarh, to understand variability of different agro-morphological traits.

Materials and Methods

The experimental material consisted of five rice germplasm accessions namely, Amajhopa, Koudidhul, Chhindguchhi, Nariyal phool and Amaruthi collected during 1972-81 by Late Dr RH Richharia and his associates at Raipur. The trials were conducted during the *kharif* seasons of 2012 and 2013 in randomized block design with three replications. The observations were recorded on 18 characters at specified stages of crop growth period when characteristics under study had full expression (IRRI, 2002). Among the 18 morphological characteristics studied, 11 where visually assessed and 7 were measured. Similarity matrix was generated using the SimQual programme NTSYS-pc software version 2.02 (Rohlf, 1998). The similarity coefficients were used in cluster analysis and dendrogram was constructed by Unweighted Pair-Group Method with Arithmetic Average (UPGMA).

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Results and Discussion

The branches of rice panicle generally bear solitary spikelets. Rare forms in which spikelets occur in clusters of 2-7 have been recorded in India, Ceylon and North Vietnam (Coyaud, 1950). The cluster habits appear to result mainly from a reduction in pedicel length. In IGKV, Raipur (C.G.) indigenous rice germplasm collection, some cultivars are available having clustered spikelets (Richharia, 1979). The agro-morphological and quality characteristics of some of the clustered accessions are presented in Table1, whereas, frequency distribution of spikelet cluster/panicle are presented in Table 2.

Amajhopa (A: 200), IC390769: It was collected from block Deobhog, Gariyaband district (Chhattisgarh). Its lemma-palea colour was and kernel colour was white and translucent. Clustered spikelets found in the range of 2 to 6 grains in most of the panicles however, clustering of 3 grains was found in large frequency (41.1%) followed by 2 grains (30.2%) in each panicle. A minimum frequency of clustering was observed for 6 grains (1.4%). Total number of grains observed was 208 divided in to 73 spikelet clusters (Table 2).

Koudidhul (K: 1849), IC390770: It was collected from block Dharamjaygarh, Raigarh districts of Chhattisgarh. Its lemma-palea colour was straw and kernel colour was deep red. Range of clustering in most of the panicles recorded was 2 to 8 grains however, occasionally clustering of 10 grains was also found in some of the panicles. Clustering of 3 grains is observed in large frequency (42%) followed by 2 & 4 grains (15% each). A minimum frequency of clustering was recorded for 8 grains (2.5%). Total number of grains recorded was 156 divided into 40 spikelet clusters (Table 2). In this accession solitary spikelet was absent in the panicle (Table 2).

Chhindguchhi (C: 739), IC390771: This accession was collected from block Bhanupratappur, Kanker district (Chhattisgarh). Its lemma-palea colour was reddish to light purple and kernel colour was white and translucent. The clustering of spikelets was recorded in the range of 2 to 4 grains whereas, occasionally clustering of 7 grains was also found in some of the panicles. Three grains clustering was observed in large frequency (33.7%) followed by 2 grains (29.4%). A minimum frequency of clustering was recorded for 4 grains (4.4%). A total number of spikelets/panicle recorded was 145, which was divided into 68 spikelet clusters (Table 2). In this accession solitary spikelets were also found in large frequency (32%) (Table 2).

Nariyal Phool (N: 796), IC390772: Place of collection was block Saraipali, Mahasamund district (Chhattisgarh). Its lemma-palea colour was gold and gold furrows on straw and kernel colour was white and translucent. In this accession clustering of spikletes recorded in broad range *i.e.* 2 to 10 grains amongst all clustered accessions available in IGKV rice germplasm. Whereas, clustering of 3 grains was found in large frequency (35.4%) followed by 4 grains (20%). A minimum frequency of clustering

Table 1. Agro-morphological and quality characteristics of some of the rice cultivars with clustered spikelets

S.No.	Name of Variety	Acc. No.	Agro-morphological traits																
			BLSC	LBC	CC	AC	CmIC	ApC	SgC	An	DF	PH (cm)	Til. No.	LmpC	ScC	TW (gm)	GRL (mm)	GRW (mm)	L/W	GT
1	Ama Ruthi	A: 643	Light purple	Green	Purple	Purple	Purple line	Purple	Purple	Absent	142	160.00	5.66	straw	White	28.80	7.70	3.50	2.20	Medium Medium
2	Koudi Dhul	K: 1849	Green	Green	Green	Green	Green	White	White	Absent	132	116.66	6.66	straw	Red	18.00	7.00	2.70	2.60	Short Medium
3	Chhind Guchhi	C: 739	Green	Green	Green	Green	Green	White	White	Short & Partially awned	138	156.66	5.66	Reddish to light purple	White	35.10	9.60	2.80	3.42	Long Slender
4	Ama Jhopa	A: 200	Green	Green	Green	Green	Green	White	White	Absent	138	152.66	5.66	Straw	White	24.50	8.30	2.80	2.96	Medium Medium
5	Nariyal Phool	N: 796	Green	Green	Green	Green	Green	White	White	Absent	144	136.66	10.00	Gold and gold furrows on Straw	White	19.00	8.50	2.60	3.26	Medium Slender

Note: BLSC: Basal leaf sheath colour, LBC: Leaf blade colour, CC: Collar colour, CmIc: Culm internode colour, ApC: Apiculus colour, SgC: Stigma colour, An: Awning, DM: Day to maturity, PH: Plant height, Til No.: Tiller number, LmpC: Lemma-palea colour, ScC: Seed coat (kernel) colour, TW (100 g): Test weight, GRL: Grain length, GRW: Grain width, L/W: length/width Ratio, GT: Grain type.

Table 2. Frequency distribution of spikelet clusters in accessions with clustered spikelets

Ama Jhopa		Koudi Dhul		Chhind Guchhi		Nariyal Phool		Ama Ruthi	
No.of spikelets occurred in cluster	Frequency of spikelet-clusters*	No.of spikelets occurred in clusters	Frequency of spikelet-clusters	No.of spikelets occurred in clusters	Frequency of spikelet-clusters*	No.of spikelets . of spikelet-clusters	Frequency of spikelet-clusters*	No.of spikelets occurred in clusters	Frequency of spikelet-clusters*
1	6.8	1	0	1	32	1	5	1	4.2
2	30.2	2	15	2	29.4	2	10.75	2	18.4
3	41	3	42	3	33.7	3	35.4	3	35.2
4	16.5	4	15	4	4.4	4	20	4	21
5	4.1	5	10	5	0	5	9.5	5	17
6	1.4	6	10	6	0	6	3	6	2.1
		7	4.75	7	0.5	7	4.6	7	2.1
		8	2.5			8	4.6		
		9	0			9	4.6		
		10	0.75			10	2.55		
Filled grains/ panicle: 202		Filled grains/ panicle: 149		Filled grains/ panicle: 141		Filled grains/ panicle: 262		Filled grains/ panicle: 224	
Unfilled grains/ panicle: 06		Unfilled grains/ panicle: 07		Unfilled grains/ panicle: 04		Unfilled grains/ panicle: 10		Unfilled grains/ panicle: 19	
Total grains/ panicle: 208		Total grains/ panicle: 156		Total grains/ panicle: 145		Total grains/ panicle: 272		Total grains/ panicle: 243	
No. of spikelet clusters : 73		No. of spikelet clusters: 40		No. of spikelet clusters : 68		No. of spikelet clusters : 65		No. of spikelet clusters : 71	
Spikelet fertility percentage: 97.11		Spikelet fertility percentage: 95.51		Spikelet fertility percentage: 97.24		Spikelet fertility percentage: 96.63		Spikelet fertility percentage: 92.18	

* Percentage; Average of three panicles

observed was 10 grains (2.55%). A total number of spikelets/panicle recorded is 272, which was distributed into 65 spikelet clusters in the panicle (Table 2).

Amaruthi (A: 643), IC390773: It was collected from block Antagarh, Bastar district (Chhattisgarh). Its lemma-palea colour is straw and kernel colour was white and chalkiness was present. Clustered spikelets found in the range of 2 to 7 grains whereas, clustering of 3 grains was found in large frequency (35.2%) followed by 4 grains/cluster (21%). A minimum frequency of clustering recorded was 7 grains/cluster (2.1%). A total number of spikelets/panicle recorded was 243, which was distributed into 71 spikelet clusters in the panicle (Table 2).

On average across all genotypes, high spikelets fertility was observed which was ranged from 92.18 to 97.24. Highest were observed in Chhind Guchhi (97.24%) followed by Ama Jhopa (97.11%), Nariyal Phool (96.63%), Koudi Dhul (95.51%) and Ama Ruthi (92.18%). The various morphological traits recorded among rice genotypes with clusterd spikelets are furnished in Table 1. The basal leaf sheath colour for rice genotypes varied from green to light purple. Genotypes Koudi Dhul, Chhind Guchhi, Ama Jhopa and Nariyal Phool had green basal leaf sheath colour while Ama Ruthi exhibited light purple. Leaf blade colour in all genotypes was green. Collar colour was found absent in all the genotypes except Ama Ruthi. Auricle colour was observed green in the genotypes Koudi Dhul, Chhind Guchhi, Ama Jhopa and Nariyal Phool, whereas it was purple in Ama Ruthi. Culm internode colour was absent in all the genotypes except Ama Ruthi. Apiculus and Stigma were colourless in four genotypes *viz.*, Koudi Dhul, Chhind Guchhi, Ama Jhopa and Nariyal Phool while, Ama Ruthi exhibited purple colour for both traits. Awning was absent in the spikelets of all genotypes except Chhind Guchhi; which exhibited short and partially awned spiklets. Lemma palea colour was recorded straw in genotypes Ama Ruthi, Koudi Dhul and Ama Jhopa while, Chhind Guchhi showed reddish to light purple colour and Nariyal Phool exhibited gold and gold furrows on straw lemma palea colour. Seed coat colour was white in all genotypes except Koudidhul which exhibited red colour. Day to maturity observed for Ama Ruthi and Nariyal Phool was late while, other three genotypes were recorded under

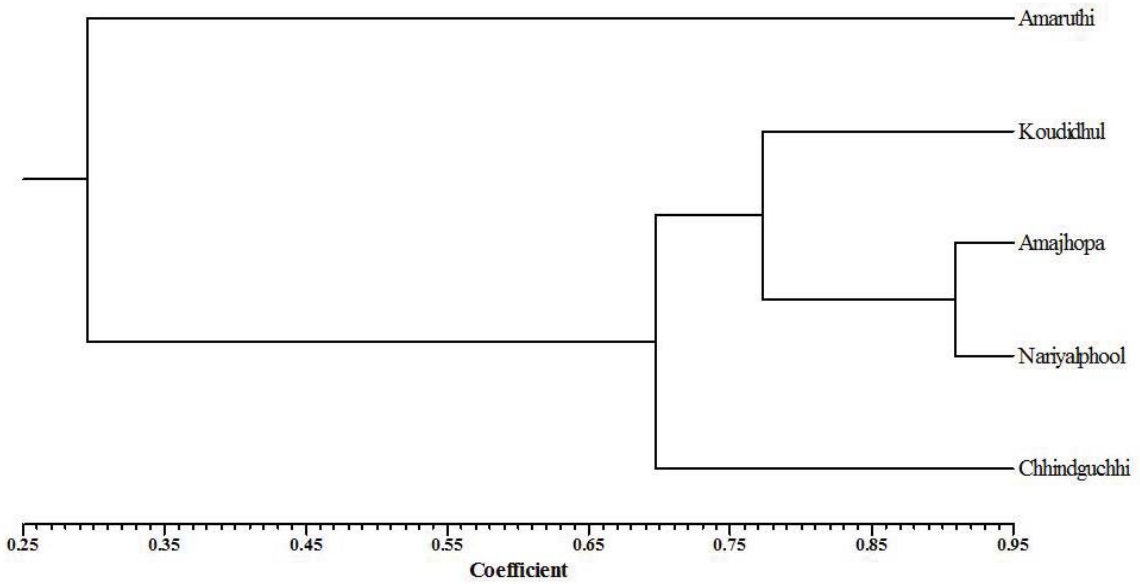


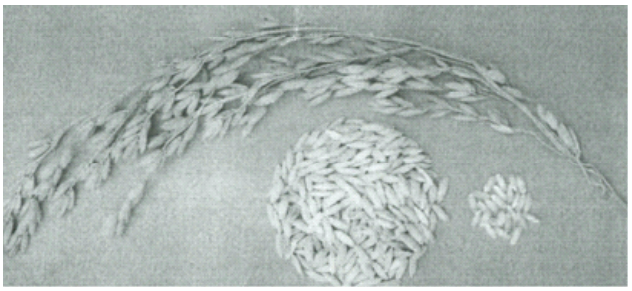
Fig. 1. Dendrogram of rice germplasm accessions based on morphological markers

medium duration. Height of plant recorded tall in all the genotypes except Koudi Dhul, which was observed as intermediate. Medium grain type was recorded in genotypes Ama Ruthi and Ama Jhopa; while Koudi Dhul exhibited short medium; long slender grain type was observed in Chhind Guchhi while, medium slender grain was recorded for the genotype Nariyal Phool.

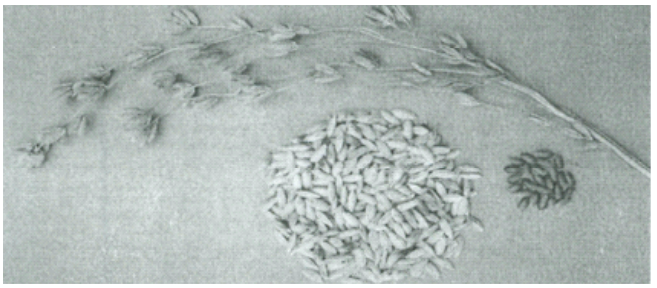
UPGMA cluster analysis was performed using SM similarity coefficient matrices calculated from morphological data to generate a dendogram for five rice genotypes (Fig. 1). The genotypes were grouped into two clusters. The similarity coefficient ranged from 0.29 to 0.91. In pair-wise comparison, the maximum similarity was obtained between Ama Jhopa and Nariyal Phool with a similarity index of 0.91, whereas Ama Ruthi showed least similarity with other genotypes (similarity index 0.29). Cluster I consisted of genotypes Ama Ruthi having 29% similarity whereas, cluster II consisted of Koudi Dhul, Ama Jhopa, Nariyal Phool and Chhind Guchhi having 70% similarity among them. Cluster II again partitioned into two sub-clusters in which one sub-cluster had Chhind Guchhi with 71% similarity, whereas another sub-culster had Koudi Dhul, Ama Jhopa and Nariyal Phool with 77% similarity among them. The basic objective of varietal characterization is to test occurrence of traits that helps in identifying a particular genotype.

As a prerequisite for efficient utilization of the germplasm, it must be properly evaluated, characterized and documented so that it could be easily retrieved and used in breeding programme (Elangovan *et al.*, 2013). The present study revealed sufficient genetic variability for most of the trait observed. Moreover response to selection is directly proportional to the genetic variability present in the material. In rice germplasm only limited accessions is available with clustered (spikelets) with vary distinct variation. Since number of filled grains/ panicle in clustered genotypes is comparatively more than other genotypes with solitary spikelets. Spikelets fertility percentage/panicle was high which can be exploited for developing superior varieties and breaking the yield plateau already fixed by the hybrid varieties. Therefore, a gene pool can be generated by crossing the germplasm lines of interest which can be further used as source material to develop high yielding varieties. These unique accessions bearing special trait of interest can be further investigated to understand its inheritance pattern. The morphological dendrogram generated for similarity or genetic distance matrices has provided an overall pattern of variation as well as the degree of relatedness among rice accessions also found by Tiwari *et al.* (2013). All the five rice accessions used in the present investigation have showed the distinct (clustered pattern) from the existing high yielding varieties which are one of the most important criteria for release of variety and also in the context of PPV&FR Act, 2001. The present accessions having the unique (clustering pattern) trait can be registered in NBPGR for future use.

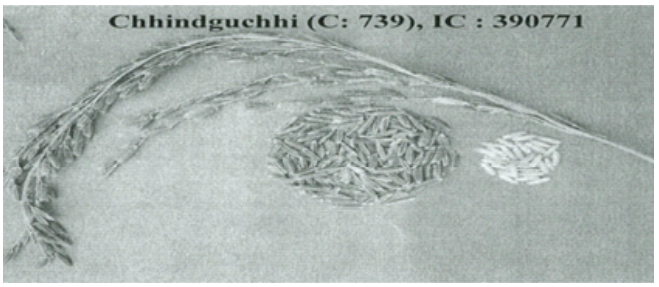
Amajhopa (A: 200), IC390769



Koudidhul (K: 1849), IC390770

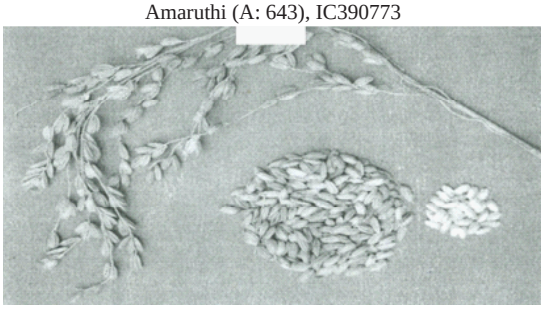


Chhindguchhi (C: 739), IC390771



Nariyal Phool (N: 796), IC390772

Amaruthi (A: 643), IC390773



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Genetic Diversity, Variability and Heritability for Root, Shoot and Water Use Efficiency Traits in Castor *(Ricinus communis* L.) Genotypes

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The present study aimed to estimate the genetic diversity; variability and heritability in 64 castor genotypes for root, shoot and water use efficiency (WUE) traits and further identify the suitable genotypes for a drought resistance breeding programme. Characters like plant height, leaf area index (LAI), stem girth and total dry matter (TDM) were significantly correlated (>0.70) with root volume and root dry weight. The genotypes were ranked based on the index in ascending order considering five important characters *viz*; LAI, stem girth, root volume, root dry weight and TDM using principal component analysis and 15 genotypes with high performance in terms of shoot and root characters were selected. These genotypes comprised 48-1, RG 2124, RG 2169, RG 2155, RG 2074, GCH-5, RG1963, RG 2094, DCS-99, RG 2153, DCS-78, RG 27, RG 1618, RG 2147 and RG 1673. High general combining ability (GCV) and heritability (>80%) for plant height, root volume, root dry weight, TDM and LAI indicate sufficient variability for selection for these characters. Heterosis was high for TDM, root dry weight, volume and LAI. Superior heterobeltiosis was observed for TDM, root volume and root dry weight. The hybrid GCH-5 with its significant heterosis, heterobeltiosis and standard heterosis for key root traits like root volume, root dry weight and TDM is worth exploring under water scarce conditions.

Key Words: Castor, Heritability, Root traits, WUE traits

Introduction

Castor, a crop more tolerant to water deficit is cultivated both as a rain-fed crop in marginal lands under harsh conditions with minimum inputs in Southern India and as an irrigated crop under intensive management conditions in North - Western India. Castor cultivation under rainfed situations is limited due to untimely and erratic rainfall exposing the crop to moisture stress at critical stages *i.e.* flowering/maturity of either one or more than one of the three spike orders *viz*., primaries, secondaries or tertiaries, more so with the latter due to cessation of monsoon season and reducing the productivity to 300 kg/ha. A large portion of these losses can be reduced through crop improvement and better drought-adapted genotypes.

Several morpho-physiological traits play a significant role in crop adaptation to drought stress during soil drying (Subbarao *et al.,* 1995). Genetic variability for traits related to drought tolerance *viz.*, water use efficiency (WUE), root characteristics (biomass, length density and depth) is scattered in germplasm accessions and may be productive when incorporated to high yielding agronomic back ground. Selection for these traits in a breeding program could result in more accurate targeting of factors limiting yield there by increasing the rate of yield improvement.

Significant improvement in productivity through enhanced WUE (Condon *et al.,* 2004; Impa *et al.,* 2005) and root traits (Li *et al.,* 2005) have been demonstrated in crops like groundnut. However, measuring WUE in large populations is difficult. Identification and use of surrogate traits for WUE that are simple and have low environmental variations under drought conditions would be more effective. Significant positive correlation of SPAD chlorophyll meter reading (SCMR) (Sheshashayee *et al.,* 2006), ^{18}O (Bindu Madhava *et al.,* 1999) and negative correlation of specific leaf area (SLA), ^{13}C (Wright *et al.,* 1994) with WUE has been established in crops like peanut.

The objective of the present study was to assess the genetic variability, heritability and genetic diversity in a set of promising genotypes of castor for the traits related to drought tolerance. In addition, the study also aimed to estimate the magnitude of heterosis for major traits related to drought tolerance in a set of four hybrids along with their parents.

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Materials and Methods

Construction of Root Structures

For screening castor germplasm and breeding lines for WUE and root traits, two structures were constructed at Narkhoda farm of Directorate of Oilseeds Research (DOR), Hyderabad. Each structure of 30 m length, 1.5 m height and 2.4 m width on either side of central 30 cm permanent wall with side collapsible walls was constructed with hollow cement bricks. The structure was secured by erecting wooden poles on either side which were held together tightly with a wire. Small drainage holes were made at regular intervals. The structures were filled with red sandy loam soil and watered regularly to allow compaction. When the bulk density of the structure reached the bulk density of that of field, sowings were done. FYM was added @ 5 t/ha. Four plants were sown per replication with spacing of 90 x 60 cm with recommended dose of fertilizers.

Genotypes

Sixty four castor genotypes including 37 germplasm lines and 27 breeding lines were sown in two structures with 32 genotypes per structure during *rabi* 2009-10. The germplasm lines with preliminary tolerance to wilt, jassids, drought and with high yield and breeding lines including four released hybrids along with their eight parents *viz.*, DCH-177 (DPC-9 x DCS-9), DCH-519 (M-574 x DCS-78), GCH-4 (VP-1 x 48-1), GCH-5 (Geeta x SH-72) and 15 parents of the experimental hybrids were studied. All the 23 parents were agronomically superior plant types with medium plant height (90-130 cm), early to medium flowering (30-55 days to 50% flowering) and maturity (100-130 days to first picking), strong stem with good branching potential (AICRP on Castor, DOR, 2006). Several parental lines like 48-1, DCS-9, DCS-78, DCS-99, DCS-100, DCS-106, DPC-9, M-574 were resistant to Fusarium wilt which is the major disease compared with 100% wilt susceptible check JI- 35.

Observations

Plants were grown for 90 days as the root growth was active till that time. Observations on growth parameters *viz.*, plant height, number of different order branches, leaf number, leaf area, stem girth, WUE traits like SPAD (soil plant analytical development) chlorophyll meter reading (SCMR) measuring leaf chlorophyll content, specific leaf area (SLA), relative water content (RWC), excised leaf water retention capacity (ELWRC) were recorded. SLA was computed by measuring leaf area and dry weight [(SLA = leaf area (dm^2) / leaf dry weight (g)]. RWC was recorded as per procedure given by Dhopte and Manuel (2002). For ELWRC measurement, the leaves with petioles were excised and fresh weight was recorded at different time intervals. ELWRC was calculated based on the percentage of weight loss of leaves from initial weight over a period of time (Clarke and Mc Caige, 1982) and expressed as percent water loss (ELWL). Plants were uprooted and washed by using water jet and root characters *i.e*. root length, root volume, root dry weight, plant growth parameters and TDM were recorded. Root volume was measured by quantifying the amount of water displaced by roots. Powdered leaf samples were sent to National Facility of Isotope Ratio Mass Spectrometer (IRMS) at University of Agricultural Sciences (UAS), Bangalore for measuring stable isotopes ^{13}C and ^{18}O which act as surrogates for WUE.

Statistical Analysis

Analysis of variance

The mean values of the data recorded from the above quantitative and physiological characters were used to study differences between genotypes for various characters with analysis of variance technique (Panse and Sukhatme, 1985). Principal component analysis was done (Dunteman, 1994) to select efficient castor genotypes with high performance in terms of shoot and root characters. The genotypes were ranked based on the index in ascending order to select efficient genotypes with high ranks. The phenotypic and genotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955).

Genetic diversity

The genetic divergence was measured by the Mahalanobis' D^2 analysis and genotypes were grouped using Tocher's method (Rao, 1952). The grouping depends on the principle that intra-group distances should be far less than inter-group distances. A principal component analysis based on Mahalanobis' D^2 (Mahalanobis, 1936) was carried out using the INDOSTAT statistical software (INDOSTAT Services, Hyderabad, India) to determine the traits most effective in discriminating between accessions. The first two components explaining the maximum variance were selected for the ordination analysis, and the correlation between the original traits and the respective principal component was calculated. The principal components with *eigen* values >1.0 were selected.

Heterosis

Three types of heterosis-heterosis, heterobeltiosis and standard heterosis was calculated for quantitative traits like plant height up to primary spike (cm), leaf number, stem girth (cm), physiological traits like LAI, TDM and root traits *viz*., root length (cm), root volume (ml) and root dry weight (g) as the percentage increase or decrease of the hybrids over the parental mean, better parent or standard check, respectively (Liang *et al.,* 1972*).*

Results

Root and Shoot Growth

The mean performance and range for different root and shoot characters of the 64 castor genotypes is presented in Table 1. The genotypes varied significantly for all the quantitative and physiological traits evaluated. Plant height up to primary spike was as low as 19 cm to as high as 160 cm with a mean of 63 cm. Node number up to primary spike which is an indication of maturity also varied from 7 to 22 nodes with a mean of 14 nodes. Among the physiological and root traits, LAI, TDM, root volume, root dry weight and ELWRC depicted higher variability. Greatest variation was observed in TDM as depicted by the high standard deviation value recorded for the trait. This was followed by root volume and dry weight.

Root volume and root dry weight were significantly correlated with TDM, stem girth and plant height (> 0.80) while root length did not show significant correlation with shoot characters *viz*., plant height, LAI, stem girth, TDM (r=0.15 to 0.47) (Table 1). In addition, correlation between shoot characters and TDM indicated that LAI is significantly and positively correlated with TDM (0.80) followed by stem girth (0.77) while plant height and leaf number were not significantly correlated with TDM**.** SCMR which measures leaf chlorophyll content based on light transmittance at blue and red wavelengths and manifested to leaf nitrogen, again related to SLA and WUE did not show strong correlation with TDM (Lakshmamma *et al*., 2010) though recorded negative correlation (-0.62) with SLA. Even SLA and ^{13}C which shows the efficiency of RuBisCO there by mesophyll capacity (Wright *et al*., 1994) also did not show good relation with TDM in this study (Lakshmamma *et al*., 2010). ^{18}O which act as surrogate for transpiration efficiency and stomatal conductance (gs) showed positive correlation with TDM (0.49) and high ^{18}O shows high amount of water transpired which is directly related to yield (Bindu Madhava *et al*., 1999). ^{13}C and ^{18}O were negatively correlated (-0.62).

Selection of Genotypes

Several promising genotypes for root traits, LAI and other morphological characters were identified based on their significantly higher values (Table 2). Genotypes

Table 1. Range, mean, correlation coefficient values for different root and shoot characters in castor genotypes

Character	Range	Mean	Correlation coefficients				
			Shoot characters	Root characters			TDM
				Length	Volume	Dry weight	
Plant height (cm)	19 -160	63	Plant height	0.47	0.85	0.82	0.69
Leaf Number	7 - 45	19	LAI	0.15	0.69	0.71	0.80
Node Number	7 - 22	14	Stem girth	0.45	0.82	0.84	0.77
Secondary branch number	0-12	4	TDM	0.26	0.84	0.88	
Tertiary branch number	0-5	1	SCMR				-0.03
Stem girth (cm)	4.9-10.5	7.0	SLA				0.08
LAI	0.29 - 5.45	1.71	^{13}C				-0.034
SLA (dm^2/g)	1.55-2.77	2.05	^{18}O				0.49
SCMR	43.2 – 57.5	49.2	SCMR vs SLA	-0.62			
TOM (g/plant)	55 - 452	175	$d^{13}C$ vs $d^{18}O$	-0.62			
Root length (cm)	125 - 235	169					
Root volume (ml)	48 - 372	143					
Root dry weight (g/plant)	8.0 – 58.1	23.5					
Root/shoot	0.08 - 0.39	0.16					
TDM/LA	0.98 - 8.45	2.46					
RWC (%)	75.1 - 95.1	88.3					
ELWRC (water loss in 2 hrs)	9.1-41.0	18.4					

Table 2. Genotypes with better root and shoot characters in castor

Lines with	Per plant	Germplasm/breeding lines
Root length	>185 cm	48-1, RG1515, RG1618, RG1626, RG1668, RG1938, RG1963, RG2074, RG2094, RG2096, RG2106, RG21 07, RG2114, RG2124
Root volume	>185 ml	48-1, DCS-78, DCS-99, GCH-5, RG27, RG1618, RG1673, RG1963, RG2074, RG2094, RG2124, RG2147, RG2153, RG2155
Root fresh weight	>194 g	48-1, DCS-78, DCS-99, GCH-5, RG27, RG1618, RG1673, RG1963, RG2094, RG2124, RG2147, RG2153, RG2155, RG2169
Root dry weight	>31 g	48-1, DCS-78, DCS-99, DCS-101, GCH-5, RG27, RG1618. RG1673, RG1963, RG2074, RG2094, RG2106, RG2124, RG2147, RG2153, RG2155, RG2169
Root/Shoot	>/0.19	RG15, RG27, RG1515, RG1618, RG1963, RG2040, RG2054, RG2064, RG2074, RG2094, RG2106, RG2107, RG2114, RG2124, RG2169
Plant height	>88 cm	48-1, Geetha, DCS-99, DCS-101, DCS-106, GCH-5, RG27, RG1673, RG1963, RG2074, RG2094, RG2124, RG2147, RG2155, RG2169
Stem girth	>8.3 cm	48-1, Geetha, DCS-78, DCS-99, GCH-5, RG27, RG1596, RG1618, RG1673, RG2074, RG2124, RG2147, RG2153, RG2155, RG2169
LAI	>2.5	48-1, Geetha,DCS-9, DCS-99, DCS-100, DCS-101, DCS-106, GCH-5, M-574, RG2094, RG2124, RG2153, RG2155, RG2169
TDM	>218 g	48-1, Geetha, DCS-78, DCS-99, DCS-100, DCS-101, GCH-5, RG27, RG1596, RG1673, RG2074, RG2124, RG2153, RG2155, RG2169
SCMR	>50	SH-72, DCS-96, RG27, RG109, RG1520, RG1596, RG1618, RG1626, RG1628, RG1673, RG1938, RG2001, RG2054, RG2106, RG2114
SLA	<1.75	DCS-78, GCH-5, RG27, RG109, RG247, RG1596, RG1626, RG1649, RG1673, RG1953, RG1963, RG2054, RG2064, RG2074, RG2106, RG2107

were ranked by developing an index based on principal components taking into consideration five important characters which showed strong positive correlations. These traits include root volume, root dry weight, stem girth, LAI and TDM. Top 15 genotypes along with their index values, growth and root characters are presented in Table 3. These genotypes include 48-1, RG 2124, RG 2169, RG 2155, RG 2074, GCH-5, RG 1963, RG 2094, DCS-99, RG 2153, DCS-78, RG 27, RG 1618, RG 2147 and RG 1673. Among these selected genotypes, 48-1 recorded highest leaf number, stem girth, root dry weight, LAI and TDM. RG 2124 recorded highest plant height, root volume, root fresh weight and root dry weight is on par with 48-1. RG 27 and RG 2074 recoded low SLA, high root shoot ratio. RG 27, RG 1618 and RG 1673 recorded high SCMR. Genotypic differences among selected genotypes were not significant for RWC and ELWRC. Data on ^{13}C and ^{18}O of the selected genotypes is also presented. ^{13}C and ^{18}O were negatively correlated (-0.62).

Among the hybrids studied, DCH-519 recorded high RWC (94.8) and ELWRC (9.1% water loss after 2 hours). Its parents also showed high percent RWC and ELWRC (M-574 with 93.1, 11.4 and DCS-78 with 89.2 and 13.3 percent RWC and excised leaf water loss). In general, female parents *viz*., Geeta, VP-1, M-574, DPC-9 showed less leaf water loss after 2 hrs with excision. High RWC and less excised leaf water loss of DCH-519 hybrid and its parents (M-574, DCS-78) show the drought tolerance capacity of this hybrid. Though female parents (VP-1, Gaeta, M-574,) of the hybrids (GCH-4, GCH-5, DCH-519) tested showed less excised leaf water loss (ELWL) after 2 hrs of excision, except DCH-519 where the male parent (DCS-78) also recorded low ELWL, other two hybrids did not show low ELWL indicating the heritability of this trait from male parent as reported by Rao *et al.* (1998).

Variability, heritability and genetic divergence: The coefficient of variation (CV), both genotypic and phenotypic indicated that there were significant differences among the genotypes for all the characters studied while the phenotypic coefficient of variation (PCV) is higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environment (Table 4). The CV is especially high for the characters like plant height, root volume, root fresh weight, root dry weight, TDM and LAI. Heritability was maximum for root volume and minimum for root length. Majority of the traits *viz.*, plant height and node number up to primary spike, fresh and dry weight of root and shoot, TDM and LAI recorded high heritability (>80). The genetic advance expected in the next generation was higher in root volume and LAI suggesting the role of dominance variance and their highly predictable

Table 3. Ranking, root, shoot growth characters and WUE traits of selected genotypes in castor

Genotype	Index (PCA*)	Rank	Plant height (cm)	Leaf No.	Node No. on primary	Stem girth (cm)	LAI	TDM (g/ plant)	SCMR	SLA (dm^2/ g)	Root length (cm)	Root volume (ml)	Root dry wt. (g/ plant)	RWC (%)	ELWRC (% water loss after 2hrs)	^{13}C	^{18}O
48-1	2.602	1	92.5	45	17	10.5	5.45	452	46.8	2.433	197	350	58.1	89.6	21.7	-22.618	22.394
RG2124	1.933	2	159.4	22	19	8.5	2.70	341	50.7	2.146	197	372	56.7	94.0	15.4	-21.701	22.713
RG2169	1.552	3	134	15	18	8.9	4.10	277	45.1	2.497	179	305	50.3	88.2	14.9	-21.543	19.765
RG2155	1.363	4	105.5	31	18	8.3	3.83	372	47.6	2.205	176	244	46.6	93.0	18.9	-21.375	21.886
RG2074	1.287	5	93.5	19	17	8.9	2.43	226	49.5	1.547	197	259	43.2	91.8	14.6	-20.038	19.576
GCH-5	1.251	6	99.0	27	17	8.9	2.98	312	50.3	1.809	179	269	42.3	92.5	12.8	-21.748	22.471
RG1963	1.219	7	107	18	22	7.4	1.8	213	48.7	1.707	203	217	37.1	84.7	18.8	-20.512	19.990
RG2094	1.205	8	88.5	11	20	8.2	2.66	210	48.5	1.991	206	232	38.0	90.2	10.6	-19.838	19.059
DCS-99	1.072	9	101.5	30	15	9.1	3.11	261	50.0	1.995	184	219	36.9	90.1	13.5	-21.471	22.586
RG2153	0.956	10	75.5	25	14	8.4	3.05	316	45.3	2.220	176	205	37.6	94.9	15.3	-21.554	23.116
DCS-78	0.890	11	85.5	24	14	8.7	1.94	300	49.2	1.748	168	248	43.1	89.2	13.3	-21.333	20.842
RG27	0.763	12	93.0	22	19	8.7	1.44	218	57.1	1.625	180	217	40.6	86.0	13.5	-20.223	19.202
RG1618	0.760	13	80.0	18	18	8.9	1.74	145	57.5	2.515	189	226	34.7	83.2	20.4	-19.857	18.615
RG2147	0.712	14	113	17	21	8.4	2.02	212	46.9	2.255	168	283	31.1	90.6	23.2	-21.697	22.864
RG1673	0.603	15	87.5	17	16	8.4	1.55	250	56.4	1.702	168	225	37.0	85.6	15.1	-19.838	19.378
Mean			63.3	19	14	7.0	1.71	174.9	49.2	2.053	169	143	23.5	88.3	18.4		
SEm±			7.12	3.3	0.99	0.71	0.32	22.3	2.2	0.18	13.4	15	4.0	2.36	2.65		
CD(0.05)			20.1	9.4	2.8	2.0	0.90	62.9	6.2	0.51	37.9	43	11.1	6.6	7.5		
CV(%)			15.9	24.7	10.0	14.2	26.3	18.0	6.3	12.4	11.2	15	23.8	3.8	20.3		

*PCA=Principal component analysis

Table 4. Coefficient of variability, heritability and genetic advance values for root and shoot characters

Character	Coefficient of variation		Heritability % (broad sense)	Genetic advance as % of mean 5%
	GCV	PCV		
Plant height	45.3	48.1	88.6	87.8
Leaf number	28.4	37.5	57.6	44.5
Node number	23.5	25.5	84.6	44.5
Stem girth	14.4	20.2	51.0	21.3
Root length	9.9	14.9	44.4	13.6
Root volume	51.0	53.2	91.8	100.7
Root dry weight	47.8	53.4	80.2	88.2
Shoot dry weight	39.9	43.7	83.5	75.2
TDM	40.2	43.7	84.2	75.9
LAI	56.6	62.3	82.6	106.0

behavior. Low genetic advance in the next generation for the traits like stem girth and root length indicate the role of additive variance.

Sixty-four genotypes were classified into 10 clusters using Euclidean^2 distances following the Mahalanobis method (Table 5). Cluster means for the high heritability traits were also presented. Cluster I included maximum genotypes (49) followed by cluster V with 7 genotypes while the remaining clusters included single genotype. The intra cluster distance among seven genotypes (7.52) was higher than 49 genotypes in Cluster I (6.95). The genotype RG 2124 is genetically divergent to the 49 genotypes in Cluster I based on inter cluster distance while RG 2107 in cluster II and 48-1 and RG-2124 in clusters VIII and X were also genetically divergent with each other. The genotype RG-2124 was also genetically divergent with a wilt and leaf hopper resistant male line, DCS-106 in cluster VII.

In the present study, four hybrids *viz.*, DCH-177, DCH-519, GCH-4 and GCH-5 along with their parents were evaluated to estimate the presence and magnitude of heterosis for physiological and root traits related to drought tolerance (Table 6). Among the four hybrids, GCH-5 alone recorded significantly positive mid parent,

Table 5. Cluster groups, distance and cluster means for root and shoot characters

Cluster groups	Intra cluster distance	Group with more inter cluster distance	Plant height	Root volume	Root DW	TDM	LAI
1 (49 genotypes)	6.95	X	51.9	110	18.7	153	1.45
II (RG2107)	0	VIII, X	59.5	146	21.1	76	0.69
III (GCH-5)	0		99.0	269	42.3	312	2.98
IV (DCS-78)	0		85.5	248	43.1	300	1.94
V (7 genotypes)	7.52		94.6	237	37.4	208	1.95
VI (RG2155)	0		105.5	244	46.6	372	3.87
VII (DCS-106)	0	X	105.0	138	18.7	193	3.66
VIII (48-1)	0		92.5	350	58.1	452	5.45
IX (RG2169)	0		134.0	305	50.3	277	4.12
X (RG2124)	0		159.5	372	56.7	341	2.70

Table 6. Heterosis and Heterobeltiosis of hybrids studied in castor

Hybrids	Plant height	Leaf no.	Stem girth	LAI	TDM	Root length	Root volume	Root dry weight
Mid Parent Heterosis								
DCH-177	-5.7	0.0	6.8	-19.0	17.6	0.53	-9.2	-13.1
DCH-519	-36.8	-23.7	-13.5	3.86	-38.2	0.76	-41.3	-44.1
GCH-4	-32.8	-33.9	-27.9	-68.6	-50.7	-18.4	-58.1	-66.1
GCH-5	6.7	33.3	7.6	27.2	51.1	11.6	76.4	60.2
Standard Heterosis								
DCH-177	-42.2	2.5	-5.3	30.8	30.9	-17.4	-31.1	-23.4
DCH-519	-37.5	-7.5	-3.03	62.1	11.0	-3.2	-23.2	-11.4
GCH-4	-36.7	7.5	-6.8	-27.4	4.1	-16.0	-33.9	-35.03
GCH-5	54.7	35.0	34.9	100.0	126.6	4.1	92.1	114.7
Heterobeltiosis								
DCH-177	-9.8	-12.5	-4.6	-35.9	-5.6	-1.7	-24.3	-30.4
DCH-519	-53.2	-24	-26.4	-11.1	-49.2	-0.9	-56.6	-59.4
GCH-4	-56.2	-51.1	-14	-80.2	-68.3	-26.7	-73.6	-78
GCH-5	-5.7	8.0	6.0	3.8	36.6	7.9	55.9	42.4

standard heterosis and heterobeltiosis for root traits like root length, root volume and root dry weight. The hybrid GCH-5 was also heterotic for other important physiological and morphological traits like plant height up to primary spike, leaf number, stem girth, LAI and TDM while the other three hybrids recorded significantly negative heterosis for all the traits except DCH-177 for stem girth and TDM and DCH-519 for LAI.

Discussion

The quantification of the existing genetic variability for the traits of interest is essential in any breeding programme to understand the genetic structure of the population and their ultimate use in development of high yielding genotypes. Genotypes selected for the study represent the sources of tolerance to major biotic stresses like Fusarium wilt and leaf hopper *etc*., which include 37 germplasm and 27 parents for the development of high yielding parents or hybrids resistant to both biotic and abiotic stresses. The present study indicated the potential of genotypes for further exploitation of the existing variability with an emphasis on traits related to drought tolerance.

The study established the presence of a large genotypic and phenotypic variation for root and shoot traits in a set of 64 castor genotypes. The characters like plant height, root volume, root dry weight, TDM and LAI with significant genetic variability and heritability (>80%) were of special interest as they will be less influenced by environment and phenotypic selection for improvement of these characters would be effective. Root volume was significantly correlated with plant height, TDM and stem girth. Among them, plant height (0.88) and TDM (0.84) were heritable and thus can be used as selection criteria for traits related to drought tolerance. However among the shoot characters, LAI was significantly correlated with TDM. Least heritability for root length indicates its sensitivity to environment and phenotypic selection

may not be that effective. The traits with high GCV, heritability also showed high genetic advancement and highly amenable for phenotypic selection. High heritability coupled with high genetic advancement for these characters is largely governed by additive gene action, which is highly amenable for visual selection (John *et al.,* 2006*).*

Majority of the genotypes (49) were classified in one group (Cluster I) for characters like plant height, root volume, root dry weight, TDM and LAI indicating geographical diversity of germplasm lines collected did not play much role in the genetic diversity especially for traits related to drought tolerance. Similar results were reported for seed yield and yield components by Durgarani *et al.* (2007). As majority of the germplasm accessions studied showed tolerance to Fusarium wilt, the possibility of linkage with drought tolerance is worth exploring in future studies. 48-1, RG 2124 and GCH-5 which were ranked as best genotypes for shoot and root characters formed as separate clusters indicating their genetic diversity for root traits. The greater inter cluster genetic diversity between RG-2124 with the genotypes in Cluster I (49), Cluster II (RG-2107) and Cluster VII (DCS-106) indicate the potential of generating genetic diversity either by recombination breeding or bi-parental mating design.

Parents like 48-1, DCS-78, DCS-99 with significantly higher root volume (>185 ml) can be directly used as male parents for generation of hybrids with drought tolerance, while the other 10 germplasm accessions *viz.,* RG-27, RG-1618, RG-1673, RG-1963, RG-2074, RG-2094, RG-2124, RG-2147, RG-2153 and RG- 2155 with higher root volume may be further used in breeding programme. As root volume was significantly correlated with plant height, TDM and stem girth, tall plant types with high TDM (>218 g) *viz.*, 48-1, Geetha, DCS-78, DCS-99, DCS-100 and DCS-101 along with germplasm accessions viz., RG-27, RG-596, RG-1673, RG-2074, RG-2124, RG-2153, RG-2155 and RG-2169 have a potential to develop high yielding varieties and hybrids with resistance to drought.

The magnitude of heterosis for root volume varied from -58.1 to 76.4% (mid-parent), -33.9 to 92.1% (standard heterosis) and -73.6 to 55.9% (heterobeltiosis). Among the four hybrids, GCH-5 alone recorded significantly positive mid parent, standard and heterobeltiosis for heritable root traits like root volume and root dry weight. The hybrid GCH-5 was also heterotic for other important physiological and morphological traits like plant height up to primary spike, leaf number, stem girth, LAI and TDM.

Among the 64 genotypes studied, 48-1, RG 2124 and GCH-5 were ranked as best genotypes for shoot and root characters. Root volume, root dry weight and TDM showed high general combining ability (GCV), heritability (>80%), heterosis and superior heterobeltiosis. These traits also showed high genetic advancement and highly amenable for phenotypic selection. Large genotypic variation available in the working germplasm for WUE and root traits related to drought tolerance can be utilized for applied breeding programme. The new sources of drought tolerance can be used for physiological and genetic studies and in drought resistance breeding programme. Root volume but not root length is the key trait that can be used as selection criteria.

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Utility of Simple Sequence Repeat (SSR) Markers to Realize Worth of Germplasm in Genus *Allium*

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Allium germplasm harbour novel genes which could be utilized in breeding programme for developing elite cultivars. Availability of wide genetic variability and its comprehensive knowledge is an important step towards the development of improved varieties in different cultivated alliums. Earlier, *Allium* germplasm characterized based on morphological markers but they are affected by environment and plant development stages which leads to biased estimates of variability. In various crop plants different molecular markers are utilized for diversity studies due to their unbiased nature and neutrality with no environmental effect. Also in genus *Allium* various marker systems such as isozymes, Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP) and Restriction Fragment Length Polymorphism (RFLP) were used but they show number of disadvantages. To overcome their drawbacks, Simple Sequence Repeat (SSR) markers were developed in *Allium cepa*, *A. fistulosum* and *A. sativum* which are being utilized for DNA fingerprinting, genetic diversity analysis and cross amplification studies for better understanding of *Allium* germplasm. In future it will be desirable to use microsatellite markers for developing high density linkage map to follow marker assisted selection. Further understanding of population structure would be beneficial to exploit natural variation by using association mapping.

Key Words: *Allium*, Germplasm, EST, SSR, Transferability, Variation

Introduction

Allium is a species rich monocot genus as it includes about 780 species (Friesen *et al*., 2006) which are utilized as vegetables, condiments, medicinal and ornamental plants (Negi, 2006). Among alliums, bulb onion and garlic are cultivated worldwide while other species of economic importance such as bunching onion, shallot, leek and chives are grown in few counties. In addition to this, semi-domesticated and wild economic species are grown in a few pockets of Indian Himalayan region by local tribes (Negi, 2006; Pandey *et al*., 2008; Khosa *et al*., 2014).

Genetic resources enable the breeders to develop productive combinations of traits in elite cultivars to fulfill the needs in various agro-systems. Evaluation of germplasm is a prerequisite for utilization and the detailed evaluation determines the potentiality of an accession for specific purpose in crop improvement. Germplasm characterization and estimation of genetic diversity in plants on the basis of morphological characteristics is not much reliable. But, with DNA-based markers it is more desirable due to precise identification and quantitative estimation of genetic diversity (Glaszmann *et al*., 2010). However, development of reliable molecular markers is a challenging task in genus *Allium* due to its huge nuclear genome among monocots as onion genome (16,415 Mbp per 1C), which is nearly 36 times larger than rice and 6 times bigger than maize (Arumuganathan and Earle, 1991). Although, RAPDs were developed and used for diversity analysis (Bradeen and Havey, 1995; Ennequin *et al*., 1997; Tanikawa *et al*., 2002), but counter repeatability problem (Eicht *et al*., 1992) has made them less attractive to the researchers. Use of RFLPs and AFLPs has also been reported (Bark and Havey, 1995; Lampasona *et al*., 2010), but RFLPs cannot be employed for studies in routine due to their high cost, labour intensive procedure and low polymorphism, while dominant inheritance of AFLPs makes it less attractive to plant biologists (McCallum *et al*., 2008; Lampasona *et al*., 2010).

To overcome these problems, SSR markers are ideal due to their co-dominant inheritance, high hyper variability, wide genomic distribution, high reproducibility, multi-allelic nature, chromosome specific locations and ease to score (Varshney *et al*., 2005). Now-a- days due to the advances in next generation sequencing

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technologies a wealth of genomic and transcriptome data was developed in various crop plants including genus *Allium* which were explored using different bioinformatic tools (Table 1) to find out SSR markers (Varshney *et al*., 2005; Baldwin *et al.*, 2012; Sun *et al*., 2012; Duagnjit *et al*., 2013). As a result, in genus *Allium*, SSR markers have been developed in bulb onion (Fischer and Bachmann, 2000; Jakse *et al*., 2005; McCallum *et al*., 2008; Baldwin *et al.*, 2012), bunching onion (Wako *et al.*, 2002; Song *et al*., 2004) and garlic (Ma *et al*., 2009; Khar, 2012) which are utilized in different studies for realizing the worth of *Allium* germplasm. In the present review, the impact of utilizing SSRs in genus *Allium* for dissecting information about genetic resources is discussed.

Bulb Onion

Allium cepa is a highly valuable crop which is reported to have originated in central Asian region. Most of cultivars developed through selection and precise estimation of genetic variability using improved techniques is pre-requisite for efficient breeding (Brewester, 2008). In this context, sequence tagged microsatellites were developed from a genomic library enriched for microsatellite markers to determine genetic relationships between onion accessions. The eighty three bulb onion accessions were analyzed for diversity analysis where germplasm was partly grouped according to their geographical origins (Fischer and Bachmann, 2000). But, these markers had not proven reliable in various genetic studies due to their complex requirements and low transferability (McCallum *et al*., 2008). To overcome these barriers, Expressed Sequence Tags (ESTs) were generated and microsatellite markers were found in EST libraries during sequence analyses (Khul *et al*., 2004). To test their utility in germplasm analysis, 35 elite populations from specific companies or breeding programmes were analyzed using EST- SSR markers and it was observed that different populations could be distinguished by them. Germplasm was found to be closely related with each other and grouping was according to their geographical origins (Jakse *et al.*, 2005). Later, more diverse germplasm was surveyed to estimate variation using 56 EST-SSR markers and four genomic SSR markers (McCallum *et al.*, 2008). Populations grown in long day, short day and Indian region clustered apart from each other (Fig. 1). They also suggested that resequencing of EST markers can readily provide SNP markers for purity testing of inbreds and other application in *Allium* genetics.

Table 1. Different bioinformatic softwares available to discover SSR markers

S. No.	Software Name	Reference
1.	Tandem Repeat Finder (TRF)	Benson *et al.* (1999)
2.	Tandem Repeat Occurrence Locator (TROLL)	Castelo *et al.* (2002)
3.	SSR Identification Tool (SSRIT)	Kantety *et al.* (2002)
4.	SSR Finder	Gao *et al.* (2003)
5.	MIcroSAtellite (MISA)	Theil *et al.* (2003)
6.	Build SSR	Rungis *et al.* (2004)
7.	SAT	Dereeper *et al.* (2007)
8.	SSR Locator	Maia *et al.* (2008)
9.	Rapid Identification of SSRs and Analysis (RISA)	Kim *et al.* (2012)
10.	GMATo	Wang *et al.* (2013)

Different diversity studies have reported uniqueness of Indian bulb onion germplasm than exotic germplasm but very few accessions/extant varieties were utilized (Mahajan *et al*., 2009). Later, greater number of accessions were used to assess the diversity of tropical Indian onion (Khar *et al*., 2011). It was reported that indigenous Indian short day onion formed separate cluster from the exotic short day and long day onions (Fig. 2). Also, Indian and North American germplasm are quite different from each other and central Asian revealed close relationship with Indian material (McCallum *et al*., 2008). It suggests that Indian cultivars and land races might provide novel germplasm sources to broaden bulb onion breeding base.

There is one concern with EST-SSR markers as they detect less number of amplicons while analyzing bulb onion germplasm. Also, onion has large genome size and low gene diversity because of which only a small region of onion genome has been explored. A new set of genomic SSR markers were developed that exhibited high allelic diversity during germplasm analysis. Most of the germplasm clustered according to their geographical origins but Algerian samples appeared to cluster across three groups and this may indicate multiple introductions into the country or independent selections (Baldwin *et al.*, 2012). In future, SSR markers will be useful to determine the levels of inbreeding and population structure for association mapping.

Bunching Onion

It is believed that bunching onion originated in North West China and is also being grown on a large scale in

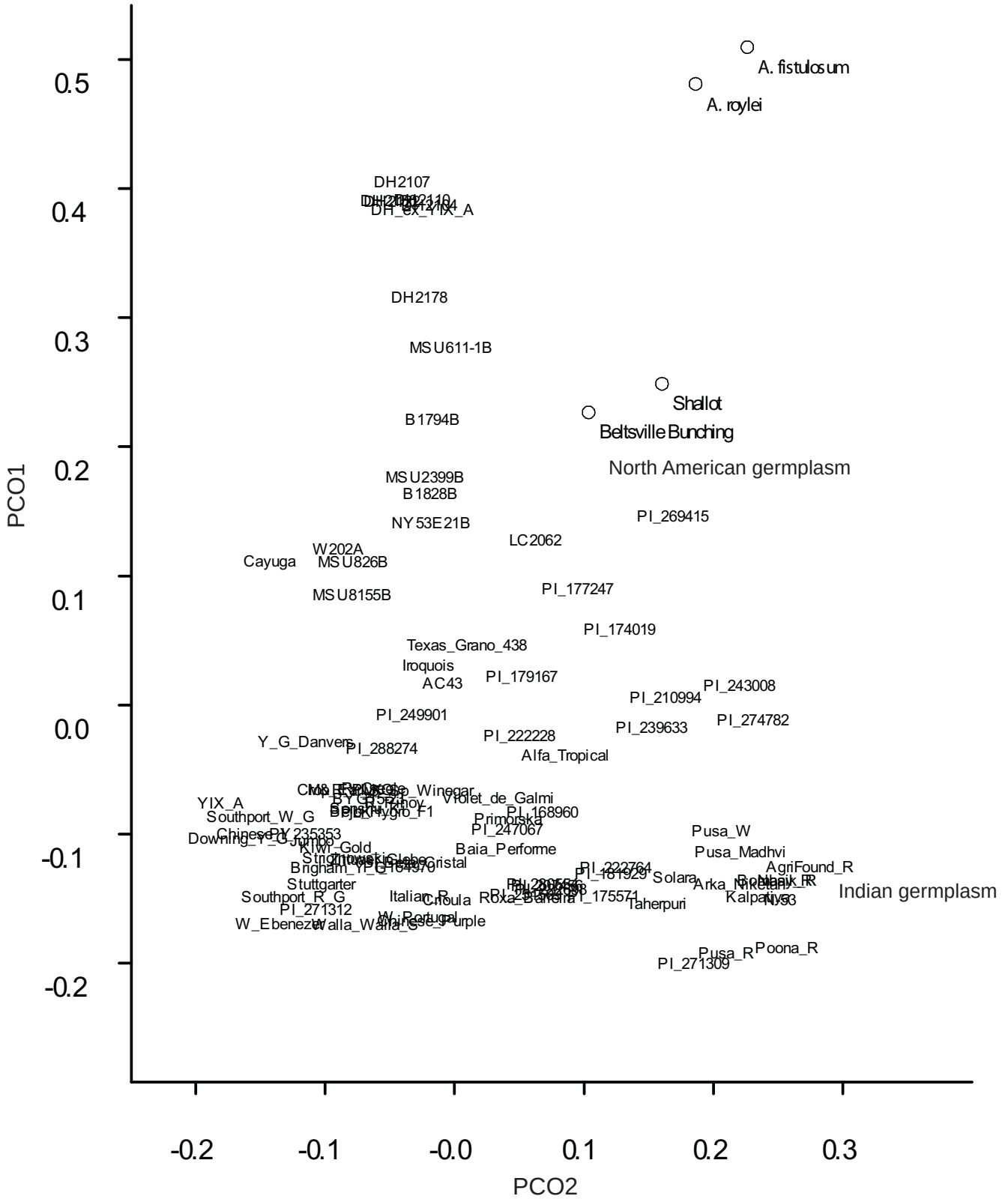

Fig.1. Principal co-ordinate analysis of Jaccard similarity matrix in bulb onion based on SSR markers (taken from McCallum *et al*., 2008)

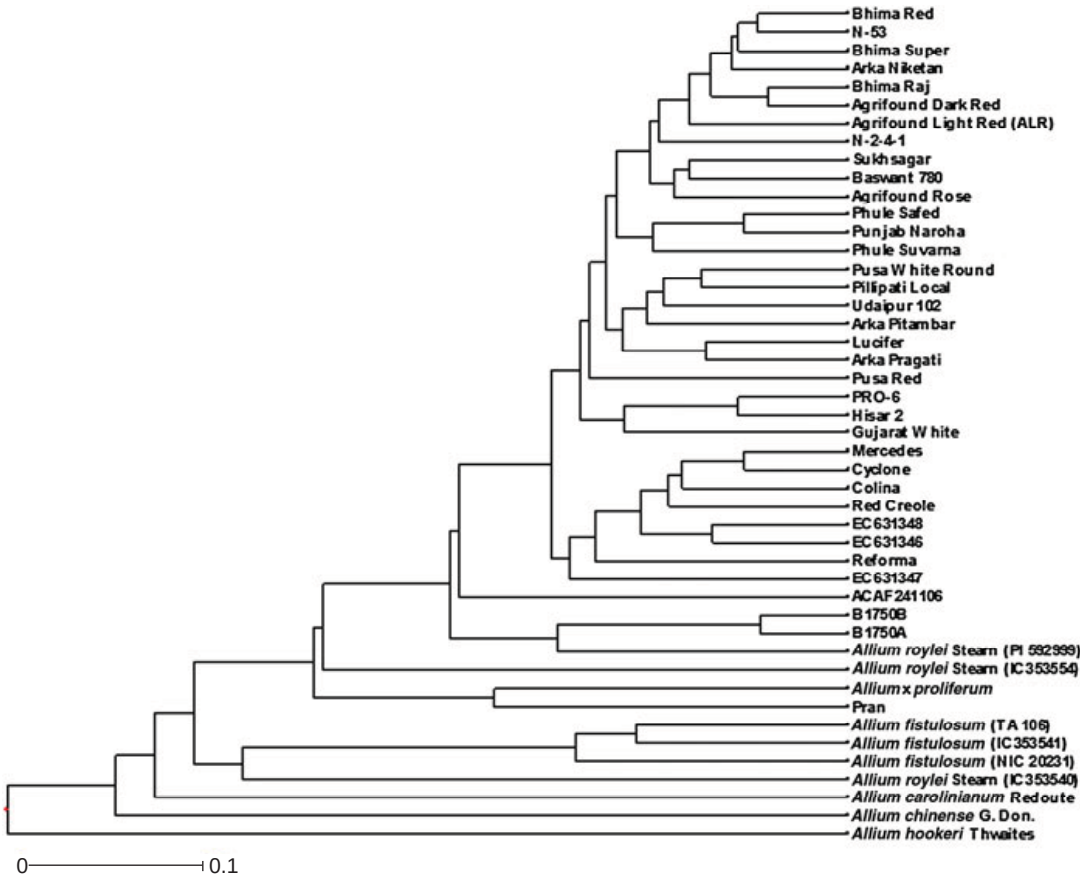

Fig.2. Clustering of bulb onion and allied species based on Jaccard dissimilarity index (Khar et al., 2011)

Japan and Korea (Brewester, 2008). In bunching onion, first set of SSR markers were developed from a genomic library and used for linkage map construction (Wako *et al.*, 2002; Song *et al.*, 2004; Tsukazaki *et al.*, 2007; 2008). SSR markers were utilized to determine genetic uniformity in bunching onion hybrids and very low were detected at different polymorphic loci suggesting high level of heterozygosity (Tsukazaki *et al.*, 2006). According to these results, SSR tagged breeding scheme was proposed in bunching onion and utilized to realize the utility of this scheme (Tsukazaki *et al.*, 2009).

Thirty bunching onion cultivars were classified using SSR markers and it was consistent with the previously reported results based up on morphological characters. Average number of amplicons per primer in this study was high (10.6) in comparison to previous studies (Song *et al.*, 2004) which indicates that high degree of genetic variability occurs in bunching onion germplasm (Tsukazaki *et al.*, 2010). In bunching onion germplasm, SSR markers were more polymorphic than Sequence Related Amplified Polymorphism (SRAP) on the basis of an average number of polymorphic alleles (Li *et al.*, 2008). But, the information given by SRAP was more consistent with morphological variability than that of SSR markers (Li *et al.*, 2008). Bunching onion accessions collected from different regions of India found to be distinctive from exotic accessions (Khosa *et al.*, 2013). In future, estimation of genetic variability in bunching onion germplasm of wide geographical origins must be investigated to detect some novel alleles.

Garlic

It is an asexually propagated *Allium*, which originated in central Asia is cultivated throughout the world (Brewester, 2008). The development of garlic cultivars has been limited to selection which hugely depends on the extent of variability available (Lampasona *et al.*, 2010). SSR markers were also developed in garlic to study genetic diversity for planning efficient strategies for germplasm conservation (Ma *et al.*, 2009; Cunha *et al.*, 2012). These studies indicated that SSR markers act as useful tool for characterization of garlic germplasm. In this context, Acharya and Simon (2010) used 20 SSR markers on 48 accessions collected from different countries and got

sufficient divergence in the germplasm. The Tunisian and French germplasm was characterized using ISSR markers where factor analysis of distances' table (AFTD) did not classify accessions on the basis of geographical origin or morpho-physiological characters, particularly bolting ability, but confirmed the appurtenance of analyzed accessions to s*ativum* botanical subspecies (Jabbes *et al.*, 2011). A core collection was developed, consisting of 95 accessions using heuristic approach which were the representative sample of whole germplasm. The degree of variability within accession (84.4%) was more than between the accessions (15.6%). There were four groups with - F_{ST} value of 0.1560, indicating a moderate differentiation among the groups (Zhao *et al.*, 2011). In China, considerable variability was observed in the garlic collections as 40 accessions were clustered into three groups (Xia *et al.*, 2012).

The garlic accessions collected from four countries were grouped into four clusters according to their geographical origin with SSR markers. It suggests that local selection pressure and differences in adaptability of garlic germplasm in particular regions is important cause of variability (Jo *et al*., 2012) Average number of alleles, observed heterozygosity, expected heterozygosity, Hardy Weinberg equilibrium, Shannon index and polymorphic information content values were 4.4, 0.468, 0.576, 1.073 and 0.518, respectively. Recently, EST-SSR markers were also developed in garlic and used for genetic diversity analysis (Ipek *et al.*, 2012; Khar, 2012). Indian garlic germplasm has considerable amount of variability and their clustering was independent of the geographical origin (Fig. 3) but based on the basis of vernalization requirement for bulb formation in garlic (Khar, 2012).

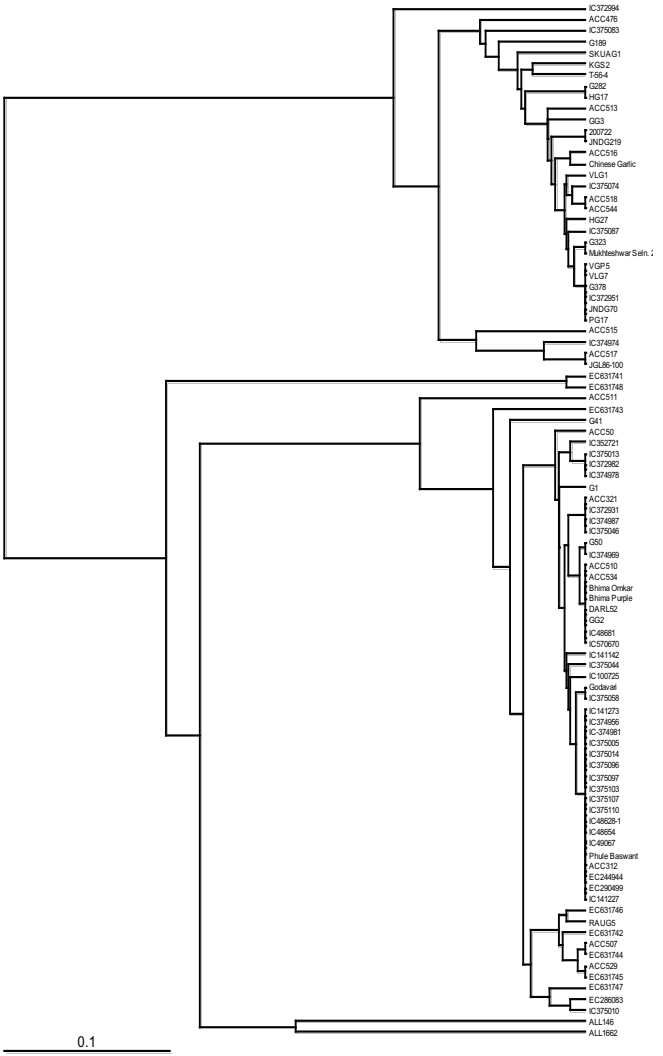

Fig. 3. The dendrogram based on Nei's genetic distance between 93 garlic accessions (Khar, 2012)

SSR Transferability

Availability of only limited number of SSR markers in *Allium* species is one of the major concerns for *Allium* research community. However, SSR transferability to related taxa is very useful approach as it was employed in various crops, which lacks sufficient sequence information (Varshney *et al.*, 2005).

Initially genomic SSR markers were screened for transferability studies but they exhibited low transferability in different *Allium* species (Fischer and Bachmann, 2000; Tsukazaki *et al.*, 2008; Araki *et al.*, 2010). It implies that markers developed from conserved coding regions would be more informative in transferability studies (Varshney *et al.*, 2005). In this context, bulb onion derived EST-SSR markers were employed for cross amplification in bunching onion and show high (75.10%) degree of transferability than genomic SSR (43.30%) markers (Tsukazaki *et al.*, 2008). Later, bulb onion derived SSR markers were used to estimate degree of transferability in wide range of *Allium* species and high transferability (100%, 87.17%, 25-91.70%) was observed in different studies (Khar *et al.*, 2011; Khosa *et al.*, 2013; Mallor *et al.*, 2014). The garlic derived SSR markers were tested for transferability in five related *Allium* species where highest transferability was observed in *A. porum* (73.00%) followed by A. *fistulosum* (48.00%) and *A. altaicum* (47.60%) which implies genome conservation among alliums (Lee *et al.*, 2011). Overall these findings suggest that in near future, SSR markers developed in bulb onion, bunching onion and garlic can be used in other *Allium* species for better understanding of *Allium* germplasm and their utilization.

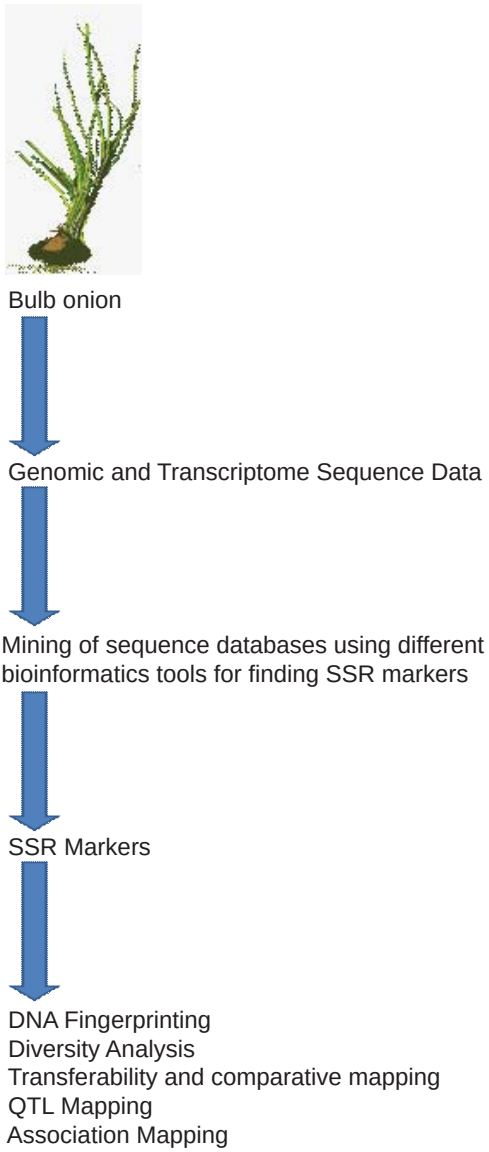

Fig. 4. A schematic flow chart for the development of SSR markers in bulb onion and their utilization

Conclusion

Utilization of SSR markers in genus *Allium* improves our understanding about genetic diversity and nature of *Allium* germplasm. This information would be useful to develop strategies for effective conservation and exploitation of *Allium* germplasm resources in improvement programs. Use of SSR markers to develop high density linkage map will facilitate the marker-assisted selection for useful traits in different *Allium* species. These markers could be utilized to study population structure which is pre-requisite to follow association mapping. Association mapping studies will be useful to find out the genomic regions associated with variability for various traits. Development of SSR-based interspecific linkage map will help us in revealing the synteny in various species. Establishment of syntenic associations will assist in the mining of orthologous genes and flow of genetic information between cultivated *Alliums* and their wild relatives for better understanding of *Allium* genomics. As transcriptome libraries were developed in garlic and bulb onion (Sun *et al.*, 2012; Duangjit *et al.*, 2013), it will be desirable to develop more EST-SSR markers to discover functional diversity in *Allium* germplasm.

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Genetic Divergence Analysis in Rice under Irrigated Conditions

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The nature and magnitude of genetic divergence were estimated in 134 rice germplasm accessions during *kharif* 2013 using Mahalanobis D^2 statistics. The genotypes were grouped into five clusters based on Euclidean cluster analysis. The pattern of distribution of genotypes into various clusters was random and independent of geographical origin or region of adoption indicating geographical diversity and genetic diversity were not related. Cluster means indicated considerable differences in the mean values of different traits. The genotypes of cluster II and cluster III exhibited high seed yield. The highest intra-cluster distance was observed among the genotypes, in cluster IV (12.19) followed by cluster III (11.03) and cluster V (10.90) indicating existence of wide genetic divergence among genotypes. Number of filled grains/panicle contributed highest towards divergence. The relative divergence of each cluster from other clusters displaced higher order of divergence between cluster IV and V followed by clusters II and V. The hybridization involving genotypes belong to these clusters is expected to give desirable segregants in rice breeding programmes.

Key Words: Clusters, Genetic divergence, Germplasm, Hybridization, Rice

Introduction

Rice is the most important staple food grain and stands next to wheat in the global food grain production. India has the largest area under rice, about 44.6 million hectare area with a production of about 106.19 million tonnes (MoA, 2014).The germplasms found in Asia, America and Europe belong to *Oryza sativa*, while *O. glaberrima* in West Africa. *O. sativa* is a cultivated diploid species with 24 chromosomes of AA genome (Brar and Khush, 1986). The nature and magnitude of genetic improvement generally depend on the amount of genetic variability present in a population. The major thrust area for such genetic improvement depends on selecting efficient breeding system and identifying desirable parents in hybridization programmes. Genetic diversity plays an important role in plant breeding since progeny originating from diverse parents exhibit greater heterosis and provide broad spectrum of variability in segregating generations (Khush, 1974). Therefore, a meaningful classification of genotypes will enable the breeder to identify the best parents with wide genetic divergence and to utilize some of the selected diverse parents in the hybridization programme. In the present study, an attempt was made to classify and understand the nature and magnitude of genetic diversity.

Materials and Methods

The experiment was carried out during *kharif* 2013 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experimental seed material comprised 134 rice genotypes collected from International Rice Research Institute, the Philippines; National Bureau of Plant Genetic Research, New Delhi; Central Rice Research Institute, Cuttack; Narendra Dev University of Agriculture and Technology, Faizabad and National Research Centre on Plant Biotechnology, New Delhi (Table 1). The nursery was sown on June 9, 2013, and 21-day-old seedlings were transplanted in a randomized block design (RBD) with three replications. Each plot consisted of five rows of 1.5 m length with spacing 15 × 20 cm. The recommended package of practices were followed for raising good and healthy crop. Observations were recorded on, days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of effective tillers/plant, panicle weight, total number of grains/panicle, filled grains/panicle, spikelet fertility percentage, test weight (g), kernel length (mm), kernel breadth (mm), kernel length/breadth ratio, kernel length after cooking (mm), grain elongation ratio and grain yield/plant. The analysis of variance was carried out for all the traits and the data were

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Table 1. List of 134 rice germplasm accessions and their collection site

Accession No.	Variety	Source	Accession No.	Variety	Source
1	HSUNG TIENG	IRRI, Philippines	68	IR 64	IRRI, Philippines
2	DULAR	IRRI, Philippines	69	SWARNA	IRRI, Philippines
3	FR13A	IRRI, Philippines	70	KASALATH	IRRI, Philippines
4	FR13B	IRRI, Philippines	71	IR 42	IRRI, Philippines
5	DHOLAMON 64-3	IRRI, Philippines	72	IR-73707-45-3-23	IRRI, Philippines
6	KARKATI 87	IRRI, Philippines	73	BARA SALI	NBPGR, New Delhi
7	JC 1	IRRI, Philippines	74	IR-36	NBPGR, New Delhi
8	JP 5	IRRI, Philippines	75	HUR-W-1	BHU, Varanasi
9	VANAN VELLAI	IRRI, Philippines	76	CHANGMAKA	NBPGR, New Delhi
10	NAALUMOLI KARUPPAN	IRRI, Philippines	77	CHOW HALA	NBPGR, New Delhi
11	ARC 614	IRRI, Philippines	78	BAGI BARDHANA	NBPGR, New Delhi
12	BIRPALA	IRRI, Philippines	79	CHANGMAN	NBPGR, New Delhi
13	BINULAWAN	IRRI, Philippines	80	BABARAKSHA KARA	NBPGR, New Delhi
14	MAPOI	IRRI, Philippines	81	JOHAINEANG (WET)	NBPGR, New Delhi
15	MENYARHUNEI	IRRI, Philippines	82	BARACHIRAMARA	NBPGR, New Delhi
16	MUYAMBA	IRRI, Philippines	83	HUKKANNA KUMBALOA	NBPGR, New Delhi
17	PAIAM	IRRI, Philippines	84	HULTA BALUNGA (WILD)	NBPGR, New Delhi
18	PALENEMA	IRRI, Philippines	85	MEGHI	NBPGR, New Delhi
19	PATAIM	IRRI, Philippines	86	JOKHRU	NBPGR, New Delhi
20	PECALO	IRRI, Philippines	87	PANIKAKUA	NBPGR, New Delhi
21	TAGBA	IRRI, Philippines	88	CHUMANSAL-39	NBPGR, New Delhi
22	TIEBIMAH	IRRI, Philippines	89	JAHABHOG	NBPGR, New Delhi
23	GODA HEENATE	IRRI, Philippines	90	CHANG MUI	NBPGR, New Delhi
24	TETEP	IRRI, Philippines	91	PANI DUBI	NBPGR, New Delhi
25	HEEN SULAI	IRRI, Philippines	92	MEGHRAJ	NBPGR, New Delhi
26	JAYMIS	IRRI, Philippines	93	ASAMIA	NBPGR, New Delhi
27	KALUWEE	IRRI, Philippines	94	CHARETSUK	NBPGR, New Delhi
28	MADAL	IRRI, Philippines	95	BAGA GOHA	NBPGR, New Delhi
29	MAHA DIKWEE	IRRI, Philippines	96	BARA RANGA	NBPGR, New Delhi
30	NCHEL PARAGAHAKALE	IRRI, Philippines	97	JAGANATHA BALLAVA	NBPGR, New Delhi
31	USA BATAPOLAAL	IRRI, Philippines	98	JALKANTHI	NBPGR, New Delhi
32	KOSHIHIKARI	IRRI, Philippines	99	CHUDI	CRRI, Cuttack
33	AUSBORO	IRRI, Philippines	100	MANOHAR SALI	CRRI, Cuttack
34	JALDUNGI	IRRI, Philippines	101	BABAI LACHHA	CRRI, Cuttack
35	NIRBOI	IRRI, Philippines	102	LUNISHREE	CRRI, Cuttack
36	PAKRIBUNA	IRRI, Philippines	103	MANDIRA	CRRI, Cuttack
37	VADAI	IRRI, Philippines	104	ASANA	CRRI, Cuttack
38	MARS	IRRI, Philippines	105	PANI DHAN-2	CRRI, Cuttack
39	CR 1009	IRRI, Philippines	106	SWARNA SUB-1	BHU, Varanasi
40	BUNTOK	IRRI, Philippines	107	BAD DHANA	CRRI, Cuttack
41	RITEK SIRENDAN MERA	IRRI, Philippines	108	ASHU BHAJNA	CRRI, Cuttack
42	AZUCENA	IRRI, Philippines	109	BAD GEDE	CRRI, Cuttack
43	HOURA KANI	IRRI, Philippines	110	PANIKEKEUA	CRRI, Cuttack
44	NALDAK	IRRI, Philippines	111	PANKEI	CRRI, Cuttack
45	BR 11	IRRI, Philippines	112	BAD JHARLI	CRRI, Cuttack
46	ZOBGUI	IRRI, Philippines	113	S-183	CRRI, Cuttack
47	SOSSON HONDON	IRRI, Philippines	114	SAMBHA SUB-1	NDUAT, Faizabad
48	VAN	IRRI, Philippines	115	JALNIDHI	NDUAT, Faizabad
49	KHAIYAN	IRRI, Philippines	116	GOTHAWA	NRCPB, New Delhi
50	LIU-TIAO-NU	IRRI, Philippines	117	KAJARAHAWA	NRCPB, New Delhi
51	MA-ZHAN(RAD)	IRRI, Philippines	118	RAJBHOG	NRCPB, New Delhi
52	MOUSSAYA	IRRI, Philippines	119	SINGHARA	NRCPB, New Delhi
53	KAOLACK	IRRI, Philippines	120	SATHI	NRCPB, New Delhi
54	NCS 348	IRRI, Philippines	121	KARIYWA	NRCPB, New Delhi
55	ZECHUM	IRRI, Philippines	122	MOTI	NRCPB, New Delhi
56	KARABONKA	IRRI, Philippines	123	SUGAPANKH	NRCPB, New Delhi
57	EMPING ARA	IRRI, Philippines	124	SARJOO-52	NRCPB, New Delhi
58	ROM RUNTIK	IRRI, Philippines	125	LALKA DHAN	NRCPB, New Delhi
59	LATSIKA	IRRI, Philippines	126	DUDHA LADU	NRCPB, New Delhi
60	SANG KHLA	IRRI, Philippines	127	S-148	CRRI, Cuttack
61	SANTI BAHN	IRRI, Philippines	128	S-177	CRRI, Cuttack
62	TAH TONE	IRRI, Philippines	129	S-138	CRRI, Cuttack
63	WAHNG	IRRI, Philippines	130	S-169	CRRI, Cuttack
64	SIPULUT PANDAN	IRRI, Philippines	131	S-141	CRRI, Cuttack
65	NANHI	IRRI, Philippines	132	S-155	CRRI, Cuttack
66	KARNAL LOCAL	IRRI, Philippines	133	KALA BUNDE	NBPGR, New Delhi
67	KHAO HLANON	IRRI, Philippines	134	KALA JOHA	NBPGR, New Delhi

subjected multivariate analysis following Mahalanobis's D^2statistics (Mahalanobis, 1936) to measure the genetic divergence followed by the clustering of genotypes based on 16 characters following Tocher's method as described by Rao (1952).

Results and Discussion

Analysis of variance revealed highly significant differences for all the characters studied, indicating a wide range of variation for all the 16 traits (Table 2). Based on the relative magnitude of D^2 values of 134 genotypes, these were grouped into five different clusters. Cluster I consist of 68 genotypes forming the largest cluster followed by cluster II comprised 22 genotypes and cluster III had 21 genotypes, cluster IV contained 10 genotypes, cluster V comprising of 2 genotypes while 11 genotypes (Rom Runtik, Ncs 348, Ritek Sirendan Mera, Kaluwee, Manohar Sali, Jalkanthi, Chang Mui, Azucena, Muyamba, Meghi and Khaiyan) were ungrouped (Table 3). The genotypes included in a particular cluster indicated their close relationship among themselves as compared to genotype in other clusters. Therefore, it could be expected that genotype within a cluster were less genetically different with each other, and were diverse from the genotype belonging to other clusters.

The highest intra-cluster distance was observed in cluster IV (12.19) followed by cluster III (11.03) and cluster V (10.90) while cluster I had lowest intra-cluster distance (Table 4). The highest inter-cluster distance was observed between cluster IV and cluster V (22.36) followed by cluster II and cluster V (21.85) and cluster I and cluster V (20.16) indicated that the hybridization between the most diverse genotypes would yield desirable segregates with the accumulation of favourable genes in the segregating generations. The lowest inter-cluster distance was recorded between cluster I and cluster IV (12.82) indicating close relationship and similarity for most of the characters of genotypes falling in these clusters. Such analysis was meant to avoid selection of parents from genetically homogenous clusters and to maintain a relatively broad genetic base. The inter-cluster distances were higher than the intra-cluster distances which indicate the existence of substantial diversity among the parents. Similar results of inter and intra cluster distances in rice were reported by Senapati and Sarkar (2005), Kuchanur *et al.* (2009) and Roy (2013).

Table 2. Analysis of variance for 16 traits in 134 rice germplasm accessions

Source of variation	Df	Mean sum of squares															
		DF	DM	PH	PL	ET	PW	FG	TG	KL	KB	TW	SF%	LB	KLAC	GER	GYP
Replicate	2	48.60	257.63	2391.04	246.13	37.78	1.88	2582.41	3094.59	1.6105	0.22	144.7	0.26	0.03	3.32	0.004	587.45
Treatments	133	2191.52**	2329.73**	1729.01**	23.65**	19.91**	1.12**	2981.16**	3501.09**	1.39**	0.196**	76.29**	15.26**	0.58**	2.19**	0.03**	128.71**
Error	266	34.39	40.07	60.05	1.89	0.43	0.02	16.60	19.69	0.03	0.01	0.67	2.717	0.02	0.1	0.0007	2.82

**Significant at 1% level of significance.

DF= Days to 50% flowering; DM= Days to maturity; ET= Number of Effective tillers/plant; FG= Filled grains/panicle; GER= Grain elongation ratio; GYP= Grain yield /plant; KB= Kernel breadth; KL= Kernel length; KLAC= Kernel lenth after cooking; LB= Kernel length/breadth ratio;PH= Plant height; PL= Panicle length; PW= panicle weight; SF= Spikelet fertility percentage; TG= Total no. of grains/panicle; TW= Test Weight

Table 3. Grouping of 134 rice germplasm accessions into five clusters by Tocher's method

Cluster number	Name of germplasm	No. of accessions
I	Asamia, Ashu Bhajna, Babai Lachha, Bad Gede, Bad Jharli, Baga Goha, Bagi Bardhana, Bara Ranga, Bara Sali, Br 11, Buntok, Changmaka, Charetsuk,Chumansal-39,Cr 1009, Emping Ara,Fr13a, Goda Heenate, Houra Kani, Hukkana KumbAloa, Hulta Balunga(Wild), Ir-36, Ir-7307-45-3-23, Jaganatha Ballava, Jahabhog, Jaldungi, Jalnidhi, Jaymis, Jc-1, Johaineang(Wet), Kala Joha, Kaolack, Karabonka, Kasalth, Koshihikari, Latsika, Lunishree, Madal, Maha Dikwee, Mandira, Mapoi, Meghraj, Menyarhunei, Naldak, Nanhi, Nchel Paragahakale, Nirboi, Paiam, Pakribuna, Palenema, Pani Dubi, Panikakua, Panikekeua, Pankei, Pecalo, Santi Bahn, Sipulut Pandan, Sosson Hondon, Swarna Sub-1, Swarna, Tagba, Tah Tone, Tiebimah, Vadai, Van, Wahang, Zobgui	68
II	Babarakshakara, Chow Hala, Chudi,Dholamon 64-3, Dudha Ladu, Gothawa, Heen Sulai, Kajarahawa, Kala BuNde, Kariywa, Karkati 87, Lalka Dhan, Mars, Moti, Naalumoli Karuppan, Pani Dhan-2, S-141, S-148, Sarjoo-52, Singhara, Sugapankh, Usa Batapolaal,	22
III	Ausboro, Barachiramara, Binulawan, Dular, Hsung Tieng, Ir-64, Jokhru, Karnal Local, Khao Hlan On, Liu-Tiao-Nu, Ma-Zhan (Rad), Moussaya, S-138, S-155, S-169, S-177, S-183, Sang Khla, Sathi, Tetep, Zechum	21
IV	Arc614,Asana, Bad Dhana, Birpala, Changman,Fr 13b, Jp5, Rajbhog, Sambha Sub-1, Vanen Vellai,	10
V	Hur-W-1, Ir-42	2
Ungrouped	Azucena, Chang Mui, Jalkanthi, Kaluwee, Khaiyan, Manohar Sali, Meghi, Muyamba, Ncs 348, Ritek Sirendan Mera, Rom Runtik	11

Table 4. Average intra and inter-cluster D2 values among five clusters of 134 rice germplasm accessions

Cluster	I	II	III	IV	V
I	9.47	13.36	13.27	12.82	20.16
II		10.71	16.04	15.00	21.85
III			11.03	17.49	19.90
IV				12.19	22.36
V					10.90

(Figures in diagonal indicates intra cluster D value)

The cluster mean values showing a wide range of variation for all the characters were taken in the study (Table 5). Cluster II exhibited highest mean values for plant height, panicle length, panicle weight, filled grains/ panicle, total number of grains/panicle, test weight and grain yield/ plant and lowest for number of effective tillers/ plant while Cluster I had the highest mean values for days to 50% flowering, days to maturity and kernel length after cooking. Similarly, cluster V exhibited highest mean values for number of effective tillers per plant, kernel length and length-breadth ratio while cluster III exhibited highest mean value for kernel breadth and lowest for filled grains/panicle. The cluster IV had highest mean value for spikelet fertility percentage and grain elongation ratio while lowest for kernel length after cooking. Thus, the accessions in cluster II, V, I and III seem to be quite promising for many of the traits which were studied. Distribution of highest and lowest mean values for different traits in distinct cluster indicated the traits contributing to the total divergence.

The contribution of characters towards the total genetic divergence is important in deciding the characters for selection. The present findings revealed that the filled grain/panicle, test weight, kernel length after cooking, days to 50% flowering and kernel length were the major contributing factors towards total divergence. Therefore, selection of genotypes would be more effective if it is based on the above said traits. Kole (2000) also reported that the traits such as kernel length, number of panicles/ plant, test weight and days to 50% flowering were the major contributors towards divergence. Similar results were obtained by Singh *et al.* (2011), Ovung *et al.* (2012) and Kumar *et al.* (2014). Clusters IV and V and Clusters II and V were diverse to each other therefore, selection of diverse accessions with desirable traits, and utilizing them in multiple crossing programmes, is expected to be effective in accumulation of favourable genes in segregating generations.

Table 6. Relative contribution of 16 characters to genetic diversity

Character	Times ranked 1st	Contribution %
50% DF	803	9.01%
Days to maturity	320	3.59%
Plant height (cm)	227	2.55%
Panicle length (cm)	15	0.17%
Effective tiller	591	6.63%
Panicle weight (g)	414	4.65%
Filled grain	2665	29.91%
Total grain	9	0.10%
Kernel length (mm)	532	5.97%
Kernel breadth (mm)	74	0.83%
Test weight (g)	1907	21.40%
Yield /plant (g)	162	1.82%
Spikelet fertility%	5	0.06%
lb ratio	6	0.07%
KLAC (mm)	952	10.68%
Elongation ratio	229	2.57%

KLAC= Kernel length after cooking

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Table 5. Cluster mean values for 16 different traits

Traits / Cluster	50% DF	DM	PH	PL	ET	PW	FG	TG	KL	KB	TW	SF%	LB	KLAC	GER	GYP
I	145.43	180.77	125.99	22.00	7.91	2.11	87.83	98.47	6.20	2.32	20.67	89.06	2.70	8.28	1.34	15.05
II	122.80	162.50	143.60	24.64	7.38	3.10	137.43	154.07	6.23	2.43	23.25	89.04	2.59	8.07	1.29	20.99
III	97.05	128.73	126.02	23.06	10.32	2.33	71.71	80.38	6.30	2.47	23.73	89.07	2.62	8.19	1.30	18.04
IV	140.40	173.67	119.80	20.11	8.18	2.33	119.39	131.19	5.50	2.11	15.21	90.59	2.67	7.97	1.45	16.35
V	93.50	128.83	111.18	24.51	10.62	1.75	81.99	92.00	8.05	2.44	14.46	88.82	3.32	8.22	1.02	12.57
Mean	140.59	178.11	125.85	22.07	7.73	2.20	95.10	106.79	6.25	2.23	21.34	88.43	2.84	8.10	1.31	15.35

DF= Days to 50% flowering; DM= Days to maturity; ET= Effective tillers/plant; FG= Filled grains/panicle; GER= Grain elongation ratio; GYP= Grain yield /plant; KB= Kernel breadth; KL= Kernel length; KLAC= Kernel lenth after cooking; LB= Kernel length/breadth ratio;PH= Plant height; PL= Panicle length; PW= panicle weight; SF= Spikelet fertility percentage; TG= Total no. of grains/panicle; TW= Test Weight

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Assessment of Morphological Diversity within Wild Rice (*Oryza rufipogon* Griff.) Germplasm of NBU Campus (West Bengal) for *In Situ* Conservation – A Case Study

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Natural population of *Oryza rufipogon* Griff. in the North Bengal University campus was characterized based on phylogeographic and morphological parameters for conservation purposes. Twenty-six different morphological characters were considered for genetic relatedness analysis within the population. Diagnostic characters were provided to delineate the species morphologically. Plants were annual ecotype having short to intermediate culm height (64-145 cm), and 0.5-1.6 cm thickness. Profuse fibrous roots of 2 mm thick and 3-9 cm long creamy-white colour emerged from the floating nodes, that was solid and pinkish (5-7 mm long). Flag leaf length ranged from 13-40 cm and 0.3-1.8 cm in width. Flag leaf blade attitude varied from deflexed to horizontal to semierect. Auricle was hard, curved, glabrous and 13-15.5 mm. Two-cleft ligule length ranged 17-35 mm. Panicle length varied from 15.4-30 cm with 1-8 cm wide with 5-13 primary branches. Attitude of primary branches was spreading, well-exserted (100%), alternately arranged on the wavy axis. Length of the lemma varies 6-11 mm and 1.4-2.3 mm wide, lemma-awn junction marked by a pinkish pubescent constriction with 23-80 mm long red awn. Yellow colour anthers varied in length 4-8 mm long. Stigma was bifurcated (> 2 mm) and purple comes out from the spikelets. Seeds (blackish) varied in length (7.5-10 mm). Density of fertile spikelets ranged from 15-82. Grain length/breadth ratio was 3.73 and average kernel length/breadth ratio was 3.99. The results suggested that the studied population were genetically diversified, heterogeneous and should be conserved *in situ* to protect precious genetic resource as separate ecological race (ecotype or intergrade) for germplasm enhancement.

Key Words: Eco-habitat, Diagnostic morphology, Genetic variation, *In situ* conservation, *Oryza rufipogon*

Introduction

The genus *Oryza* (Poaceae) includes two cultivated species (*Oryza glaberrima* Steud. and *O. sativa* L.) and 22 wild species. *O. glaberrima* is restricted only Western Africa, but *O. sativa* is cultivated globally (Vaughan, 1994; Kovach *et al*., 2007) due to its wide adaptability to different habitats and growing conditions. The species *O. sativa* can be grouped into two subspecies, *Oryza sativa* ssp. *japonica* and *O. sativa* ssp. *indica*, based on a number of physiological and morphological traits (Second, 1982; Oka, 1998). *Oryza sativa* ssp. *indica* was domesticated within a region south of the Himalaya mountain range, lowland of tropical Asia likely eastern India, Myanmar, and Thailand, whereas *Oryza sativa* ssp. *japonica* was domesticated from wild rice in the upland hills of southern China, southeast Asia, and Indonesia, and also outside of Asia (Africa, North America, and South America) (Khush, 1997; Londo *et al*., 2006). *Oryza sativa* L., represents the world's most important staple food crop, feeding more than half of the human population (supplying 20% of the world's total caloric intake). Despite this essential role in world agriculture, the history of cultivated rice's domestication from its progenitors (ancestors) and evolutionary pathways remains unclear. Phylogeographic studies indicate that India and Indochina may represent the centre of diversity of one of the 22 wild rice species *O. rufipogon* Griff. Wild rice species, *O. rufipogon*, grows across this entire range. *O. sativa* L. and *O. rufipogon* Griff. share the similar vegetative growth and other eco-geographical characters including the same AA genome and is widely recognised as a progenitor of cultivated rice (*O. sativa* L.) (Khush, 1997; Londo *et al*., 2006; Vaughan, 2008). *O. rufipogon* is a perennial species and cultivated rice is an annual species, it has been proposed that the annually occurring form of *O. rufipogon*, *O. nivara* (Sharma *et* Shastry, 1965), may represent the most recent ancestor of *O. sativa*. During the course of domestication from

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wild rice to cultivated rice, many genes were lost through natural and human selection, leading to the lower genetic diversity of the cultivated rice (Zhu *et al*., 2007). These wild species are the reservoirs of many useful genes/ QTLs particularly for resistance to major biotic and abiotic stresses (Xiao *et al*., 1996; Sanchez *et al*., 2013). The most successful examples are the use of genes from *Oryza nivara* to breed rice varieties with long-lasting resistance to grassy stunt virus (Khush, 1977) and the use of wild abortive cytoplasmic male sterility from *O. spontanea* to hybrid rice (Lin and Yuan, 1980). Broad spectrum blast resistance gene(s) and yield improving potentials have been introgressed for the development of new cultivar, Dhanarasi using *O. rufipogon* as donor (Ram *et al*., 2007a; 2007b). Green leafhopper resistance gene has been introgressed into cultivated species through molecular breeding from *O. rufipogon* (Fujita *et al*., 2003). Many useful genes from *O. rufipogon* have been successfully introgressed into the cultivated background (Wright and Gaut, 2005). Yield-enhancing traits/QTLs/ genes were mapped and identified from *O. rufipogon* and incorporated into the genetic background of IR64/ other cultivars for yield increase (Septiningshih *et al*., 2003; Thomson *et al*., 2003; Tian *et al*., 2006; McCouch *et al*., 2007). Today, the wild species exists in only a few severely fragmented populations that may be remnant of a formerly more continuous widespread range (Gao, 2004; Londo *et al*., 2006). Populations of *Oryza rufipogon* have gradually reduced due to ecological stresses.

Due to long term neglect, wild rice population in NBU campus (North Bengal University) are being lost at an alarming rate. NBU campus has received little attention to *Oryza rufipogon* populations. It needs immediate attention with high priority before agriculturally important *Oryza* genepool is lost.

After exhaustive reviewing of the literature and considering the importance of origin of problem of wild rice genetic resources, the present investigation was made for the first time to characterize the germplasm of *O. rufipogon* from the campus of North Bengal University (NBU) based on ecological and morphological parameters to provide much needed data to maintain and implement *in situ* conservation strategies.

Material and Methods

Plant Material

Natural population of wild rice *Oryza rufipogon* Griff. in the campus of the University of North Bengal (NBU) was surveyed for the present study including the growing conditions, ecological environments, water availability and morphological characteristics. Some specific ecological environments are supporting wild rice *Oryza rufipogon* Griff. population in the NBU campus as natural habitat (Fig. 1), which is located at Latitude of 26º 84′ North and Longitude of 88º 44′ East, near Siliguri, Dist-Darjeeling, WB, India. The area is seasonally dry and water logged. During summer this region is completely dry but during monsoon June to September there is plenty of water in the ponds and ditches.

Soil Testing

Soil samples were collected from the rice field during March (2014) according to the standard protocol and sent to the Tea Science Department, NBU for analysis (Tea Board approved soil testing lab) on payment basis.

Methodology for Morphological Trait Analysis

Plant materials (*Oryza rufipogon* Griff.) were directly used for morphological trait measurement and analysis in the natural field conditions in the NBU campus. Twenty-five plants were selected for recording twenty-six morphological features for genetic variation study. All the phylogeographic and morphological observations were recorded and measured as per standard protocol for wild rice characterization (IBV/IRRI). Eighteen quantitative morphological traits were considered for the present study *viz.*– panicle length, flag leaf length/ width, spikelet number per panicle, seed length/width, awn length, stigma length, anther length and plant height, uppermost internode distance, primary branching, ligule, auricle, palea length, sterile lemma, kernel length/ breadth, etc. The average quantitative trait value for each variable from all individuals in a population was generated and used for analysis. Eight qualitative traits were considered in the present study – attitude of panicle branches, panicle curvature, panicle exsertion, attitude of flag leaf, spikelet anthocyanin, keel edge, stigma colour, and lemma colour at maturity.

Results and Discussion

Wild rice of NBU campus were identified as *Oryza rufipogon* Griff. based on data on phylogeography and morphological traits analysis. Morphological characteristics measurements were statistically analysed using SPSS-15 software and summarized in Table 1 and graphically represented in Fig. 3.

Fig. 1. Location of surveyed population of wild rice *Oryza rufipogon* **in the NBU campus**

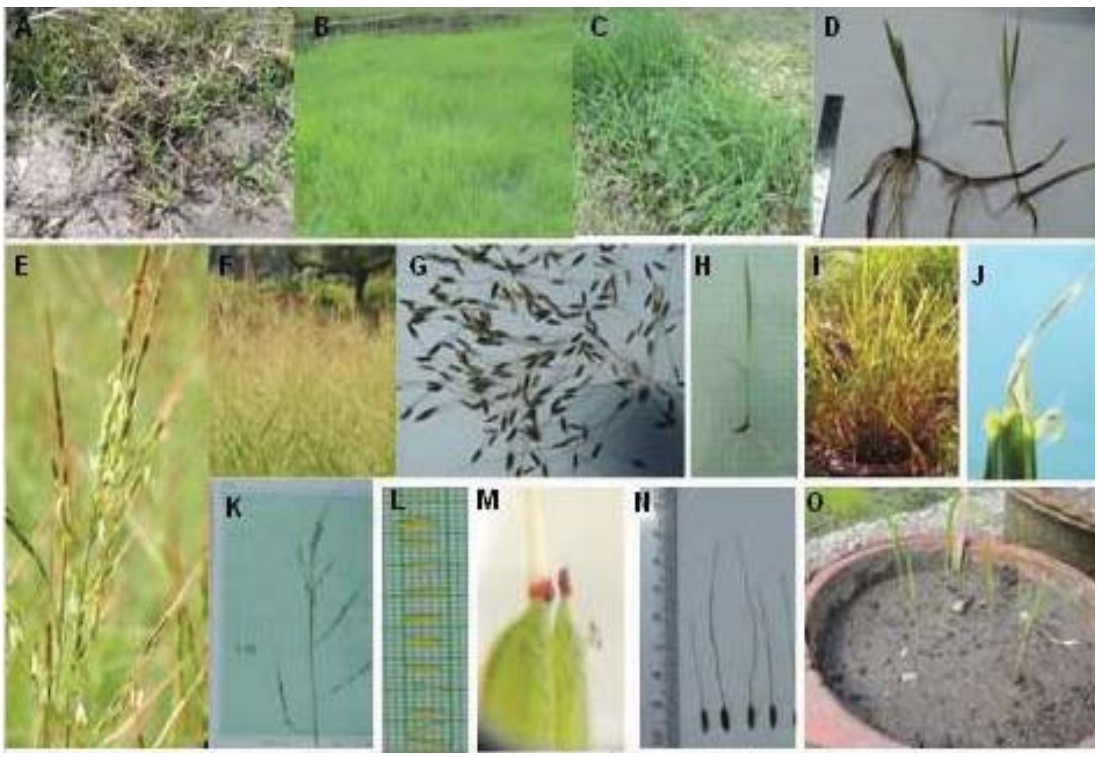

Fig. 2. Different morphological traits and measurement for characterization of wild rice *Oryza rufipogon* Griff. of NBU campus. A : Plants with stem stolon survive in dry summer, B: Vegetative propagation in monsoon, C: Stem stolon grown in water tanks for propagation and conservation, D: Tillering with roots from nodal region, E: Panicle with spikelets showing protruding anthers and stigmas, F: Starts seeds shattering during maturity, G: Mature black seeds with long awn, H: Mature seed germinated and measured seedling length, I: Profuse tillering from node of a stem part, J: Showing auricle and ligule, K: Panicle length measurement, L: Anther length, M: Dark red point at awn base, N: Seed length, O: Germinated seeds in pot during *kharif* 2014

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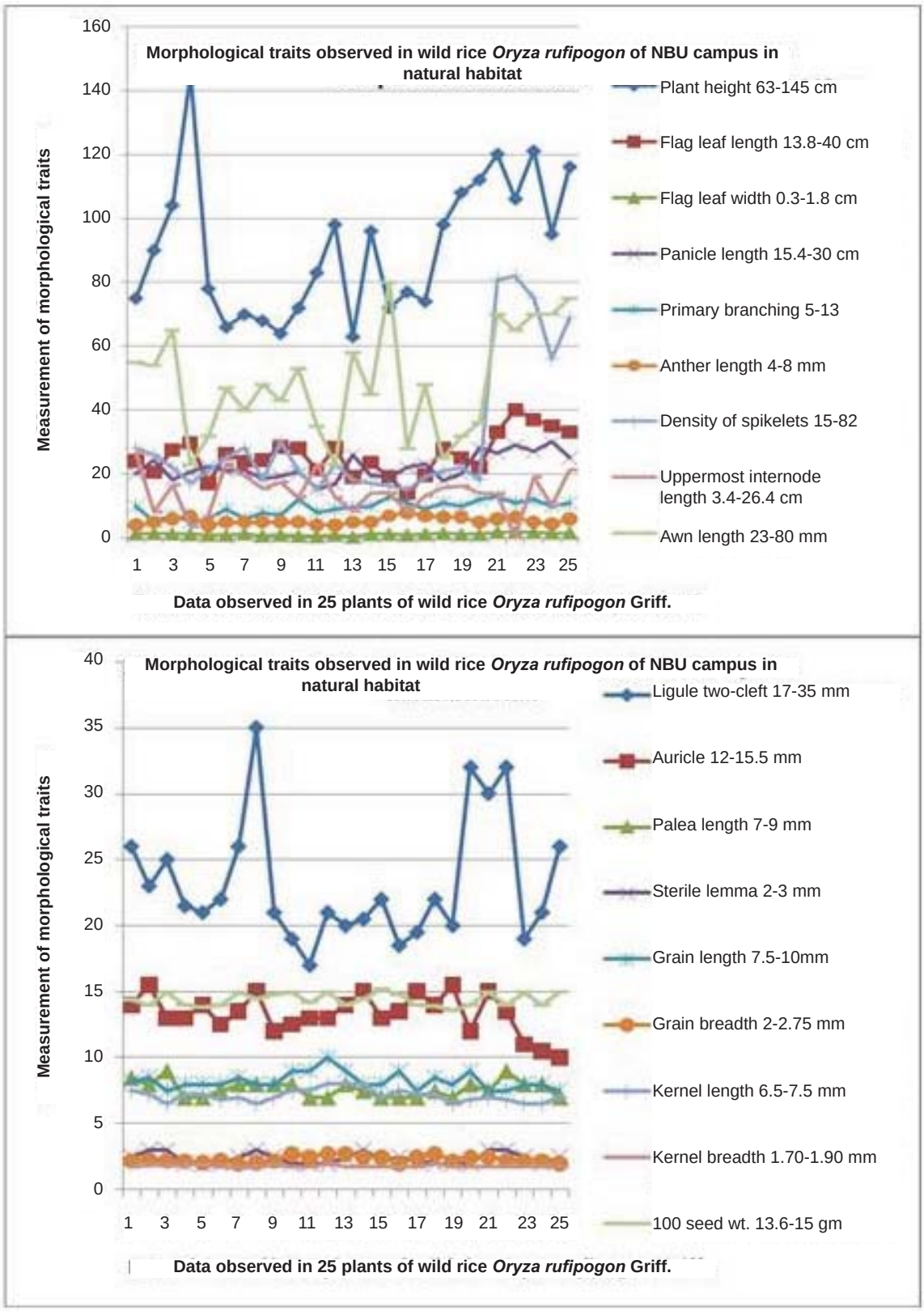

Fig. 3. Graphical representation of some morphological traits observed in *Oryza rufipogon* Griff. of NBU campus in natural habitat

Habitat and Ecology

Plant is annual ecotype, sometimes rhizomatous, short to intermediate height (64-145 cm). It is found growing in swampy areas (shallow water, up to 0.3 m), at edge of ponds and tanks, in ditches around the river of Magurmari which flows through the campus of the University of North Bengal, which is seasonally dry and open habitats. Plants start flourishing during the rainy season June-July of every year mostly through clonal propagation, flowering in September-October and seed shedding November-December and then dried up (Fig.1 & 2). Low population are due to destruction by human activities (poor women collect wild green vegetables along with wild rice during monsoon period) and over grazing.

Morphological Diversity

Culms: Geniculately ascending/sub-erect or decumbent (prostrate), 64-145 cm long, 0.5-1.6 cm thick, spongy lower part floating on the water surface with profuse fibrous rooting at the node region often with rhizomes, roots are 2 mm thick and 3-9 cm in length, creamy-white in colour present in the subsoil culms at the node region, node region is solid, hard and pinkish in colour (5–7 mm).

Roots: Roots fibrous, often with rhizomes. Fibrous root produces from nodal region of floated stems/stolons (Fig. 1 D).

Leaf Morphology: Leaf blades linear, lanceolate, flat, somewhat glaucous, scabrid on margins and main nerves, base rounded, margin tentate, apex acuminate, leaf blade surface scabrous or smooth, flag leaf 13-40 cm long and 0.3-1.8 cm width. Flag leaf blade attitude- deflexed/ horizontal/semierect. Leaf sheath loose, cylindrical, smooth, glabrous on surface, generally cover the whole intermodal region with distinct auricle at the junction with the blade. Auricles 13 mm-15 mm in size, narrow, curved, hard, glabrous or lined with long hairs to 2 mm long. Ligule- two-cleft, V-shaped, triangular, an unfringed membrane up to 17-35 mm long.

Inflorescence: Panicle, open, linear, nodding, 15-30 cm long, 1-8 cm wide; primary branches 5-13; attitude of branches –spreading, well exserted (100%). Panicle before anthesis erect and compact but after anthesis spikelets primary branches spread from the panicle axis, primary branches alternately arranged on the axis and axis is wavy. Flowering time September-October.

***Fertile Spikelets*:** Spikelets oblong, laterally compressed, 5-9 mm long, 1.6-3.5 mm wide with pedicel.

***Functional Florets*:** Lemma 6-11 mm long, 1.4-2.3 mm wide, straight or curved, lemma-awn junctions marked by a purplish, pubescent construction, awns 23-80 mm long. Awn bicolour, hard and rough surface, lower part creamy-white before anthesis and upper part reddish colour at maturity. Palea–elliptic, 7 mm long, coriaceous, 3-veined, 1-keeled, surface scabrous, apex acute. Glumes 2-3 mm long, ovate, and unequal.

Flowers: Lodicules 2, membranous, stamens 6, anthers 4-8 mm long, yellow in colour, stigma bifurcated, purple-brown in colour comes out from the spikelets through lemma and palea, ovary 1 mm long.

Fruits: Caryopsis with adherent pericarp 7.5-10 mm long, 2-2.75 mm wide, broadly elliptic or oblong, reddish-brown to dark blackish-red, embryos 1-1.5 mm. Most of the seeds are shed before harvesting due to shattering nature. Seeds harvested during November-December.

Wild rice of NBU campus is considered as a variant ecotypic race of *Oryza rufipogon* Griff. due to distinct characteristics specially anther length (4-8 mm), stigma >2 mm and sterile lemma 2-3 mm long. In most cases, individuals within populations showed different levels of morphological variability (Table 1 and Fig. 2). It is consistent with earlier report (Dong *et al*., 2010). In case of plant height and spikelet density Sd value is 21.74, and 21.87, respectively, which clearly indicating that morphological data are highly variable (Table 1). There was no report of secondary panicle branching in the present observation that was not supporting the earlier observation (Dong *et al.,* 2010). Morphological variation existed within the populations may be due to the existence of variety of ecological parameters include temperature, water, soil and associated plants communities, among others (Gao, 2004). Soil is loam type containing 40% silt, 20% clay and 40% sand, with acidic pH 5.69. Proportion of organic matter was 2.41 %, organic carbon 1.40 %, nitrogen 0.12 %, K_2O 89.8 ppm, P_2O_5 18 ppm and sulphur 40.5 ppm. Panicle is less than 30 cm in length with 15-80 spikelets per panicle. Spikelet tip was marked with a deep pink colouration. Plenty of fibrous roots were evident in many individuals. Morphological variation were observed in the present study may be due to the introgression of genetic factors from *Oryza sativa* to *O. rufipogon* (Dong *et al*., 2010). The two taxa (*O. nivara* and *O. rufipogon*) are recognized as distinct

Table 1. Morphological data of *Oryza rufipogon* of NBU campus

		Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Panicle length (cm)	Primary branching	Anther length (mm)	Spikelets density	Upper most internode (cm)	Awn length (mm)
N	Valid	25	25	25	25	25	25	25	25	25
	Missing	0	0	0	0	0	0	0	0	0
Mean		90.8400	25.8720	1.1400	22.0440	9.3800	5.4800	31.3200	13.9840	48.8000
SEm		4.34921	1.28398	0.08062	0.79103	0.47546	0.22076	4.37596	1.23994	3.43511
SD		21.74603	6.41992	0.40311	3.95517	2.37732	1.10378	21.87982	6.19971	17.17556

		Ligule size (mm)	Auricle size (mm)	Palea length (mm)	Sterile lemma (mm)	Grain length (mm)	Grain breadth (mm)	Kernel length (mm)	Kernel breadth (mm)	100 seed wt. (g)
N	Valid	25	25	25	25	25	25	25	25	25
	Missing	0	0	0	0	0	0	0	0	0
Mean		23.2000	13.3200	7.6600	2.3960	8.2480	2.3364	7.1160	1.8120	14.4280
SEm		0.94074	0.29563	0.12490	0.08072	0.12585	0.04907	0.09340	0.01589	0.10042
SD		4.70372	1.47817	0.62450	0.40361	0.62923	0.24537	0.46698	0.07943	0.50210

species (Sharma *et* Shastry, 1965; Banaticla-Hilario *et al*., 2013) but others considered *O. nivara* to be the annual ecotype or subspecies of *O. rufipogon* (with *O. rufipogon sensu stricto* as the perennial ecotype) due to their continuous variation (morphological and genetic) including interfertility. Presence of stolons and long, strong, and spreading culms make *O. rufipogon* suitable for permanently inundated habitats. Stigma and anther are longer and panicles are more exerted and open in this outcrossing *O. rufipogon* than in inbreeding *O. nivara* (Table 2). *O. rufipogon* is photoperiod sensitive (Banaticla-Hilario *et al*., 2013). Gene flow between populations of *Oryza rufipogon* (*sensu lato*) and *Oryza sativa* is highly probable due to their overlapping distribution in the same area (Oka, 1998; Vaughan *et al*., 2008). However, hybrid populations between *O. nivara* and *O. rufipogon* are rarely reported as they are hardly found growing side by side in the same area. There are some intermediate populations (morphologically and genetically) of the two wild species in some part of Thailand and Vietnam but not considered as a hybrid of *O. nivara* and *O. rufipogon*, instead they may be hybrid of *O. sativa* with *O. nivara* or *O. rufipogon* (Banaticla-Hilario *et al*., 2013). The wild rice taxon of NBU campus has been identified as *Oryza rufipogon* based on morpho-ecological parameters although it is not matching all the characteristics of its previous reports (Table 2). Deviation from the previously reported morphological features may be due to its adaptation in different environmental factors. Before the establishment of the University (1962), the lands were used for rice cultivation due to lowland habitat, ditches, and ponds around the small flowing River Magurmari. During that period (1962s) there may be some kind of gene flow between *O. sativa* and *O. rufipogon*, and thus the wild taxon of this NBU campus showing deviated morphological features from *O. rufipogon* and may be considered as intermediate form (intergrade) (Table 2). Morphological differentiation and variation within and among population has been studied to diagnosing species boundary (Elizabeth *et al*., 2008). Genetic diversity assessment within the species has been basis to utilize and manage germplasm resources (Wright and Gaut, 2005) and particularly crucial to its conservation. Many rice scientists have studied the genetic structure within and among the *O. rufipogon* based on morphology, ecology and DNA markers (Sun *et al*., 2001; Dong *et al*., 2010).

Conclusion

The present ecogeographical and morphological characteristics showed that high level of genetic diversity in the populations of *O. rufipogon* in NBU campus. Thus, wild rice population of NBU campus is considered as separate ecological race (ecotype) and may carry some important genes/alleles and hence considered as precious germplasm for crop genetic improvement. Ecological

Table 2. Comparison of NBU wild rice with reference data of other wild rice species

Morphological traits	*Oryza rufipogon*	*Oryza nivara*	Wild rice NBU
Plant height (cm)	136 – or >170	50-150 or <170	64 – 145
Flag leaf length (cm)	7 – 20	30 – 49	13 – 40
Flag leaf width (cm)	0.4 - 0.95	1.1 - 1.8	0.3 - 1.8
Panicle length (cm)	19.8-37.6	14-16	15.4-30
Attitude of panicle branches	Spreading	Compact/spreading	Compact/spreading
Panicle exsertion	Well exserted	Well exserted	Well exserted
Uppermost internode length (cm)	1.6 – 2.6	0.9 – 1.8	3.4 – 26
Attitude flag leaf blade	Horizontal	Semierect	Deflexed/Horizontal/ Semierect
Ligule (mm)	18 – 30	21 – 44	17 – 35 two-cleft
Awn length (mm)	40 – 67	50 – 88	23 – 80
Anther length (mm)	> 3.7	< 3.7	4 – 8
Pollination	Cross pollination	Self pollination	Cross pollination
Stigma length (mm)	1.8 – 2.8	1.4 – 1.8	>2
Sterile lemma (mm)	0.5 – 0.76	0.83 – 1.2	2 – 3
Grain length (mm)	7 – 10	6 – 10.4	7.5 – 10
Grain breadth (mm)	1.8 – 2.3	2.8 – 3.4	2 – 2.75
Kernel length (mm)	5 – 7	5.5 -8.5	7.5 – 8
Kernel breadth (mm)	2.2 – 2.7	0.65 – 0.92	1.7 – 2
Life cycle	Perennial/annual	Annual	Annual

diversity of the wild rice species should be protected and maintained. The population should be conserved *in situ* conditions to understand the morphological diversity within the populations and make convenient habitat for evolution. In addition, competitive associated plant species in protected areas should be controlled and the level of intra- and inter-population gene flow in protected populations should be monitored. This type of well-defined eco-phenotypes based species delineation will help gene bank people in dealing with misidentified accessions and in maintaining intermediate forms. Population of *Oryza rufipogon* of NBU campus should be maintained at *in situ* condition to conserve this valuable wild rice germplasm as important genetic resources.

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Combining Ability Analysis for Yield and its Related Traits in Pearl Millet

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A 10×10 half diallel excluding reciprocals was evaluated in 3 environments to study the combing ability and gene action involved in respect of yield and its attributers in pearl millet. The environment wise combining ability analysis revealed significant differences for GCA (general combining ability) and SCA (specific combining ability) variances for characters *viz.* days to 50% flowering, days to maturity, productive tillers/plant, plant height, panicle length, panicle girth, biological yield/plant, dry fodder yield/plant, grain yield/plant, harvest index, test weight and protein content in all the three environments, except GCA for productive tillers per plant in E_2 and panicle girth in E_3 and SCA for panicle girth in E_3, indicating the importance of both additive and non-additive gene effects for the genetic control of all the characters studied. The estimates of GCA effects indicated that the parents 71-75 and 76-80 emerged as good general combiners for grain yield and its components in the entire environment. Out of 45 crosses combinations only seven combinations such as 26-30 x 71-75, 26-30×RIB-135-144, 31-40×76-80, 31-40×RIB-135-144, 31-40×101-105, 41-50×RIB-20 and RIB-20×71-75 showed significant and positive SCA effects in all the three environment for grain yield and other yield attributing characters. These parents and crosses have immense potential for pearl millet improvement and may be utilized in multiple crossing programme.

Key Words: Combining ability, Environments, GCA, Gene action, SCA

Introduction

Pearl millet (*Pennisetum glaucum* L.) is the world's sixth important and widely grown potential cereal crop. In India pearl millet is the fourth most important food grain after rice, wheat and sorghum. Pearl millet is highly cross pollinated crop with the advantages of huge genetic variability, protogyny and availability of efficient cytoplasmic genetic male sterility system. These characteristics, offer great possibilities of crop improvement through hybridization. Selection of suitable parent is an important step in a crop improvement programme.

Materials and Methods

Ten inbred lines *viz*. 26-30, 31-40, 41-50, RIB-20, 61-70, 71-75, 75-80, 51-60, RIB-135-144 and 101-105 were crossed in a diallel fashion excluding reciprocals during *kharif* season 2011. These 10 parents and their $45F_1$'s were evaluated in randomized block design with three replications under three environments at Agronomy Research Farm, Jobner (Jaipur) during *kharif* season, 2012. Environment created by dates of sowing viz. 2 July, 2012 {first date of sowing (E_1)}, 14 July, 2012 {second date of sowing (E_2) and 28 July, 2012 {third date of sowing (E_3)}. Each entry was sown in a two row of 3.0 m length with row-to-row and plant-to-plant distances of 50 cm and 15 cm, respectively. The observation were recorded on five randomly selected plants from each replication and environment, for the characters namely; days to 50% flowering, days to maturity, productive tillers/plant, plant height, panicle length, panicle girth, biological yield/plant, dry fodder yield/plant, grain yield /plant, harvest index, test weight and protein content while, days to 50% flowering and days to maturity were recorded on plot basis. The combining ability analysis was done according to Griffing (1956) Method-2, Model-1 using SAS 2005 package from Zhang *et al.* (2005).

Results and Discussion

The general combining ability (GCA) and specific combining ability (SCA) variances were highly significant for days to 50% flowering, days to maturity, productive tillers/plant, plant height, panicle length, panicle girth, biological yield/plant, dry fodder yield/plant, grain yield/plant, harvest index, test weight and protein content in all the three environments, except GCA for productive tillers per plant in E_2 and panicle girth in E_3 and SCA for panicle girth in E_3, indicating the importance of both additive and non-additive gene effects for the genetic control of all the characters studied. However, GCA: SCA variance ratio being less than the unity showed that the non-additive gene action was more important for all the characters in three environments (Table 1).

These findings were supported by Vagadiya *et al*. (2010), Jethva *et al*. (2011), Yadav *et al*. (2012) and Parmar *et al*. (2013).

Nature and magnitude of combining ability effects provide an idea about the relative role of fixable and non- fixable gene effects in the inheritance of different characters. Thus, it helps in identifying suitable parents for crossing programme. In the present study, out of 10 parents only two parents such as 71-75 and 76-80 showed significant and positive general combining ability (GCA) effects in all the three environments for grain yield and other yield attributing characters. While parent 31-40 was found to be uniformly undesirable parent across the environment with high negative effects (Tables 2 and 3). These parents may be used in a multiple crossing programme to synthesize a dynamic population with most of the favourable genes accumulated (Griffing, 1956). In pearl millet, parents having good GCA have been reported by Shanmuganathan and Gopalan (2006), Rohitashwa *et al*. (2006), Dangaria *et al*. (2009) and Chaudhary *et al*. (2012).

There was no consistency over environment for the ranks of crosses with high SCA effects. Furthermore, a number of crosses exhibited changes in the magnitude and direction of SCA effects in different environments, which might be consequence of high SCA x environment interaction. Out of 45 crosses combinations only seven combinations such as 26-30×1-75, 26-30×RIB-135-144, 31-40×76-80, 31-40×RIB-135-144, 31-40×101-105, 41-50×RIB-20 and RIB-20×71-75 showed significant and positive specific combining ability (SCA) effects in all the three environment for grain yield and other yield attributing characters (Tables 2 and 3) These crosses have immense potential for pearl millet improvement, they may be utilized in multiple crossing programme and crosses 76-80×51-60, 31-40×101-105 and 41-50×RIB-135-144 in E_1, 26-30×41-50, 61-70×71-75 and RIB-20×71-75 in E_2 and 31-40×101-105, 41-50×RIB-20 and 31-40×76-80 in E_3 were identified on the basis of high SCA effects for specific environment for grain yield per plant and related traits (Table 4). These finding were corroborative with the results obtained by Rasal and Patil (2003), Bhanderi *et al*. (2007) and Chotaliya *et al*. (2010). These crosses offer good promise for improvement of respective component trait and ultimately grain yield in respective environment.

Conclusion

This study concludes that the SCA variance was greater than the GCA variance for most of the traits among the pearl millet population, indicating non-additive genetic effects as the most important in control of the studied traits. Since non-additive gene action was more important for grain yield, simple recurrent selection that emphasises selection for SCA could be employed in the breeding

Table 1. Analysis of variance for combining ability in individual environment in pearl millet

Source of variance	d.f.	Env.	Mean sum of square											
			Days to 50% flowering	Days to maturity	Productive tillers/ plant	Plant height (cm)	Panical length (cm)	Panical girth (cm)	Biological yield/ plant (g)	Dry fodder yield/ plant (g)	Grain yield/ plant (g)	Harvest index (%)	Test weight (g)	Protein content (%)
GCA		E_1	33.858**	42.823**	0.432**	258.517**	5.555**	0.893**	2391.863**	972.834**	14.434**	9.201**	2.515**	1.304**
		E_2	5.700**	15.555**	0.085**	524.367**	5.452**	2.447**	345.647**	452.764**	5.475**	2.022*	3.294**	0.771**
	9	E_3	14.106**	7.931**	0.005	676.653**	8.457*	0.535	132.082**	75.494*	3.1627**	102.617*	2.907**	1.042**
SCA		E_1	27.159**	31.279**	0.523**	1029.576**	17.496**	1.622**	4563.391**	3915.447**	15.864**	14.468**	1.643**	2.406**
		E_2	10.557**	19.218**	0.072**	413.973**	9.738**	1.928**	763.663**	762.552**	7.291**	5.979**	2.173**	2.152**
	45	E_3	9.695**	14.900**	0.010*	392.611**	9.367**	0.568	65.694*	46.862*	6.495**	926.338**	1.582**	2.200**
Error		E_1	0.565	1.128	0.017	1.388	0.488	0.028	525.240	155.629	0.632	0.979	0.353	0.091
		E_2	0.614	1.248	0.015	3.259	0.190	0.008	40.770	7.606	0.381	0.689	0.007	0.055
	105	E_3	0.438	2.139	0.006	3.888	2.557	0.107	34.339	24.620	0.703	445.227	0.004	0.024
GCA/SCA		E_1	0.104	0.115	0.068	0.020	0.024	0.045	0.038	0.018	0.075	0.050	0.139	0.043
		E_2	0.042	0.066	0.102	0.105	0.045	0.105	0.035	0.049	0.061	0.021	0.126	0.028
		E_3	0.123	0.037	-0.039	0.144	0.072	0.077	0.259	0.190	0.035	0.036	0.153	0.038

*and**significant at 5% and 1% level of significance, respectively

Table 2 Estimate of GCA and SCA effects of some promising parents and crosses for grain yield/plant in all the three environment

Parents/Crosses	Days to 50% flowering			Days to maturity			Productive tillers/plant			Plant height (cm)			Panicle length (cm)			Panicle girth (cm)		
	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
71-75	0.083	0.011	0.922**	-0.556	-0.933**	0.633	0.039	0.110**	-0.010	-1.895**	-4.248**	-3.206**	0.006	-0.218	-1.633**	0.366**	0.182**	0.398**
76-80	-0.306	0.344	-0.828**	-1.056**	0.928**	-0.506	-0.094*	0.038	0.029	4.561**	16.277**	16.522**	-0.184	0.853**	1.091*	0.216**	0.011	-0.008
SEgi	0.215	0.224	0.189	0.304	0.320	0.418	0.038	0.036	0.023	0.337	0.516	0.564	0.200	0.125	0.457	0.048	0.026	0.094
26-30 X 71-75	-6.306**	-5.311**	-0.636	-7.601**	-5.467**	-4.578**	-1.103**	-0.243*	-0.079	-22.934**	-21.017**	3.306	-2.459**	-4.443**	-2.460	-1.255**	0.537**	0.400
26-30 X RIB-135-144	1.111	-1.311	1.558*	2.593**	-3.384**	1.811	-0.247*	0.223	0.038	59.938**	17.297**	2.334	-2.752**	0.691	3.613*	0.091	-0.270**	-0.032
31-40 X 76-80	4.222**	0.967	-1.081	4.538**	-0.384	-2.217	0.447**	-0.038	-0.068	-12.829**	31.936**	-8.449**	-1.250	-2.927**	-1.391	1.551**	1.164**	0.321
31-40 X RIB-135-144	-6.417**	1.634*	-2.636**	-8.101**	0.894	-2.634	-0.297*	-0.043	0.021	-4.768**	2.608	6.039**	1.794**	0.703	1.002	-0.986**	-0.557**	0.243
31-40 X 101-105	-2.944**	-3.449**	-2.497**	-1.351	-3.134**	-4.912**	0.825**	-0.016	0.049	5.749**	3.014	19.706**	1.061	-0.205	0.794	1.051**	0.023	-0.767*
41-50 X RIB-20	4.028**	-0.422	0.086	0.955	3.477**	2.394	-0.897**	-0.160	-0.040	9.330**	0.306	10.517**	-3.262**	3.917**	1.552	-0.159	-1.825**	0.526
RIB-20 X 71-75	-4.083**	0.939	1.503*	-3.851**	-1.995	-0.162	-0.319*	-0.182	-0.029	27.293**	22.347**	2.517	6.496**	-0.754	-3.933**	2.238**	2.218**	-0.450
SEsij	0.693	0.722	0.610	0.978	1.029	1.347	0.123	0.115	0.075	1.085	1.663	1.817	0.644	0.402	1.473	0.155	0.083	0.302

*=Significant at 5%level of significance, **=Significant at 1%level of significance

Table 3 Estimate of GCA and SCA effects of some promising parents and crosses for grain yield/plant in all the three environment

Parents/Crosses	Biological yield/plant (g)			Dry fodder yield/plant (g)			Grain yield/plant (g)			Harvest index (%)			Test weight (g)			Protein content (%)		
	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
71-75	7.508	6.017**	-1.642	0.384	6.091**	-1.551	1.852**	1.259**	0.777**	1.136**	0.548*	2.041**	-0.301	-0.284**	-0.343**	0.040	-0.034	-0.124**
76-80	11.241	5.784**	6.677**	4.798	4.420**	3.871**	1.337**	0.856**	1.019**	0.641*	-0.087	-0.298	-0.430*	-0.312**	-0.477**	-0.321**	-0.244**	-0.219**
SEgi	6.555	1.826	1.676	3.568	0.789	1.419	0.227	0.177	0.240	0.283	0.238	0.581	0.170	0.024	0.020	0.086	0.068	0.044
26-30 X 71-75	-84.992**	-15.222*	0.247	-39.419**	-21.954**	0.227	2.499**	2.318**	2.164**	10.706**	3.325**	2.975	0.230	-0.150	0.260**	1.334**	1.189**	0.958**
26-30 X RIB-135-144	68.414**	40.114**	-3.467	65.841**	36.711**	-8.648	3.545**	3.628**	3.929**	-1.600	-0.269	9.004**	1.332*	2.756**	1.961**	0.394	1.024**	0.629**
31-40 X 76-80	-33.883	30.300**	1.089	-37.764**	34.529**	-1.711	4.970**	2.427**	3.992**	5.472**	-1.110	6.878**	0.866	0.674**	0.364**	2.443**	1.501**	2.293**
31-40 X RIB-135-144	-30.484	20.236**	2.628	-42.629**	6.857**	-0.630	3.015**	1.840**	3.725**	4.144**	-0.839	6.924**	-0.054	0.660**	0.213**	-0.678*	-1.269**	-0.895**
31-40 X 101-105	38.340	14.134*	-1.384	29.740*	0.935	-4.458	6.504**	3.968**	4.765**	0.729	1.564*	9.952**	0.005	-0.097	0.121	-0.088	0.302	0.450**
41-50 X RIB-20	3.661	22.677**	6.125	-53.739**	13.202**	1.070	2.551**	2.939**	4.539**	1.075	0.227	5.865**	-1.141**	-1.744**	-1.841**	-0.813**	-0.559*	-0.470**
RIB-20 X 71-75	51.251*	18.069**	-0.986	57.052**	8.780**	-1.261	5.639**	4.120**	2.343**	-0.990	1.301	5.804**	-0.129	-0.212**	-0.060	-2.962**	-2.786**	-3.415**
SEsij	21.111	5.882	5.398	11.491	2.540	4.571	0.732	0.569	0.773	0.912	0.765	1.870	0.548	0.077	0.065	0.278	0.217	0.142

*=Significant at 5%level of significance, **=Significant at 1%level of significance

Table 4. Top three parents and crosses for grain yield/plant on the basis of high GCA and SCA effects

Characters	Environments	GCA	SCA
Grain yield/plant	E_1	71-75, 76-80 and 41-50	76-80×51-60, 31-40×101-105 and 41-50×RIB-135-144
	E_2	71-75, 76-80 and 61-70	26-30×41-50, 61-70×71-75 and RIB-20×71-75
	E_3	76-80 and 71-75	31-40×101-105, 41-50×RIB-20 and 31-40×76-80

programme. The study also concludes that an astounding level of variability existed in the population because of the enormous level of high SCA among the hybrids, indicating the possibility of getting better combinations from segregating generations of these crosses.

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Indian Collections of Turmeric (*Curcuma longa* L.): Genetic Variability, Inheritance, Character Association and Performance

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Twenty seven genotypes of turmeric (*Curcuma longa* L.) were evaluated to estimate the variability and inheritance pattern, to suggest suitable breeding strategies and to identify productive genotypes. Highly significant mean squares for all the traits indicated large variation among genotypes. High genetic gain through selection is expected for shoot length, leaf area, rhizome yield and dry matter yield because of additive gene inheritance; while curcumin accumulation in rhizome could be improved by selecting the heterotic seedlings as it is governed by non-additive gene. Furthermore, leaf length and curcumin content could be the most effective and reliable selection indices, as indicated by correlation and path coefficients, in identifying the curcumin-rich productive genotypes. A variety of North East India 'Megha Turmeric-1' excelled for the traits of commercial importance (dry matter recovery and curcumin yield). Conclusively, the genotypes of North East India were superior to other parts of India for most of the economic traits and potentially useful for genetic enhancement as well as for varietal improvement of turmeric.

Key Words: Curcumin, Heritability, North East India (NEI), Turmeric (*Curcuma longa*), Variability, Yield

Introduction

Turmeric (*Curcuma longa* L.) is one of the most widely cultivated spice crops in North-eastern region of India because of agro-climatic suitability, rich genetic diversity and high curcumin content. India is the largest producer, consumer and exporter of turmeric accounting for about 80%, 90% and 60% share, respectively of the world's total (Anonymous, 2012). In India, turmeric is extensively cultivated in the states having high rainfall such as Andhra Pradesh, Tamil Nadu, Odisha, Karnataka, West Bengal, Gujarat, Maharashtra, Assam and Meghalaya. The distinctive yellow-orange curcuminoids (curcumin, demethoxycurcumin and bisdemethoxycurcumin) are important bioactive compounds that occur in the rhizomes. Among curcuminoids, curcumin is a major colour pigment whose concentration varies from 4.0–9.0% amongst genotypes. Turmeric possesses anti-inflammatory, hepatoprotective, antitumor, antiviral and anticancerous properties, and is also beneficial in treating gastrointestinal and respiratory disorders (Ammon and Wahl, 1991; Polasa *et al*., 1991; Anwarul *et al*., 2006). Recent data also suggest that curcumin and other antioxidant products from the dried rhizome may be useful in the treatment of some age-related degenerative processes (Miquel *et al*., 2002).

Indian states of the North East India (NEI) especially Mizoram, Meghalaya and Assam are endowed with a wide range of genetic variability in *C. longa* and other *Curcuma* species and with geo-climatic conditions of the region favouring higher accumulation of curcumin in rhizomes (Singh *et al*., 2013a; 2013c). The curcumin content is one of the major criteria for its export to the global markets. Alleppey turmeric, world's most outstanding and demanded grade, is the richest source of curcumin and it is extensively cultivated in Kerala. Turmeric is a cross-pollinated triploid species (2n = 3x = 63), very shy in flowering requiring, needs specific climatic conditions for flowering and has pollen fertility less than 60% (Nambiar, 1979; Nair *et al*., 2004). The aforementioned factors make its hybridization tedious and almost ineffective in most of the cases. Being propagated commercially by rhizomes and with flowering complexities, the genetic improvement programmes in turmeric are largely restricted to clonal selection and induced mutation. Moreover, limited viable seed setting in open-pollination and controlled crosses explore the possibility of recombination breeding through hybridization, and hence few varieties such as IISR Prabha and IISR Pratibha have been released through progeny selection of open-pollinated seedlings (Sasikumar *et al*., 1996).

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Considerable genetic variation for various traits of economic importance has been reported, especially among Indian collections excluding NEI (Babu *et al*., 1993; Sasikumar 2005). Those from this region have one of the best agro-climatic conditions for production of curcumin-rich turmeric, the potential for genetic improvement and production is still to be exploited. Therefore, the aim of the present study was to estimate the variance components, heritability, expected genetic advance and character association of important traits related to vegetative growth, rhizome yield and curcumin content, and its agronomic performance for various economic traits between and within Indian turmeric genotypes/ collections from a wide range of latitudes and longitudes. The findings pertaining to genetic variation and inheritance pattern would be helpful to the plant breeders in selecting the breeding approaches (clonal selection and/or hybridization), genotypes and traits more appropriately and efficiently.

Materials and Methods

Field experiments were conducted at the Research Farm, ICAR-RC-NEH Region, Mizoram Centre, Kolasib, Mizoram during 2008–2009. The experimental material comprised 27 genetically diverse genotypes, including 11 released varieties and 16 germplasm collections (Table 1). These 27 genotypes were categorised into two groups i.e. (i) NEI collections: belonged to North East India and (ii) other parts of India (OPI) collections: belonged to other than North-eastern region of India. The growth parameters like shoot length, leaf length, leaf width, leaf area, shoot thickness near base and numbers of tillers/ plant were measured 120 days after planting. The observations pertaining to growth parameters were recorded on 15 randomly chosen plants in each plot. For measuring the leaf length, leaf width and leaf area, third leaf from top was selected. Days to maturity were counted at 50% neck-fall stage. Rhizome yield (q/ha) and dry matter content (%) were determined as per

Table 1. Details of basic experimental materials

S.No.	Genotype	Developing organization/ region of collection
	Released variety	
1	Megha Turmeric-1	ICAR-RC-NEH Region, Shillong, Meghalaya
2	Suranjana	UBKV, Pundibari, Cooch Behar, West Bengal
3	Narendra Haldi-1	NDUAT, Kumarganj, Faizabad, Uttar Pradesh
4	IISR Alleppy Supreme	IISR, Kozhikode, Calicut, Kerala
5	IISR Kedaram	
6	IISR Pratibha	
7	Duggirala Red	Dr YSRHU, Jagtial, Andhra Pradesh
8	BSR-2	TNAU, Coimbatore, Tamil Nadu
9	Rajendra Sonia	TCA, RAU, Dholi, Bihar
10	Rasmi	HARS, OUAT, Pottangi, Odisha
11	Roma	
	Germplasm	
12	Local-4	Barapani, Shillong, Meghalaya
13	Local-5	
14	Local-7	Silchar, Assam
15	Local-9	Dulte, Champhai, Mizoram
16	Local-10	Phaileng, Mamit, Mizoram
17	Local-11	Rotlang, Lunglei, Mizoram
18	IC0588788	Vengthar, Kolasib, Mizoram
19	IC0588789	
20	IC0588790	Kawnpuii, Kolasib, Mizoram
21	IC0588791	
22	IC0588792	Theiva, Saiha, Mizoram
23	IC0588793	
24	IC0588794	
25	IC0588795	
26	IC0588796	Siphir, Aizawl, Mizoram
27	IC0588797	

standard procedure (Bavappa, 1985). Curcumin content in turmeric powder was estimated by following the American Spice Trade Association method (ASTA, 1997). Finally, dry matter yield (q/ha) and curcumin yield (kg/ha) were calculated. The data were analysed statistically for analysis of variance (Singh and Chaudhary, 1977); variability, heritability and genetic advance (Burton and DeVane, 1953); correlation (Searle, 1961); and path coefficient (Dewey and Lu, 1959).

Results and Discussion

Highly significant mean squares for all the morphological and quality traits in 27 genotypes of turmeric (*Curcuma longa* L.) are presented in Table 2. It is clear from the data that there is natural variation among genotypes which can be improved by various breeding strategies. The extent of variability (Table 2) among genotypes was estimated in terms of range, coefficient of variation (CV), genotypic and phenotypic variance (σ^2g and σ^2p), and genotypic and phenotypic coefficient of variation (GCV and PCV). There was sufficient variation with respect to plant growth, maturity, yield and curcumin content. The magnitude of PCV was higher than the corresponding GCV for all the parameters which reflects the influence of environment on the expression of these traits. The respective PCV and GCV were higher for shoot length, leaf length, shoot thickness, leaf area, rhizome yield, dry matter yield and curcumin yield; whereas these were lower for leaf width, numbers of tillers/plant, days to maturity, dry matter content and curcumin content. The traits with high GCV possess a higher magnitude of variability and thus, present a better possibility of improvement through breeding approaches. Significant variations for various parameters were also reported by various workers (Babu *et al*., 1993; Manohar et al., 2004; Sasikumar, 2005; Pothitirat and Gritsanapan, 2006; Jan *et al*., 2011; 2012; Singh *et al*., 2013b,d; Rajyalakshmi *et al*., 2013).

Heritable variation among genotypes could be anticipated by calculating the estimates of heritability and genetic advance as percentage of mean. The magnitude of heritability (Table 3) varied from 62.7–92.9% (moderate to high). High heritability (> 80%) was estimated for

Table 2. Mean squares for morphological and quality traits in turmeric genotypes

Source of variation	d.f.	Mean square											
		Shoot length	Leaf length	Leaf width	Shoot thickness	Leaf area	No. of tillers/ plant	Days to maturity	Rhizome yield	Dry matter content	Dry matter yield	Curcumin content	Curcumin yield
Replication	2	26.8	4.67	0.24	3.08	788	0.012	19.3	1382	3.93	50.0	0.010	2231
Genotype	26	1071.2**	218.68**	8.09**	37.88**	130043**	1.858**	464.9**	14017**	40.61**	741.9**	1.091**	43452**
Error	52	26.7	7.85	1.34	2.32	4456	0.266	46.8	912	2.18	56.6	0.049	2241

*,** Significant at $P < 0.05$ and $P < 0.01$, respectively.

Table 3. Estimates of variance, heritability and genetic advance for economic and quality traits in genotypes of turmeric

Parameter	Range	CV (%)	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2 (%)	GA	GA as %age of mean
Shoot length (cm)	53.6-135.2	6.06	348.1	374.9	21.9	22.7	92.9	37.0	43.4
Leaf length (cm)	28.1-68.2	6.65	70.3	78.1	19.9	21.0	90.0	16.4	38.9
Leaf width (cm)	8.9-17.5	9.05	2.3	3.6	11.7	14.8	62.7	2.4	19.1
Shoot thickness (mm)	10.3-26.2	9.15	11.9	14.2	20.7	22.6	83.6	6.5	39.0
Leaf area (cm^2/leaf)	190-1146	13.20	41863	46318	40.5	42.6	90.4	400.7	79.2
No. of tillers/plant	2.4-6.8	11.87	0.5	0.8	16.8	20.5	66.6	1.2	28.2
Days to maturity	180-228	3.30	139.4	186.2	5.7	6.6	74.8	21.0	10.1
Rhizome yield (q/ha)	158-500	9.94	4368.3	5280.1	21.8	23.9	82.7	123.8	40.8
Dry matter content (%)	10.0-27.5	7.01	12.8	15.0	17.0	18.4	85.5	6.8	32.4
Dry matter yield (q/ha)	26.0-93.7	11.85	228.4	285.0	23.8	26.6	80.1	27.9	43.9
Curcumin content (%)	5.01-7.51	3.60	0.3	0.4	9.6	10.3	87.7	1.1	18.6
Curcumin yield (kg/ha)	151.0-646.2	12.04	13737.2	15977.9	29.8	32.2	86.0	223.9	57.0

CV: Coefficient of variation (%) σ^2g: Genotypic variance σ^2p: Phenotypic variance
GCV: Genotypic coefficient of variation PCV: Phenotypic coefficient of variation h^2: Heritability GA: Genetic advance

shoot length (92.9%), leaf length (90.0%), shoot thickness (83.6%), leaf area (90.4%), rhizome yield (82.7%), dry matter content (85.5%), dry matter yield (80.1%), curcumin content (87.7%) and curcumin yield (86.0%). A high heritability for a trait indicates that a large portion of phenotypic variance is contributed through genotypic variance and therefore, a reliable selection could be made for these traits. However, moderate heritability (50–80%) indicates considerable influence of environment on the expression of leaf width, numbers of tillers/plant and days to maturity. High heritability for plant height and leaf width as well as moderate to low heritability for yield have been reported by Babu *et al*. (1993).

The efficacy of genetic gain and gene action responsible for a particular trait could be revealed by the estimates of genetic advance. Heritability values along with genetic advance as percentage of mean are better tools in predicting gain under selection than either of them alone. Genetic advance as percentage of mean ranged from 10.1–79.2% (Table 3). Its magnitude was high (> 40%) for shoot length, leaf area, rhizome yield, dry matter yield and curcumin yield; moderate (30 – 40%) for leaf length, shoot thickness and dry matter content; and low (< 30%) for leaf width, number of tillers/plant, days to maturity and curcumin content. In the present study, a high heritability accompanied with high genetic advance for shoot length, leaf area, rhizome yield, dry matter yield and curcumin yield clearly suggest the role of additive gene action, and hence a high genetic gain is expected from selection for these traits; while non-additive gene action was responsible for curcumin as revealed by low genetic advance along with high heritability which could be enhanced by heterosis breeding. Heritability and genetic advance were observed to be high for rhizome yield and number of tillers/plant (Rajyalakshmi *et al*., 2013). According to Manohar *et al*. (2004) there was moderate to high heritability and genetic advance for cured yield, fresh weight of the mother rhizome and number of secondary finger rhizomes. High heritability coupled with moderate genetic advance for leaf length, shoot thickness and dry matter content indicate the involvement of both additive and non-additive gene action.

Correlation coefficient measures the degree and direction of relationship between various characters, and determines the component characters on which selection can be made efficiently. The coefficient of genotypic correlation was higher in magnitude than its related phenotypic correlation (Table 4) which indicates that the apparent association of two traits is not only because of genetic architecture but also due to influence of environmental interactions. The meager the difference, the lesser is the environmental impact. The significant positive correlation of shoot length, leaf length and shoot thickness along with rhizome yield, dry matter content and curcumin content (0.689, 0.710 and 0.676; 0.550, 0.562 and 0.432; and 0.557, 0.555 and 0.427, respectively) indicates that plant vigour influences the yield, recovery (dry matter) and quality (curcumin content) of turmeric very significantly. However, days to maturity had positive association with dry matter content which indicated that selection for short duration cultivars would adversely affect the dry matter recovery of turmeric. Rhizome yield and curcumin content had a strong positive correlation; meaning improving either of these traits will take care of the other simultaneously.

Correlation coefficients indicate only the general association between any two traits without tracing any possible cause of such association. Hence, the path coefficient analysis at genotypic level (Table 5) was done to partition the correlation coefficient into direct and indirect effects by taking rhizome yield as a dependent variable. Here, only directly measured traits (leaving deduced parameters such as dry matter yield and curcumin yield) were taken into consideration to avoid masking effects by deduced parameters. Most of the traits, except days to 50% maturity and dry matter content, were influenced by positive indirect effects of leaf length. However, positive direct effects on rhizome yield were high for leaf length (2.070) and curcumin content (0.617) which is higher or fairly close to its significant correlation coefficients indicating that a direct selection based on leaf length and curcumin content would be the most effective and reliable tool to identify productive and curcumin-rich genotypes of turmeric.

With respect to range and mean performance of 27 genotypes (also categorized into two groups as per their source of collection i.e. NEI collection and OPI collection), there was a variation within and between category(ies) for various traits in general (Table 6). The NEI collections were significantly superior to OPI collections with respect to shoot length, leaf length, shoot thickness, leaf area, rhizome yield, dry matter yield, curcumin content and curcumin yield with their respective values being 40.4%, 33.0%, 91.8%, 23.3%, 33.3%, 34.0%, 13.5% and 52.4% (Table 6). This is attributable

Table 4. Correlation coefficients for economic and quality traits in genotypes of turmeric

Economic traits		Shoot length	Leaf length	Leaf width	Shoot thickness	Leaf area	No. of tillers/ plant	Days to maturity	Rhizome yield	Dry matter content	Dry matter yield	Curcumin content	Curcumin yield
Shoot length	g	–	0.991**	0.758**	0.563**	0.969**	0.191	–0.388*	0.689**	–0.043	0.550**	0.557**	0.600**
	p	–	0.954**	0.600**	0.550**	0.911**	0.206	–0.322	0.606**	–0.024	0.497**	0.499**	0.552**
Leaf length	g		–	0.813**	0.677**	0.980**	0.252	–0.369	0.710**	–0.037	0.562**	0.555**	0.610**
	p		–	0.718**	0.620**	0.962**	0.268	–0.321	0.609**	–0.010	0.502**	0.525**	0.567**
Leaf width	g			–	0.904**	0.828**	0.256	–0.176	0.618**	0.056	0.525**	0.328	0.512**
	p			–	0.683**	0.794**	0.254	–0.139	0.460*	0.080	0.419*	0.258	0.419*
Shoot thickness	g				–	0.750**	0.229	–0.334	0.676**	–0.156	0.432*	0.427*	0.473*
	p				–	0.671**	0.200	–0.253	0.585**	–0.105	0.409*	0.347	0.442*
Leaf area	g					–	0.157	–0.467*	0.716**	–0.091	0.520**	0.534**	0.571**
	p					–	0.173	–0.403*	0.609**	–0.053	0.464*	0.499**	0.529**
No. of tillers/ plant	g						–	0.536**	0.487*	0.253	0.562**	0.360	0.552**
	p						–	0.374	0.383*	0.166	0.430*	0.276	0.437*
Days to maturity	g							–	–0.122	0.657**	0.348	–0.240	0.192
	p							–	–0.115	0.545**	0.266	–0.158	0.161
Rhizome yield	g								–	–0.158	0.753**	0.757**	0.839**
	p								–	–0.160	0.754**	0.615**	0.813**
Dry matter content	g									–	0.524**	–0.134	0.347
	p									–	0.511**	–0.115	0.359
Dry matter yield	g										–	0.557**	0.952**
	p										–	0.457*	0.948**
Curcumin content	g											–	0.781**
	p											–	0.710**
Curcumin yield	g												–
	p												–

*,** Significant at $P < 0.05$ and $P < 0.01$, respectively; g: genotypic level; p: phenotypic level

Table 5. Genotypic path coefficients for various traits of turmeric showing the direct and indirect effects on fresh rhizome yield

Parameter	Shoot length	Leaf length	Leaf width	Shoot thickness	No. of tillers/ plant	Days to maturity	Dry matter content	Curcumin content	'r' value with rhizome yield
Shoot length	**-1.660**	2.051	0.282	-0.160	-0.019	-0.165	0.017	0.344	0.689**
Leaf length	-1.644	**2.070**	0.302	-0.193	-0.025	-0.156	0.014	0.343	0.710**
Leaf width	-1.258	1.681	**0.372**	-0.257	-0.026	-0.074	-0.023	0.203	0.618**
Shoot thickness	-0.933	1.399	0.336	**-0.285**	-0.023	-0.141	0.060	0.263	0.676**
No. of tillers/plant	-0.317	0.523	0.096	-0.066	**-0.100**	0.228	-0.099	0.222	0.487*
Days to maturity	0.643	-0.762	-0.065	0.095	-0.054	**0.425**	-0.256	-0.148	-0.122
Dry matter content	0.071	-0.075	0.022	0.044	-0.026	0.280	**-0.389**	-0.083	-0.157
Curcumin content	-0.924	1.149	0.122	-0.122	-0.036	-0.102	0.052	**0.617**	0.757**

Residual effect = 0.457; The Bold values indicate direct effect, while others indicate indirect effect.
*,** Significant at $P < 0.05$ and $P < 0.01$, respectively.

to the NEI having favourable climatic conditions (mild temperature and high rainfall) for turmeric cultivation. However, with respect to leaf width, numbers of tillers/ plant, days to maturity and dry matter content there was no significant difference between the two groups. Pothitirat and Gristsanapan (2006) have reported lower content of curcuminoids under cooler and drier climate.

The dried turmeric rhizomes are mostly processed into powder and oleoresin (40–55% curcuminoid and 15–20% volatile oil). Considering the economic importance and commercial value, dry matter yield (factor of dry matter content and rhizome yield) and curcumin yield (factor of curcumin content and rhizome yield) were calculated to find out the actual quantity of

Table 6. Category-wise mean performance and range of turmeric genotype for various economic traits

Particular		Shoot length (cm)	Leaf length (cm)	Leaf width (cm)	Leaf area (cm^2/leaf)	Shoot thickness (cm)	No. of tillers/ plant	Days to maturity	Rhizome yield (q/ ha)	Dry matter content (%)	Dry matter yield (q/ ha)	Curcumin content (%)	Curcumin yield (kg/ ha)
All collections	Range	53.6–135.2	28.1–68.2	8.9–17.5	190.3–1145.8	10.3–26.2	2.4–6.8	180.0–228.0	158.3–500.0	10.0–27.5	26.0–93.7	5.01–7.51	151.0–646.2
	Mean	85.4	42.1	12.8	505.7	16.6	4.3	207.5	303.6	21.1	63.5	6.12	393.1
OPI collections	Range	53.6–83.3	28.1–43.4	8.9–15.0	190.3–488.3	10.4–17.9	2.8–6.1	190.0–228.0	158.3–369.0	10.0–27.5	26.0–88.2	5.01–6.17	151.0–540.8
	Mean	68.0	34.9	12.1	320.5	14.5	4.4	213.7	251.0	20.8	52.3	5.64	295.5
NEI collections	Range	65.3–135.2	34.2–68.2	9.1–17.5	339.4–1145.8	10.3–26.2	2.4–6.8	180.0–228.0	216.7–500.0	16.3–27.5	48.7–93.7	5.25–7.51	284.7–646.2
	Mean	95.5	46.4	13.2	614.6	17.9	4.3	203.8	334.6	21.2	70.1	6.40	450.4
Advantage of NEI collections over OPI collections (%)		40.4	33.0	9.3	91.8	23.3	-0.5	-4.6	33.3	1.8	34.0	13.5	52.4

economic produce. The present study clearly revealed the genetic potential of NEI collections over OPI collections which have 34.0–52.4% yield advantages of economic produce i.e. dry rhizome and curcumin yield (Table 6). Dry matter recovery and curcumin yield among various genotypes ranged from 29.5–89.4 q/ha and 172–620 kg/ha, respectively (Table 7). The best performing top 10 genotypes (Megha Turmeric-1, Local-4, Local-5, Local-7, Local-9, Local-11, IC0588791, IC0588795, IC0588796 and IC0588797) belong to NEI for both the

Table 7. Mean performance (in descending order) of genotypes for dry matter yield and curcumin yield

Dry matter yield		Curcumin yield	
Genotype	Quantity (q/ha)	Genotype	Quantity (kg/ha)
Megha Turmeric-1	89.4	Megha Turmeric-1	620
Local-9	87.2	IC0588797	578
Local-11	84.0	IC0588796	552
IC0588797	78.8	Local-4	524
IC0588795	76.5	Local-5	513
Local-4	76.1	IC058879	504
Local-5	75.1	Local-11	500
IC0588796	74.9	Local-9	491
IC0588791	71.2	IC0588795	459
Local-7	70.8	Local-7	455
IISR Pratibha	69.1	IISR Alleppy Supreme	408
IC0588788	67.5	IISR Pratibha	401
IISR Alleppy Supreme	67.3	IC0588788	389
Roma	66.2	Local-10	387
IISR Kedaram	64.8	Roma	382
Rasmi	60.8	IISR Kedaram	366
Local-10	60.8	IC0588793	357
IC0588793	58.5	IC0588789	353
IC0588794	58.4	IC0588794	350
IC0588789	57.0	Rasmi	329
IC0588792	54.4	IC0588792	328
Duggirala Red	51.0	IC0588790	298
IC0588790	50.5	Duggirala Red	272
Suranjana	47.3	Suranjana	256
BSR-2	36.5	BSR-2	190
Rajendra Sonia	30.2	Rajendra Sonia	179
Narendra Haldi-1	29.5	Narendra Haldi-1	172

traits of commercial importance (dry matter recovery and curcumin yield). Furthermore, 'Megha Turmeric-1' had excelled with respect to all the aforementioned traits; while other two varieties such as 'IISR Alleppy Supreme' and 'IISR Pratibha' were better among OPI collections. Singh *et al*. (2013b) reported that the varieties such as 'Megha Turmeric-1', 'IISR Pratibha', 'Duggirala' and 'Roma' performed better under different planting dates at Kolasib, Mizoram. Recently, in a 'genotype × environment' trial (11 cultivars including 1 from NEI, 10 environments for fresh yield, and 5 environments for curing per cent, curcumin and dry yield) across India; three cultivars ('Megha Turmeric-1', 'IISR Kedaram' and 'IISR Prathiba') were recommended as preferred genetic source for stability in breeding for high dry yield and curcumin content (Anandaraj *et al*., 2014).

Conclusion

Two economic parameters namely leaf length and curcumin content could be the most effective and reliable tools for identifying productive and curcumin rich genotypes and to realize maximum genetic gain in turmeric breeding. The best performing top 10 genotypes belong to NEI ('Megha Turmeric-1' ranked first) for both traits of commercial importance (dry matter recovery and curcumin yield). Therefore, the NEI genotypes should be given importance in the programmes of genetic enhancement and varietal improvement of turmeric.

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Genetic Divergence Studies for Yield Components and Root Traits in Castor (*Ricinus communis* L.)

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Magnitude of genetic divergence among 27 castor accessions was studied to identify diverse parents. Genotypes were characterized for physiological, morphological and root traits in an elevated root structure. Study identified seven clusters. Cluster means for traits showed considerable differences. Highest inter-cluster distance was found between clusters I and IV. Cluster I had highest variance for eight characters. Cluster II recorded the highest intra cluster distance. Seed yield recorded maximum divergence of 31.91% while root length, total root length, diameter, laterals and weight together contributed to 8.54% and showed significant correlation. The probability of obtaining better segregants and recombinants is expected when SKI-215, PCS-106 of cluster VII and II as females and Haritha, Kranthi, Kiran of cluster I can be used as male parents. Haritha, RG 48, Kranthi and SKI 215 which showed superior root and shoot characters, can be candidates in breeding for drought tolerance.

Key Words: Castor, Carbon isotope discrimination, D^2 analysis, Genetic divergence, Root length

Introduction

Castor (*Ricinus communis* L.) 2n = 20, a member of the family Euphorbiaceae is cultivated throughout the world. The productivity of crop in India in 2011-12 is 1417 kg/ha *vis-a-vis* world average of 850 kg/ha. Under rainfed conditions crop productivity is low at 400-600 kg/ha. To bring about crop improvement through breeding programmes, it is necessary to quantify the available variability for effective use in planning the crossing programme (Ramesh *et al*., 2012). Further, selection of diverse parents for hybridization programme will be effective by the identification of characters responsible for the total genetic diversity among the populations (Singh and Chaudhary, 1977). In case of roots, spatial distribution *i.e*., the ability of root system to take up water and not root mass per se (Draye *et al*., 2010), distribution of ca. 1 cm root/cm^3 of soil (root length density) is an ideal root system suitable for most field conditions (Tardieu *et al*., 1992). Steeper root angles and less branching are traits associated with drought tolerance in field (Hund *et al*., 2009). Crosses between divergent parents usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971). Improvement in yield is normally attained through exploitation of the genetically diverse parents as divergent parents throw heterotic crosses and also more variability could be expected in the segregating generations. In this context, Mahalanobis D^2 statistic provides an effective tool in quantifying the degree of divergence at genetic level and it also provides quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). D^2 is also a valuable tool to study genetic divergence at inter-varietal and sub-species level in classifying the crop plants (Rodge *et al*., 2003). Earlier, Bhatt and Reddy (1987), Chakrabarty and Banu (1999) and Lakshmamma *et al*. (2002) studied genetic diversity in castor genotypes through Mahalanobis D^2 statistic and identified the parents for future heterosis breeding. The present study was therefore carried out to measure the nature and magnitude of genetic divergence among the accessions to select superior material to be used in breeding programmes.

Materials and Methods

The experimental material consisted of 27 germplasm accessions obtained from RARS, Palem, Professor Jayashankar Telangana State Agricultural University (PJTSAU), and Directorate of Oilseeds Research

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(DOR), Hyderabad. The material includes twelve elite lines, three pistillate lines, four germplasm accessions, one male line and four checks (Table 1). The genotypes were selected based on their early flowering and tolerance or resistance to Fusarium wilt, Reniform nematode and leaf hopper. The accessions were planted in a specially designed temporary root structure of 25 m length, 4 m width and 1.5 m height in randomized block design with a permanent wall separating the replications (Lakshmamma *et al*., 2010). Crop was raised for two consecutive years with same set of 27 genotypes with two replications with spacing of 90×45 cm during late *rabi* 2012 and 2013. Observations were recorded on four plants in each replication for 15 quantitative traits. Data was recorded before dismantling of root study structure in respect of SPAD chlorophyll meter readings (SCMR), Relative Water Content (RWC), fluorescence, plant height up to primary raceme, number of nodes up to primary raceme, effective length of primary spike, hundred seed weight and seed yield (kg/ha). Carbon Isotope Discrimination (CID) were quantified (‰) in Isotope Ratio Mass Spectrophotometer (IRMS) facility in UAS, Bengaluru. CID is a tool that helps to understand photosynthesis and its coordination with water use in ecological and physiological studies in C_3 species (Farquhar *et al*., 1989). Structure was dismantled at 110 DAS when root growth was maximum and data was recorded on root system architectural traits (RSA) *viz*., root diameter, root length, number of laterals, total root length and root dry weight. Group distance was measured on multiple characters following Mahalanobis (1928). Clustering of genotypes was done according to Tocher's method.

Results and Discussion

This study revealed significant difference among the accessions for the characters studied. Based on the relative magnitude of D^2 values, 27 genotypes were grouped into seven clusters by Tocher's method (Fig. 1). Cluster II was the largest with 16 genotypes followed by cluster III (four), cluster I (three) while clusters IV, V, VI and VII possessed one genotype each (Table 2). Inclusion of maximum genotypes in one cluster revealed that the genotypes did not have wider diversity or limited gene exchange or narrow range of selection.

Table 1. Castor genotypes used in present study with source and available information

S.No.	Genotypes	Source	Remarks
1	DPC-9	DOR, Rajendranagar	Pistillate line
2	RG-48	DOR, Rajendranagar	Elite line (germplasm accession)
3	RG-43	DOR, Rajendranagar	Early flowering, resistant to reniform nematode and leaf hopper
4	RG-1354	DOR, Rajendranagar	Fusarium wilt resistant
5	RG-47	DOR, Rajendranagar	Fusarium wilt resistant and root rot
6	RG-67	DOR, Rajendranagar	Elite line (germplasm accession)
7	RG-1686	DOR, Rajendranagar	Male line (germplasm accession)
8	DCS-78	DOR, Rajendranagar	Male line
9	RG-20	DOR, Rajendranagar	Elite line (germplasm accession)
10	PCS-293	RARS, Palem, AP	High yielding
11	PCS-312	RARS, Palem, AP	High yielding
12	PCS-106	RARS, Palem, AP	High yielding, wilt resistant
13	PCS-236	RARS, Palem, AP	High yielding, wilt resistant
14	PCS-252	RARS, Palem, AP	High yielding
15	PCS-230	RARS, Palem, AP	High yielding
16	PCS-171	RARS, Palem, AP	High yielding, condensed internodes, cup shaped leaves
17	PCS-265	RARS, Palem, AP	High yielding, wilt resistant
18	PCS-228	RARS, Palem, AP	High yielding
19	PCS-224	RARS, Palem, AP	Early flowering
20	PCS-302	RARS, Palem, AP	Divergent branching
21	JP-65	Junagadh	Pistillate line
22	SKI-215	S.K. Nagar, Gujarat	Male line
23	M-574	DOR, Rajendranagar	Pistillate line, convergent branching, semi compact spike
24	RG1(Aruna)	DOR, Rajendranagar	Check variety
25	Kiran	RARS, Palem, AP	Check variety, Red stem, double bloom, monoecious
26	Kranthi	RARS, Palem, AP	Check variety, Red stem, double bloom, monoecious, shallow cup leaf
27	Haritha	RARS, Palem, AP	Check variety, Green stem, double bloom, monoecious, shallow cup leaf

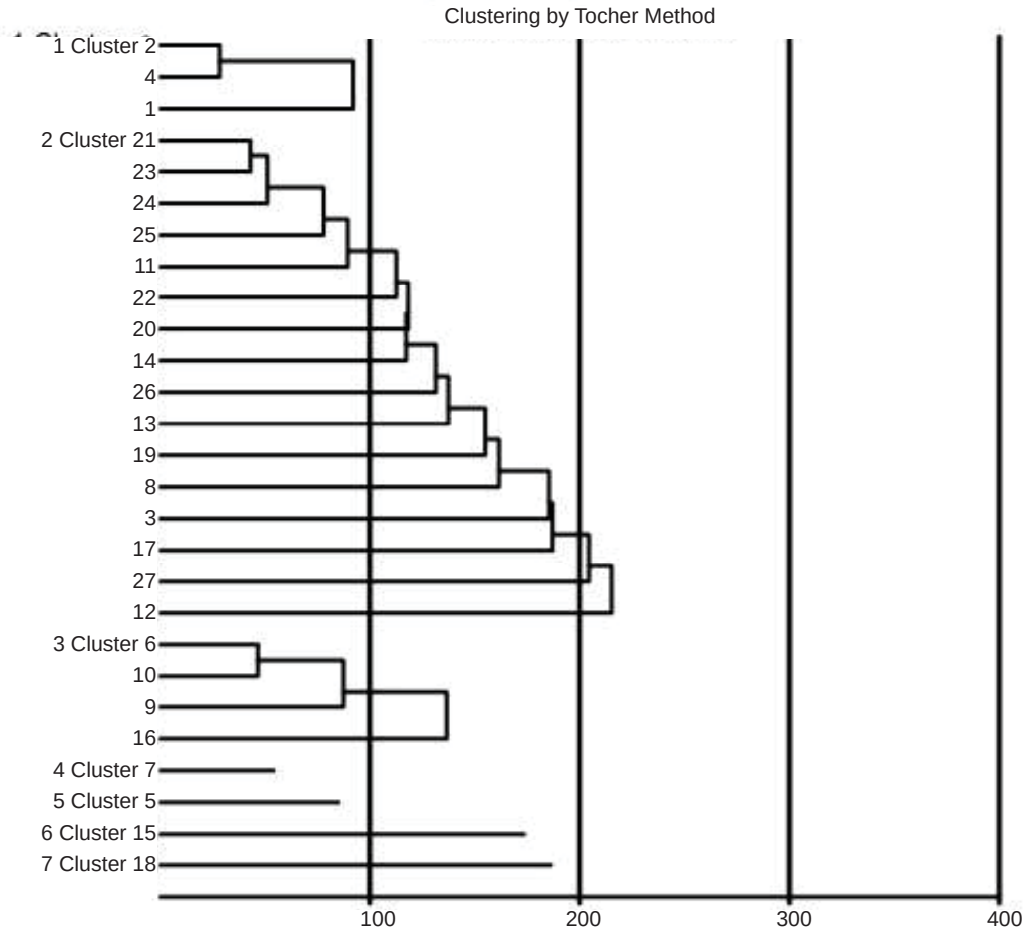

Fig. 1. Clustering pattern of 35 castor genotypes formed by Tocher's method

However, it was interesting to note that three pistillate lines *viz*., DPC9, JP 65 and M 574 were placed in the same cluster II. Occurrence of genotypes in the same cluster indicated the same genetic background (Prasad and Kumar, 2013) or absence of geographic diversity (Ganesh and Thangavelu, 1996). RG-43 which is early flowering, resistant to reniform nematode and leaf hopper was placed in separate cluster V. Elite lines occurred randomly in clusters. Any crossing programme taken up between genotypes of different clusters can have selective advantage when constant selection is practiced in the segregating populations (Ramesh *et al*., 2012).

Table 2. Distribution of castor genotypes into different clusters

Cluster No.	No. of genotypes	**Genotypes**
I	3	Haritha, RG-48, Kranthi
II	16	DCS-78, RG-20, PCS-302, M-574, PCS-106, JP-65, PCS-265, PCS-236, RG-1686, Kiran, PCS-171, RG-47, DPC-9, PCS-230, PCS-224, RG-67
III	4	PCS-293, RG-1 (Aruna), PCS-312, RG-1686
IV	1	RG-1354
V	1	RG-43
VI	1	PCS-252
VII	1	SKI-215

The intra-cluster distance was highest in cluster II (13.27) followed by cluster III (11.94) and I (10.08) (Table 3). The cluster II was widely separated from cluster VI (34.84) which involved only one genotype PCS 252. Cluster VI recorded maximum variance for total root dry weight (39 g) and total dry matter (134 g). Crossing of genotypes of clusters II and VI can result in transgressive recombinants with superior root characters. Four clusters IV, V, VI and VII possessed one genotype each. Zero cluster distance has been attributed to the similarity in their source of cytoplasmic genetic male sterility or share the same genetic background or may belong to the same geographical area (Prasad

Table 3. Average intra and inter cluster distance (D^2) values

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	10.08	38.84	27.76	47.18	42.34	18.44	19.62
Cluster II		13.27	20.39	17.07	16.24	34.84	27.15
Cluster III			11.94	25.28	22.72	19.78	21.25
Cluster IV				0	9.22	42.06	37.59
Cluster V					0	38.70	33.08
Cluster VI						0	20.46
Cluster VII							0

and Kumar, 2013) in pigeonpea. Genotypes belonging to same cluster showed smaller D^2 values than those belonging to different clusters (Parameshwarappa and Palakshappa, 2010).

The relative divergence of each cluster from other clusters (inter-cluster divergence) indicated high order of divergence between cluster I and IV (47.18) followed by I and V (42.34), IV and VI (42.06) and I and II (38.84). The least inter-cluster distance was found between cluster IV and V (9.22). Cluster I showed highest variance for eight characters such as root diameter (8.60 cm), RWC (83), SCMR (52), fluorescence (0.66), number of nodes (13), effective spike length (29 cm), 100 seed weight (28 g) and seed yield (1508 kg/ha). Haritha, RG 48 and Kranthi belonged to this group. These genotypes are at present used as male lines. Cluster II with 16 genotypes, recorded lower mean values for seven characters. Genotype DPC 9 of this cluster specifically showed S type pistillate nature and M-574 is presently used as a pistillate line in breeding programmes (DOR, 2013). Cluster III included four genotypes. Cluster V with only genotype RG 43 recorded resistance to reniform nematodes and leaf hoppers (DOR, 2013). Cluster VII which consisted of only one genotype SKI 215 showed superior mean values for number of laterals (43), root length (226 cm), total root length (1342 cm), plant height (74 cm) and CID (-19.33 ‰) (Table 4). The superior root architectural traits of SKI-215 point towards its ability to mine water. SKI 215 at present is used as a male line in breeding programmes (DOR, 2013). In contrast, cluster IV genotype namely RG 1354 recorded low values for as many as seven characters (Table 4). RG 1354 was found to be wilt resistant (DOR, 2013). Castor being monospecific genus, diversity is based on geographical, genetic and morphological characters (Mallesh, 2007). The genotypes belonging to these clusters separated by high statistical distance have been attributed with greater genetic divergence. The genotypes of cluster I were highly divergent to those of cluster VII indicating the scope of generating heterotic hybrids in a crossing programme. SKI 215 of cluster VII, PCS 106 of cluster II as female lines and Haritha, Kranthi as male lines of cluster I can be utilized in line × tester or diallel analysis. All the elite lines which occurred randomly in clusters can be considered as potential divergent lines for future breeding programme.

Table 4. Cluster means for evaluated traits of 27 castor accessions

	Root diameter (cm)	No. of laterals	Root length (cm)	Total root length (cm)	Root dry weight (g)	Total dry matter (g)	RWC (%)	SCMR	Fluore-scence	Plant height (cm)	No. of nodes	Effective spike length (cm)	100-seed weight (g)	Yield (kg/ha)	CID kg/ha (%)
Cluster I	8.60	21	164	1138	32	127	83	52	0.66	55	13	29	28.00	1508	-18.73
Cluster II	5.86	18	115	778	10	57	74	50	0.58	48	10	19	22.31	704	-18.66
Cluster III	7.50	28	132	1011	24	98	78	49	0.61	48	10	19	19.63	645	-18.57
Cluster IV	4.50	24	89	909	3	14	79	47	0.59	36	10	13	19.00	595	-17.80
Cluster V	7.70	21	142	1292	8	19	81	49	0.66	52	10	12	25.50	858	-17.56
Cluster VI	8.35	40	158	1025	39	134	77	48	0.63	56	10	13	19.50	876	-17.57
Cluster VII	8.30	43	226	1342	29	89	76	51	0.63	74	11	27	26.50	1288	-19.33
Range	3.68 -8.75	16.3-74.8	74.5 - 226	503 - 1341	1.8 - 38.9	26.8 - 138	67.3 - 83.3	45.9 - 51.8	0.52 - 0.68	33.5-85.5	9-14	12-30.3	17.5-28.6	517-1622	-17.6-19.3
Mean	6.58	35.5	128	906	15	71.7	76.2	49.7	0.6	49.6	10	19.7	22.5	814	-18.6

CID: carbon isotope discrimination; RWC: relative water content; SCMR: SPAD chlorophyll meter reading

The contribution of individual character towards the divergence was maximum for seed yield (31.19%) followed by total dry matter (23.36 %), fluorescence (13.96 %), 100-seed weight (13.96%) and root dry weight (5.70 %). Root traits together contributed to 8.54%. Four root characters showed significant correlation with seed yield and included root diameter (0.5838), root length (0.5626), total root length (0.5393) and root dry weight (0.5785). In other studies, oil content, seed yield and 100 seed weight recorded higher contribution (Ramesh, 2008). Least contributors for divergence included, root diameter, number of laterals and plant height (Table 5). Genetic drift and selection in different environments have been reported to cause greater diversity than geographic distance (Murty and Arunachalam, 1966). In the present study, crossing between genotypes of cluster I with cluster II and VII could be better for obtaining high heterosis.

The new information generated through this research for identification of the genetically divergent material as per the need of breeder, which was hitherto lacking, has significant bearing on the development of new heterotic hybrids aimed towards the improvement of yield traits in castor. Haritha, RG 48, Kranthi and SKI 215 showed superior root and shoot characters which make them likely candidates in breeding for drought tolerance.

Table 5. Contribution of characters towards genetic divergence

Character	Time ranked first	Contribution (%)
Root diameter (cm)	0	0.00
No. of laterals	0	0.00
Root length (cm)	7	1.99
Total root length (cm)	3	0.85
Root dry weight (g)	20	5.70
Total dry weight (g)	82	23.36
Relative water content (%)	10	2.85
SPAD chlorophyll meter reading (SCMR)	1	0.28
Fluorescence	49	13.96
Plant height (cm)	0	0.00
No. of nodes	1	0.28
Effective spike length (cm)	8	2.28
100-Seed weight (g)	49	13.96
Yield (Kg/ha)	112	31.19

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SHORT COMMUNICATION

Evaluation of F_2 Population Derived from *Cucumis melo* var. *momordica* X *C. melo* var. *reticulatus* in Konkan Region based on Morphological Characters

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The present investigation was aimed for assessing the morphological parameters of the F_2 population of 10 promising hybrids between snap melon and musk melon. The hybrids $SM_2 \times MM_4$ and $SM_5 \times MM_2$ were found to be promising for plant architecture, yield and attractive golden fruit colour. The hybrid $SM_1 \times MM_4$ can be rated extremely well for yield. The component characters recorded may be utilized for developing desirable plant type.

Key Words: Evaluation, F_2 population, Morphological characters, Snap melon, Tribal food

Tribal people cultivate various cucurbits for their day to day needs in Kitchen garden. The genetic variability among cucurbits is still ambiguous (Kulkarni and Kumbhojkar, 2004). Indian scientists have carried out research on *Cucumis melo* and wide variability of dessert melons as well as non-dessert (non-sweet) forms and land races were found in India. Phoot or Chibud commonly known as Snapmelon [*Cucumis melo* L. var. *momordica* (Roxb.) Duthie & J.B. Fullar] is an important vegetable cum fruit in tribal region of Konkan. Germplasm collection of this species and their scientific evaluation pertaining to morphological variation and qualitative and quantitative characters of F_2 population is essential for development of desired character combinations (Patil, 1994). Seshadri and More (2008) have carried out research on *Cucumis melo* var. *momordica* Duthie & Fullar for resistance to powdery mildew (*Sphaerotheca fuliginea*), downy mildew (*Pseudoperonspora cubensis*) and *Cucumber green mottle mosaic virus* (CGMMV). There are cucumber-like forms (used as salad) with crisp flesh like Kakri (*Cucumis melo* var. *utilissimus* Duthie & Fullar) from North India and Vellarikkai (or Vellarikkaya) and Vellari of South India (Sheshadri, 1991). These valuable forms are important food resources of local people.

The genus *Cucumis* (Cucurbitaceae) comprises about 30 species and is of great economic importance (Kirkbride, 1973). *Cucumis melo* var. *momordica* are widely grown by tribal communities for their edible fruits used both as vegetable and fruits. However, the crop is least attended and remained unexploited. Variability studies have indicated scope for improving the quality aspects, plant architecture and season insensitivity (Deshmukh, 1991). In another study, it has been revealed that the snap melon can be freely crossed with muskmelon, thereby providing a scope for inducing the quality aspects like non cracking behavior which is a severe problem of snap melon and seasonal insensitivity (Datta and Nath, 1969). Krishna Reddy *et al*. (2005) studied genetic and biochemical parameters in introduced and indigenous germplasm in snap melon. Such a distant crossing is expected to create a great degree of variability, which is a basis for success of further breeding programmes. When six lines of snap melon were crossed with four testers of musk melon good combining ability for important traits was observed. Therefore, the present investigation was undertaken to evaluate the F_2 with desirable plant types suitable for *kharif* season cultivation in Konkan region.

Seeds of 10 promising hybrids of snap melon × musk melon, namely, '$SM_1 \times MM_4$', '$SM_2 \times MM_2$', '$SM_2 \times MM_3$', '$SM_2 \times MM_4$', '$SM_5 \times MM_2$', '$SM_5 \times MM_3$', '$SM_5 \times MM_4$', '$SM_6 \times MM_2$', '$SM_6 \times MM_3$', '$SM_6 \times MM_3$', '$SM_6 \times MM_4$' were selected. The experiment was laid out in a compact family block design, with two replications. The experimental conditions were

tropical climate, laterite soil of pH 5.6 to 6.5 with good drainage and high humidity. The distance between plant to plant was 1 meter and row to row was 0.75 meter. The nutrients were applied (N:P:K) at the rate of 80, 50 and 30 kg/ha, as urea, single super phosphate and muriate of potash, respectively. Plant protection measures were applied as per requirement. The fruits of F_2 population were harvested at full ripe stage (full maturity). The data on quantitative aspects were recorded for each hybrid. Present study encompasses characters like stem length, number of branches, leaf area, fruit development period, first fruit initiation, length and diameter of fruits, flesh thickness, edible portion and total yield/vine.

Statistical analysis was done in two stages first form the main plot values, the variance between families and corresponding error was calculated in second, treating the experiment as one in simple randomized block (Panse and Sukhatme, 1967).

Formation of a population with genetic variability for the characters of interest is a pre-requisite for crop improvement programme. Genetic improvement mainly depends upon the amount of genetic variability present in a population. The mean values of hybrids for different characters of growth, yield and a quality is mentioned in Table 1.

The overall mean showed maximum variation within the progenies. Hybrids $SM_1 \times MM_4$ showed maximum vine length of 399.80 cm followed by those belonging to $SM_6 \times MM_4$ (377.80 cm.). The progenies of $SM_2 \times MM_3$ attributed minimum average vine length 250 cm. It was observed that number of primary branches of $SM_1 \times MM_4$ was 10.70 followed by 9.80 in $SM_2 \times MM_4$. The lowest number of branches (7.00) were noticed in hybrid SM6 × MM4. The highest mean performance for total number of branches/vine was exhibited by $SM_1 \times MM_4$ (25.60) followed by $SM_2 \times MM_4$ (23.60) and $SM_2 \times MM_2$ (21.00). The lowest performance was noticed in $SM_6 \times MM_4$ (16.70). The highest average leaf area/vine was recorded in the hybrid $SM_1 \times MM_4$ (412.16 dm^2/vine). It was lowest in the hybrid $SM_6 \times MM_2$ (165.49 dm^2/vine). Highest performance in secondary branches (14.90) was recorded in hybrid $SM_1 \times MM_4$. The number of secondary branches/vine is the principle determinants of number of fruits/vine and hence the fruit yield/vine in cucurbits (Nath and Vashistha, 1969, 1970; Moon, 1989). The hybrid means for fruit development period ranged between 27.3 in $SM_5 \times MM_2$ to 36 days in $SM_6 \times MM_2$. Considering shorter fruit development period as a criteria for selection hybrid $SM_5 \times MM_2$ may be considered as most promising. The hybrid $SM_5 \times MM_4$ recorded maximum average fruit length (18.80 cm) followed by those belonging to hybrid $SM_5 \times MM_3$ (16.15 cm). The hybrids $SM_2 \times MM_3$ showed

Table 1. Mean values of F_2 population of Snapmelon cross

S. No.	Family	Main stem length (cm)	No. of primary branches/ vine	No. of secondary branches/ vine	Total no. of branches/ vine	Leaf area (dm^2)/ vine	Fruit devp. period in days	Days to first fruit	Average length of fruit (cm)	Average diameter of fruit (cm)	Flesh thickness of fruit (cm)	Edible portion in %	Average weight of fruit (kg)	Total yield/ vine (kg)
1	SM1 × MM4	399.8	10.7	14.9	25.6	412.16	29.5	91.8	13.91	9.44	2.73	86.2	1.015	3.87
2	SM2 × MM2	317.7	9.1	11.9	21	284.31	29.7	91	14.16	8.69	2.97	85.64	0.852	2.376
3	SM2 × MM3	250	8.3	9.9	18.2	204.83	30.5	88.1	12.07	8.17	3.13	83.71	0.527	1.291
4	SM2 × MM4	361.75	9.8	13.8	23.6	205.12	29.5	87.6	14.01	9.96	3.2	85.29	0.878	1.953
5	SM5 × MM2	326.25	8.5	12.2	20.7	219.82	27.3	86.1	13.15	10.09	3.27	86.45	0.954	2.489
6	SM5 × MM3	342.8	8	11.4	19.4	215.95	32.1	89.8	16.15	10.96	3.23	86.43	1.216	2.786
7	SM5 × MM4	371.5	9.5	10.8	20.3	265.76	31.7	91.8	18.8	9.49	3.06	84.86	1.046	2.104
8	SM6 × MM2	326.8	7.7	10.5	18.2	162.49	36	9.8	12.72	8.88	2.58	89.67	0.783	1.094
9	SM6 × MM3	351.4	7.7	10.6	18.3	253.2	35.2	92.8	15.16	9.68	2.9	89.02	0.829	1.287
10	SM6 × MM4	377.8	7	9.7	16.7	254.2	33.1	95.2	14.28	10.54	3.48	88.71	0.968	1.577
	Avg. Mean of Hybrids	342.58	9.5	11.57	20.2	247.78	31.5	90.8	14.44	13.56	3.05	87.38	0.907	1.983
	Avg. Mean of Parents	333.14	9.5	14.68	21.07	333.7	31.78	86.28	19.5	9.59	3.26	89.27	1.31	2.73

minimum average fruit length (12.07 cm). The progenies of $SM_5 \times MM_4$ may be regarded as promising as it shows maximum average fruit length. The maximum flesh thickness (3.48 cm) was noticed in hybrid $SM_6 \times MM_4$ followed by $SM_5 \times MM_2$ (3.27 cm) and $SM_5 \times MM_3$ (3.23 cm). The lowest flesh thickness was noticed in $SM_6 \times MM_2$ (2.58 cm). The flesh thickness is an important aspect related to yield of edible portion. The maximum weight of edible portion was recorded in $SM_6 \times MM_2$ (89.67) followed by $SM_6 \times MM_3$ (89.02). The highest mean performance 3.70 was exhibited by hybrid $SM_1 \times MM_4$ followed by $SM_5 \times MM_2$ (2.90) and $SM_2 \times MM_2$ (2.50) for average number of fruits. The hybrid mean 3.87 kg/ vine was recorded in $SM_1 \times MM_4$ followed by $SM_5 \times MM_3$ (2.79 kg/ vine) for total yield/vine. The lowest hybrid mean was recorded in $SM_6 \times MM_2$ (1.09 kg/vine). These hybrids may be regarded as promising types for total/ vine yield.

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Spatial Distribution of Trait-specific Diversity in Indian Wheat Collections

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A total of 5,930 accessions of wheat were collected in collaboration with crop-based institutes of Indian Council of Agricultural Research (ICAR) and State Agricultural Universities (SAUs) from diverse areas of the country during the period 1976-2013. Of these, 3,973 accessions were short-listed with details on state, district, village, collector number, latitude (N) and longitude (E) of the collection sites to understand the diversity distribution pattern. The geo-referenced map of collected diversity depicted that Himachal Pradesh and Uttarakhand states were extensively explored for *Triticum aestivum* and Karnataka, Gujarat and Madhya Pradesh for *T. turgidum* subsp. *durum*. Among the local landraces, drought tolerant Jautri local type from Madhya Pradesh; awnless types Lakh, Dhavati and Hansy from Uttarakhand; and non-shattering types Kankoo and Dharmauri from Himachal Pradesh were some notable collections. Besides, the priority areas for collection of cultivated species of wheat distributed in different agro-ecological regions were identified and discussed in the present communication.

Key Words: Diversity distribution, GIS, Landraces, Trait-specific germplasm

Introduction

Wheat is widely cultivated as a cash crop because of good unit area production. It grows well in a temperate climate even with a moderately short growing season. Wheat has more than 60% share of calories in human diet, together with rice and maize (Gill *et al.,* 2004). *Triticum aestivum* L. (bread wheat), *T. turgidum* L. subsp. *durum* (Desf.) Husn. (durum wheat) and *T. turgidum* L. subsp. *dicoccon* (Schrank) Thell. (emmer wheat) are three main species of wheat under cultivation in India. Among these, bread wheat is grown in about 95% area, durum wheat in 4% and emmer wheat in only 1% area (Gupta, 2004; Singh, 2006). *T. aestivum* has superior bread-making qualities, and traditionally dominates under cultivation in the north-western part of continent and the Ganges valley. *T. turgidum* subsp. *durum* is hardier, drought resistant, generally provides grittier flour and often traditionally used in grits, sweets, base for pizza, burger, etc. (Ambasta *et al.,* 1986). *T. turgidum* subsp. *dicoccon* has high fibre and antioxidant compound concentration, is particularly suitable for diabetes (Annapurna, 2000), also possesses high lysine content and minerals than bread and durum wheat (Zaharieva *et al.,* 2010).

In India, wheat is mainly grown in Punjab, Haryana, Gujarat, Rajasthan Uttar Pradesh, and West Bengal. Presently the wheat growing areas are experiencing the major impact of climate change and changes in cultivation pattern in the country; the cool period of crop growing duration is shrinking, while the threat of terminal heat stress is increasing (Rane *et al.,* 2000; Sharma *et al.,* 2002). The high temperature stress could be a significant factor in reducing yield and quality of wheat (Stone and Nicolas, 1995). Therefore, to combat biotic (yellow and brown rust, loose smut, etc.) and abiotic stresses (moisture stress at different stages, terminal heat, etc.), there is a need to collect trait-specific germplasm of landraces/ local cultivars as well as the wild *Triticeae* from areas of diversity (Gupta and Lakshmi Kant, 2012; Singh *et al.,* 2006).

Presently limited studies have been conducted on agro-ecological distribution pattern of *Triticum* spp. in India as compared to other crops. Geographical Information System (GIS) is an efficient tool that supports the analysis of exploration and collection, characterization and evaluation, genebank and herbarium databases to elucidate genetic, ecological and geographical distribution patterns of the crops and wild species (Hijmans and Spooner, 2001; Semwal, 2009). This tool has been used to analyse the data pertaining to management of plant genetic resources of various crops and crop wild relatives *viz.,* wild potato, wild *Vigna*, wild peanut, *Jatropha* and

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Brassica spp. (Hijmans *et al.*, 2000; Jarvis *et al.*, 2002; Dutta, 2008; Sunil *et al.*, 2009; Abraham *et al.*, 2010; Semwal *et al.*, 2013). Keeping this in view, DIVA-GIS software has been used in the present study to identify the high diversity rich and under-explored/ unexplored areas using passport data of collected germplasm.

Materials and Methods

Wheat germplasm was assembled from different wheat growing regions of India through crop-specific and multi-crop explorations in collaborative mode with ICAR crop-based institutes/State Agricultural Universities/ Krishi Vigyan Kendras by Plant Exploration and Germplasm Collection Division of National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India. Germplasm collection and conservation databases, plant collection reporters, NBPGR annual reports and other published literature were used for the analysis of passport and related information. Out of 5,930 assembled accessions of three different *Triticum* spp., a total of 3,973 accessions were short-listed with detailed information pertaining to state, district, village, collector number, latitude (N) and longitude (E) of the collection sites for the present study. In order to know the spatial distribution and assessment of diversity richness, DIVA-GIS version 7.3 was used for point to grid analysis using simple/circular neighborhood method (Hijmans *et al.*, 2001).

Results and Discussion

Mapping of Collected Diversity and Collection Sites

In the present study, 2,090 villages belonging to 213 districts and 22 states were surveyed and 5,930 accessions of *Triticum* germplasm were collected. By screening the passport data of collected germplasm, only 3,973 accessions comprising of *T. aestivum* (2,745 accessions), *T. turgidum* subsp. *dicoccon* (61 accessions), *T. turgidum* subsp. *durum* (1,167 accessions) could qualify the parameters to pool for further analysis.

The analysis of information has shown that majority of the accessions were assembled from seven states. A total of 732 accessions were assembled from 397 villages of 12 districts of Himachal Pradesh. Like-wise, 652 accessions from 326 villages of 44 districts in Madhya Pradesh; 612 accessions from 379 villages of 12 districts in Uttarakhand; 554 accessions from 305 villages of 25 districts in Rajasthan; 455 accessions from 195 villages in 14 districts of Karnataka; 375 accessions from 216 villages of 22 districts in Gujarat and 279 accessions from 84 villages of 12 districts in Jammu & Kashmir (Fig. 1 and Table 1).

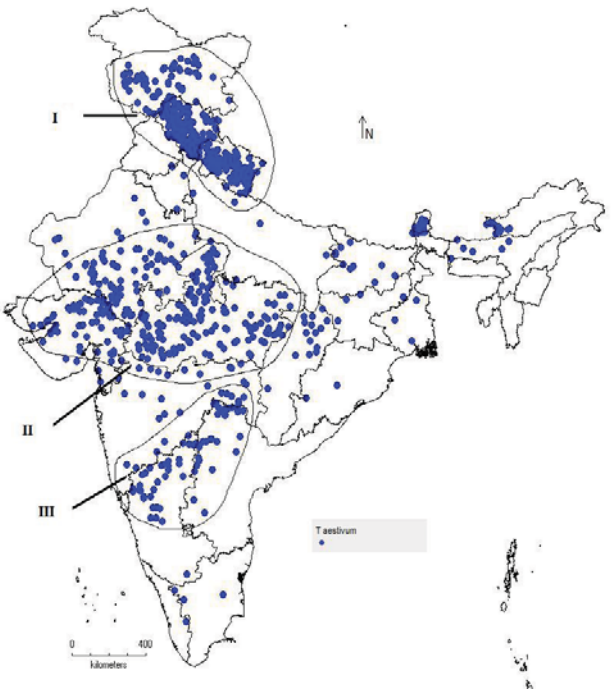

Fig. 1. Collection sites of *Triticum aestivum*

Keeping in view the diversity distribution pattern of *Triticum* species in different agro-ecological regions of the country, it was clearly observed that *T. aestivum* is under cultivation in 22 states but majority of accessions were collected from Himachal Pradesh (722) followed by Uttarakhand (611), Madhya Pradesh (377), Jammu & Kashmir (279), Rajasthan (260) and Gujarat (178) (Table 1). Analysis of the passport data indicated that *T. aestivum*, region I was extensively explored as compared to region II, whereas region III was meagerly explored (Fig. 1). For further collections, meagerly explored areas can be surveyed on priority basis. GIS mapping has successfully been used in identifying the areas of high diversity in *Phaseolus vulgaris* (Jones *et al.*, 1997), wild potato (Hijmans *et al.*, 2000), wild peanut (Jarvis *et al.*, 2002), mustard (Dutta, 2008), *Jatropha* (Sunil *et al.*, 2009), wild *Vigna* (Abraham *et al.*, 2010), eggplant (Gunjeet *et al.*, 2013) and rapeseed-mustard (Semwal *et al.*, 2013).

The emmer wheat is mainly grown in northern Karnataka, southern Maharashtra, the Saurashtra region of

Table 1. Species-wise accessions of wheat collected from different states

Species	State (accessions)	Total
Triticum aestivum	Andhra Pradesh (35), Arunachal Pradesh (48), Assam (18), Bihar (12) Chhattisgarh (19), Gujarat (178), Haryana (15), Himachal Pradesh (722), Jammu & Kashmir (279), Jharkhand (4), Karnataka (52), Kerala (1), Madhya Pradesh (377), Maharashtra (52), Manipur (1), Odisha (1), Rajasthan (260), Sikkim (48), Tamil Nadu (11), Uttarakhand (611), Uttar Pradesh (7), West Bengal (4)	2,755
T. turgidum subsp. *dicoccon*	Andhra Pradesh (1), Gujarat (11), Himachal Pradesh (2), Karnataka (31), Kerala (2), Madhya Pradesh (2), Maharashtra (4), Tamil Nadu (7), Uttarakhand (1)	61
T. turgidum subsp. *durum*	Andhra Pradesh (1), Gujarat (186), Haryana (4), Himachal Pradesh (8), Karnataka (372), Madhya Pradesh (281), Maharashtra (10), Rajasthan (294), Tamil Nadu (1)	1157
Total		3,973

coastal Gujarat, parts of Tamil Nadu and Andhra Pradesh (Hanchinal *et al.*, 2005). But presently it was seen under cultivation in about nine Indian states and from these 61 accessions could be assembled. Maximum number of accessions were collected from Karnataka (31) followed by Gujarat (11), Tamil Nadu (7), Maharashtra, Himachal Pradesh, Kerala, Madhya Pradesh, Uttarakhand and Andhra Pradesh (Table 1). The dry tracts of northwestern part of Karnataka were extensively explored (Fig. 2, encircled region I). Very few accessions were made from others areas of the country (Fig. 2 and Table 1).

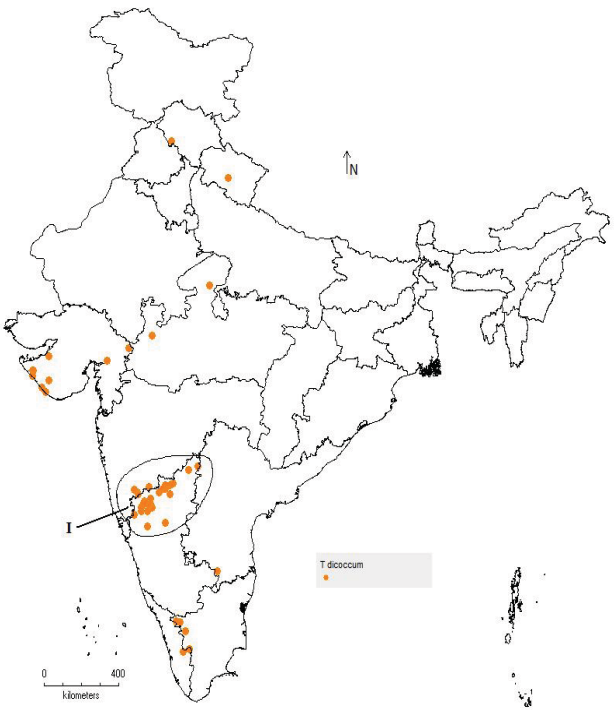

Fig. 2. Collection sites of *Triticum turgidum* subsp. *dicoccon*

Durum wheat is cultivated in a small portion of the total wheat grown area mainly under rainfed conditions in Madhya Pradesh, Gujarat, Karnataka, south Rajasthan, and Maharashtra, except in some irrigated areas of Gujarat. Efforts were made to collect 1,167 accessions in durum wheat from these states but majority of accessions were from northern Karnataka (372) followed by Rajasthan (294), Madhya Pradesh (281) and Gujarat (186) (Fig. 3 and Table 1).

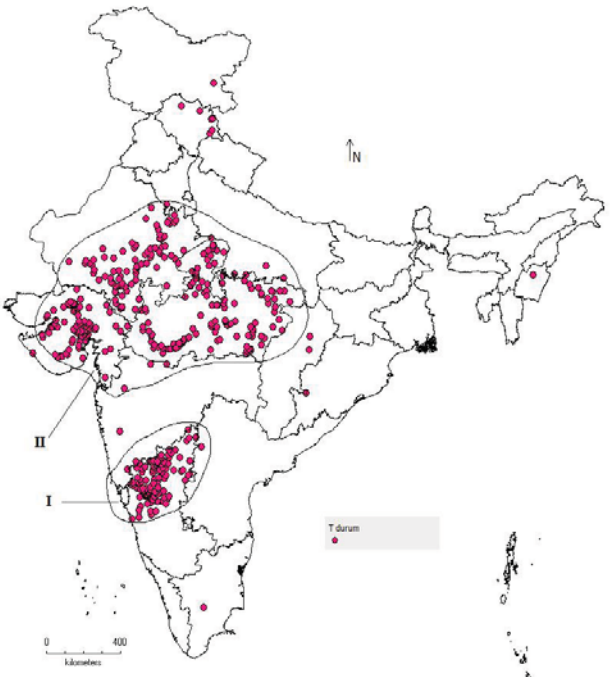

Fig. 3. Collection sites of *Triticum turgidum* subsp. *durum*

Mapping of collected diversity indicated that some of the diversity rich states viz., Himachal Pradesh, Jammu & Kashmir, Uttarakhand, Gujarat and Madhya Pradesh were extensively explored for collection of bread wheat germplasm. Similarly, Madhya Pradesh, Gujarat and Karnataka were explored extensively for collection of emmer and durum wheat. However, still

there is a scope for execution of specific explorations mainly for collection of trait-specific germplasm and wild species from under-explored/ un-explored areas in Tamil Nadu, Jharkhand, Kerala, Odisha, West Bengal and Uttar Pradesh keeping in view the availability of diverse germplasm.

Trait-specific Variability Collected

The crop landraces/local cultivars are geographically or ecologically distinctive populations, which are conspicuously diverse in their genetic composition both between populations and within them (Zeven, 1998). Wheat landraces/local cultivars have been largely displaced by high-yielding cultivars in many developing countries hence is rarely observed under cultivation due to their low yield potential and susceptibility to pests. However, landraces and old cultivars out-yield, and have better quality attributes than high-yielding cultivars under organic and low-input farming systems (Jaradat, 2011). During germplasm collection, rich variability was observed in landraces/local cultivars of wheat for different agro-morphological traits *viz.*, plant height, tiller number, ear head size, ear head types (lax/loose), awn colour (yellow, black, red or brown), awned and awnless types, grain size, grain colour (red, amber and white), shattering types, straw colour (yellow, dull yellow with brown tinge and shining yellow), etc. Different landraces/local cultivars collected from 13 states are listed in Table 2. Some of the notable landraces/local cultivars *viz.*, Kankoo and Dharmauri observed as highly non shattering types, tall and good for bread making collected from Sirmour district; tall with high tillering *viz.*, Dharnon, Shruin, Mundan, Daru and Bhangaru from rainfed areas of Mandi and Kullu districts; similarly other cultivars *viz.*, Bada kanak, Chhiti kankoo, Dharmodi, Lalpuri, Mandalum, Mundal kankoo, Shruin from Banjar, Sainj, Soja, Garsa and Parvati valleys and Mundri, Mundru, Kanku, Dharmodi, Kasyali from Hamirpur and Una districts of Himachal Pradesh (Anonymous, 1976-2012). According to Pal *et al.*, (2007) and Gupta and Lakshmi Kant, (2012), local cultivars *viz.*, Bharadoo, Chawera, Cheeuni, Desi mundal, Gazaria, Jael, Joth, Jhuladi, Kasieun, Kothek, Kothi, Kiawali, Lal kanak, Latar, Kalee bauri, Mundra, Marodum, Misri, Mundu, Paluwa, Ralieum, Rigaliya, Rundan, Trimudi are still under cultivation in different parts of Himachal Pradesh. Some of the landraces/ local cultivars *viz.*, Jael, Joth, Jhuladi, Kothek, Mundra and Rundan were assembled (Table 2).

In Uttarakhand, good variability was observed in bread wheat (*T. aestivum*) for traits like grain colour (deep amber to light amber white) and grain size, while tillering was shy (3-4) and awned types were more common. Landraces/ local cultivars in awnless types *viz.*, Lakha, Dhavati, Hansy and Donya were collected from Bageshwar districts. Safed mundri and Lal mundri considered as drought-tolerant; Jhusia, Kishva and Churi known for high yield potential; and Bhuri mundiya for high biomass were some notable collections from Uttarakhand. Among these, Mundiya landrace has been

Table 2. List of some landraces/local cultivars collected from different states

State	Landraces/Local cultivars
Andhra Pradesh	Erragoduma, Goduma, Godumalu, Goduma vadlu, Katta koduma, Machhu godumalu, Neeti godumalu and Tella goduma
Arunachal Pradesh	Buku, Feuk, Fu, Fugiri, Kangla, Kho, Koh, Nai and Rambu
Assam	Bhutia gom, Molllah gom and Ranto wheat
Gujarat	Dukhani ghau
Himachal Pradesh	Amreek gandham, Baasthi gehun, Bangla kalyan, Bariharu, Brehar, Haans, Jael, Jiri kanak, Joth, Jhuldi, Jhurti, Kali bhauri, Kali and Safed dharmodi, Kankoo, Kashmal, Keshwali, Kishaal, Kothek, Lamtara, Mundra, Rindyu, Rundan, Serohan and Sherwan
Jammu & Kashmir	Kashur kanak, Moond kanuk, Tro and Toe
Karnataka	Beligodi, Goi, Jawari kadli, Kolavi sadak, Lokapur sadak, Moolagodhi, Neeragodhi and Ravagodhi
Madhya Pradesh	Gajri, Jautri, Hasia gehun, Jalalia, Kali muchh gehun, Kacchi pissi, Kariya-sukra, Kathia gehun, Kathia, Kali pissi, Karodpati gehun, Lajya gehun, Lal kathi, Lal pissi, Mundi lal and Safed mundi
Maharashtra	Khapali gahun
Rajasthan	Gehun katha
Sikkim	Ghaow, Knoo, Menchak and Semia
Tamil Nadu	Ettagodhi, Gothumai, Mullu gothum and Sambagodhumai,
Uttarakhand	Bareek lal, Bhotia gehun, Bona, Chanosi, Chini, Churiya gehu, Cheuri, Dabdi gehun, Dapati gehun, Daulatkhani, Dhol churia, Dhudia, Dogla gehun, Donia, Dug gehun, Gerua, Gharia, Ghegua, Jhusal gehun, Jhausa, Jiswal gahun, Juinsi Ninsa, Jusia gehun, Kisala, Kontha Gainhu, Lakha Gainhu, Lal mishri, Lal sungari, Laldandi gehun, Lal kishwa, Lal mundiya, Messa, Munara, Munda, Mundania, Muneri, Munnar, Palthi gehun, Radh, Raje gehun, Ratta, Ryat gehun, Safed mundri, Safed mundiya, Setta, Syatgehun, Tank, Thaenkna, Thangi and Thull

reported to be suitable both for drought and higher biomass production (Mehta *et al.,* 2009). Some other potential landraces *viz.*, Naphal is known for softness and good quality biscuit making; Lal gehun for tastier chapati; Rata for good dalia and better fodder quality and Bhati for excellent fodder for livestock were also collected from parts of Uttarakhand. Vivekanand Parvatiya Krishi Anusandhan Shala (VPKAS), Almora has also registered a landrace 'Tank' from Uttarakhand is known for long awns and small grains, which is not damaged by monkeys (Gupta *et al.,* 2009). Some of the local landraces/local cultivars *viz.*, Chanosi, Chini, Chotia safed, Chyud, Dapti, Dhang, Dhaulia, Dualatkhani, Dudgyn, Doldakhani, Dudh, Geruwa, Intor, Kanyari, Kavjhusi, Lal misri, Lalnoi, Mangraje, Munda gehun, Munar, Naulia, Pothi, Safed jhusia, Safed misri, Setta and Thull collected are also popular in the different pockets of hills of Uttarakhand (Mehta *et al.,* 2009).

Kharchia landrace, known for salinity tolerance is largely cultivated in saline areas of Barmer and Jalore districts of Rajasthan has been utilized for the purpose. The farmers in Sirohi, Pali, Nagaur, Churu and Jhunjhunu districts of Rajasthan use brackish water reserved in wells for irrigation of wheat fields. The landraces/ local cultivars *viz.*, Bajia, Contoli gehun, Chapadia, Deshi lal, Desi safed, Dhoiti, Dhola gehun, Mangsi, Pissi, Rata, Safed kanak and Pili kanak collected from these areas could be important source to utilize as salinity tolerant germplasm. Some other notable landraces/ local cultivars *viz.*, Dholia, Kharchia, Katta, Katbajya, Moti and Teria with long ear heads were also collected from Southeast Rajasthan. Likewise, Vajya, Lal gehun, Kharchia, Sachiya and Bundiya gehun in bread wheat; Popatiya and Putra gehun in emmer wheat and Kathia, Futel, Bansi, Arnej katha, Bhatiya desi, Dant khani and Poona giri in durum wheat were collected from salinity and drought affected districts of Gujarat (Ahmedabad, Amreli, Banaskantha, Bhavnagar, Jamnagar, Junagarh, Kachchh, Porbandar and Rajkot) and Rajasthan (Barmer, Jalore, Jodhpur, Pali and Sirohi) (Anonymous, 1976-2012).

In durum wheat, a medium tall variety Kathia collected from Madhya Pradesh was distinct from local landraces. It appeared in two forms (ear head colour) on maturity, one with reddish-brown ear heads and the other with whitish-yellow ear heads, extensively grown in Chhatarpur, Damoh, Dewas, Khargone, Raisen, Rewa, Satna, Shahdol and Sidhi districts of Madhya Pradesh (Arora and Koppar, 1979). A long culmed trait of landrace/ local cultivar Jautri identified as drought tolerant was collected from dry tracts of Madhya Pradesh. Some other notable landraces/ local cultivars *viz.*, Beligodi, Goi, Jawari kadli, Kolavi sadak, Lokapur sadak, Moolagodhi, Neeragodhi and Ravagodhi grown during *kharif* season in Karnataka exhibiting variability in plant height, tillers per plant, straw colour (yellow, dull yellow with brown tinge and shining yellow), ear length and grain colour (red/deep amber) were also collected.

Future Thrust

The gaps identified during exploration and collection of *Triticum* species indicated that representation of germplasm collections from Uttar Pradesh, Punjab and Haryana states was meager because landraces/ local cultivars have been replaced by high yielding hybrid varieties that narrowed down the genetic base in the area. In such situation, collection of landraces/primitive cultivars which have been grown by the farmers for thousands years in such areas can be of great help. Moreover, collection of wild Triticeae needs to be made to broaden the genetic base. Broadly all wheat growing states have been surveyed and assembled the diversity. However, based on gaps identified in the collection and genebank holdings, trait-specific and unique germplasm need to be assembled. Traits recorded in the field by the collectors need further validation through field evaluation studies. Keeping in view the diversity assessment of wheat *vis-à-vis* germplasm collected from diverse localities, thrust would be laid on the following:

- Cultivated species with important traits identified for abiotic stresses with their presence in respective priority areas *viz.*, intensive survey for heat tolerance in arid tracts of Rajasthan, Gujarat, Madhya Pradesh and Karnataka and for cold tolerance in Nilgiri hills of Tamil Nadu, Ladakh region of Jammu and Kashmir and Lahaul and Spiti of Himachal Pradesh.
- Collection of trait-specific landraces/local cultivars from areas prone to flood, drought, salinity, heat, cold and its detailed evaluation for validation of traits.
- Collection of wild and weedy relatives of wheat (wild *Triticaceae* such as species of *Aegilops*, *Elymus* and *Eremopyrum*) distributed mainly in western/ north-western Himalaya to enhance the genetic base of the wheat.

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SHORT COMMUNICATION

Stability for Yield and its Component Traits in Durum Wheat (*Triticum durum* Desf.)

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Fifty genotypes of durum wheat were evaluated over four diverse environments for grain yield and its component traits (tiller number, grains/spike and 100 grain weight). Genotype × environment interaction was found significant for all the traits except 100 grain weight. Further, linear component of G×E interaction was significant for 100 grain weight suggesting that the variation in performance of different genotypes could be predicted. The genotypes IDYT-CA-05-47, NI 146, PDW 215, IDYN 46 and IDYN 49 were found to desirable and stable across the environments for grain yield. Thus, these genotypes could be included in the hybridization programme to converge the stability characteristics of grain yield for the development of a stable variety adapted to wider range of environments.

Key Words: Durum wheat, G×E interaction, Grain yield, Linear component, Stability

Wheat is the second most important food crop in India after rice, both in terms of area and production. In any breeding programme it is necessary to screen and identify phenotypically stable genotype for yield which could perform more or less uniformly under different environmental conditions. It is an established fact that yield is a complex character (Whitehouse *et al.*, 1958) and largely depends upon its components characters, with an interaction with the environments resulting in to the ultimate product i.e. yield. So for breeding a stable variety, it is necessary to get the information on the extent of genotype×environment (GE) interaction for yield and its component characters. To meet the objective of developing varieties with high yield potential a wide collection of germplasm must be available so that the evaluation for desirable traits for yield can be exercised and a breeding programme for an ideal plant type concept can be made accordingly. A phenotype is the product of interplay of genotype and its environment. A specific genotype does not exhibit the same phenotype under the changing environments and different genotypes respond differently to a specific environment. This variation arising from the lack of correspondence between the genetic and non-genetic effects is known as genotype × environment interaction. G × E interactions are generally considered impediment in plant breeding as it baffles the breeder in judging the real potential of a genotype when grown in different environments. The existence of interaction between genotype and environment has been recognized by Fisher and Mackenzie (1923). Several workers considered G×E interactions as linear functions of environment and proposed regression of yield of a genotype on the mean yield of all genotypes in each environment to evaluate stability of performance of genotype (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Perkinis and Jinks, 1968).

The main objective of a breeding programme is to develop varieties that perform well over a broad spectrum of environments. According to Frey (1964), a variety having wide or good adaptability is one which gives consistently superior performance over several environments. Thus, the assessment of the nature and extent of genotype×environment interaction and identification of phenotypically stable genotypes, showing low genotypic×environment interaction, becomes important. This requires the screening of promising and stable genotypes over a set of environmental conditions. It is observed that the phenotypic response to change in environment is not the same for all the genotypes. The consequences of variation in phenotype depend upon the environment. Genotype-environment interaction are of major consequence to the breeders in the process of evolution of improved genotypes when the varieties/ genotypes are grown at several locations for testing their

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performance, their relative ranking do not remain the same, this cause difficulties in demonstrating significant superiority of any genotype. The information about phenotypic stability is useful for the selection of crop varieties as well as for breeding programmes. In durum wheat few studies are available on these aspects Kaya *et al.*, 2002; Benmahammed, 2010. The objective of the present study is to explore the effect of genotype (G) and genotype × environment (GE) on grain yield.

Materials and Methods

The experimental material for the present study comprised of 50 durum wheat genotypes made available from Directorate of Wheat Research (DWR), Karnal. These 50 durum wheat genotypes were grown in simple randomized block design experiment (RBD) in three replication as timely (22 Nov.) and late sowing (18 Dec.) for two years (2010-11 and 2011-2012) at Research and Demonstration Farm of Kisan (P.G.) College, Simbhaoli, Ghaziabad (UP) in each year, thus giving four environments. Each genotype was grown in a single row plot of 3m length with a distance of 25 cm and 10 cm between rows and plants, respectively.

All the recommended cultural and agronomic practices including pest control measures were adopted to raise good crop. To identify the comparative behavior of different genotypes under different environment, observations were recorded on five randomly selected plants for tiller number, grains/spike, 100-grain weight (g) and grain yield (g). In all the experiments, plot means (mean of five plants) were used for environment-wise analysis of variance and pooled analysis of variance for the estimation of G x E interaction effects and stability analysis as suggested by Eberhart and Russell (1966). In this model, regression coefficient (b) is considered as parameter of response and S^2d as parameter of stability. Assuming S^2d equal to zero, the high value of 'b' means more change in Y for unit change in I, in other words variety is more responsive. Such variety may, therefore, be recommended only for highly favourable environment. A relatively lower value of 'b' say around one, means less responsive to the environmental changes and, therefore, more adaptive. However, if 'b' is significantly less than one, the variety may be grown only in poor environment.

The unit value of 'b' considered as most desirable, indicating that the mean performance of a genotype increases with an average amount as conditions improve. The smaller values simply failure to take advantage of better environments, while larger values imply serious yield decline when environments are unfavorable. S^2d, if, significant from zero will invalidate the linear prediction. If S^2d is non-significant, the performance of a genotype for a given environment may be predicted. Accordingly, a variety whose performance can be predicted (i.e. $S^2d = 0$) is said to be stable. Here stability means predictability, or in other words phenotypic stability of individual variety is the function of two parameters, namely linear (b) and non-linear (S^2d) sensitivity coefficient.

Results and Discussion

The environment-wise analysis of variance (Table 1) was significant for all the traits in all the environments suggesting sufficient genetic variability in the material. One regression approach (Eberhart and Russell, 1966) has been applied to understand the genotype × environment interaction effects and stability of 50 genotypes grown under four environments. In the pooled analysis of variance for different traits also exhibited highly significant differences among the genotypes for all the traits further suggesting enough genetic variability among the genotypes (Table 2). The variances associated with genetic effects were smaller than the variances associated with environmental effects for all the characters i.e. the number of grains/spike, tiller number, 100 grain weight and grain yield which contradicted the observations of Rharrabti *et al.* (2003). This shows that under the present environmental conditions for determination of such characters, the genotypes need to be evaluated in multi environmental trials. Furthermore, the larger variances associated with genetic effects than the variances associated with genotype × environment for number of grains/spike, tiller number, 100 grain weight and grain yield indicates a greater influence and stability of genetic factors relative to the variability associated with the interaction of genotype × environment for these characters in durum wheat. Mean squares due to environments were also significant for all the traits indicating that the environments under study were diverse enough. Further, genotype × environment (G × E) interaction were also significant for all the traits except 100 grain weight suggesting that the traits responded to the environments differently. The G × E linear component was significant for 100 grain weight suggesting that the variation in performance of different genotypes is due to the regression of genotypes on environments and hence the performance is predictable in nature. The

List of genotypes used in the present study and their pedigree

S.No.	Name of Genotype	Pedigree
1	Macs-2856	CPAN 6079/MACS 2340
2	IDYT-CA-05-59	STJ3//Bcr/Lks4
3	IDYT-CA-05-40	Plc/Ruff//Gta/Rtte
4	IDYT-CA-05-48	Jori c69/Hau
5	IDYT-CA-05-47	FG. S. TAKCO, G11'S' (BAXI/E2198)
6	NI-146	Old released variety pedigree not available
7	PDW-215	RAJ 911//AA'SD#2E/3/DWL 5002
8	Behar Wheat	A land race of bread wheat type
9	Bejaga Yellow	M. LOCAL/GAZA
10	DWL-5023	CR'S'-LD'S'-GR'S'
11	NI-59	Released variety
12	Kiran	BIJAGA-YELLOW/A-206
13	MPO-215	Released variety
14	MASA-35	Exotic line of durum
15	Malwa Raj	Released variety
16	PKD-5	Released variety
17	JAI	Released variety
18	HD 4502(Malvika)	PI'S72*BY//TC60/3/ZENATI/BTL//WLS
19	Meghdoot	HI-6-23/HY-23//NP-404
20	Jai Raj	Released variety
21	Motia	(S) LV-BOMBAY;(S) LV; BANSI
22	PDW 254	Advance durum line
23	Vijay	NATURAL CROSS MOTIA/KHP (dm)
24	HI -8381(MALVASHIRI)	Released variety
25	EC34	Jori c69/Hau
26	EC38	20048 Traikia (Mor)/Mrb5//Stj3
27	EC39	Bicrederaa1/Azeghar2//Icajihan25
28	IDSN-72	BELLAROI/4/BCRIS/BICUM//LLA RETA INIA/3
29	IDSN-148	SOOTY-9/RASON-37//LLARETA INIA/10/ALTAR 84
30	IDSN-49195	PLATA-7/ILBOR-1//SOMAT-3/3/SORA/2*PLATA-12
31	IDYN-46	PLATA-6/GREEN-17//SNITAN/4/YAZI-1/AKAKI-4//SOMAT-3/3
32	IDYN-49	SOMAT-3/GREEN-22/4/GODRIN/GUTROS//DUKEM/3/THKNEE-11/6
33	IDYN-76	SOMAT-3/GREEN-22/4/GODRIN/GUTROS//DUKEM/3/THKNEE-11/7
34	EDUYT-54	MAALI/6/MUSK-1//AC089/FNFOOT-2/4/MUSK-4/3/PLATA-3
35	DDW-01	PDW 233/DCB 25
36	DDW-05	GULAB/DCB 53
37	DDW-06	RASCON 30/3/CELTA//WH 896
38	IDSN-76	LABUD/NIGRIS-3//GAN/3/AJAIA-13/YAZI/10
39	IDYN-100	PH 896-21/5/BRAK-2/AJAIA-2//SOLGA-8/5
40	IDSN-236	PH 896-21/5/BRAK-2/AJAIA-2//SOLGA-8/3
41	EDUYT-64	TARRO-1/2*YUAN-1//AJAIA-13/YAZI/3/3/SOMAT-3/PHAX-1
42	RAJ-1555	COCORIT 'S'/RAJ 911
43	PDW 233	YAV'S'/TEZ ''S''
44	WH 896	STIL''S''/YAV'IS7/PEN''S
45	NI-5749	G-4-48*N59
46	IDYT-CA-0561	ICAMORTA0472/Ammar7
47	IDYT-CA-0562	Stj3Lks4
48	IDYT-CA-0563	Plc/Ruff//Gta/Rtte
49	IAIISWIP-D/1 DON06-IRR-41	OROBEL//BUSHEN-4/2*GREEN-18/8/GEDIZ/FGO
50	IAIISWIP-D/1 DON06-IRR-42	HUBEI//SOOTY-9/RASCON-37/3/2*SOOTY_9

Table 1. Environment-wise analysis of variance for yield and yield traits in durum wheat

Source of variation	d.f.	Mean squares			
		Tiller number	Grains/spike	100-grain weight	Grain yield
Environment I					
Replication	2	286. 75	131. 76	1. 07	243. 45
Genotypes	49	3. 24**	224. 89**	0. 99**	10. 41**
Error	98	0. 88	8. 04	0. 54	0. 75
Environment II					
Replication	2	292. 43	1. 92	00. 31	208. 42
Genotypes	49	3. 91**	9. 05**	0. 24**	3. 12**
Error	98	0. 92	0. 56	0. 03	0. 72
Environment III					
Replication	2	257. 77	9. 53	3. 15	110. 92
Genotypes	49	5. 54**	37. 52**	5. 45**	23. 48**
Error	98	0. 97	3. 13	0. 68	1. 83
Environment IV					
Replication	2	289. 99	1. 71	3. 26	124. 03
Genotypes	49	7. 02**	22. 03**	1. 54*	42. 70**
Error	98	0. 34	7. 4	0. 80	2. 30

*,**= Significant at P = 0. 05 level and P = 0. 01 level.

Table 2. Joint regression analysis for yield and yield related characters in durum wheat

Source of variation	d.f.	Mean squares			
		Tiller number	Grains/spike	100-grain weight (g)	Grain yield (g)
Genotype (G)	49	2. 10**	129. 64**	2. 49**	5. 14**
Environment (E)	3	51. 20**	10644. 36**	55. 23**	374. 97**
GXE	147	1. 16**	24. 41**	0. 39	3. 78**
E+GXE	150	2. 16	236. 81	1. 48	11. 20
E (linear)	1	358. 39**	74510. 46**	386. 62**	2624. 87**
GXE (linear)	49	0. 85	27. 68	0. 87**	3. 19
Pooled deviation	100	1. 19**	23. 39**	0. 30**	3. 80**
Pooled error	392	0. 60	9. 73	0. 48	0. 82

**= Significant at P = 0. 01 level.

mean square due for pooled deviation is significant for all the traits but mean square for G × E (linear) is non-significant for grains/spike, tiller number and grain yield suggesting that variation in performance of genotypes is entirely unpredictable. Similar to the present results the importance of G×E interaction in durum wheat have been recognised by several workers (Akcura *et al.*, 2009; Gohil and Jadeja, 2009; Mohammedi *et al.*, 2010, 2014; Sakin *et al.*, 2011; Hassan *et al*., 2013). Eberhart and Russell (1966) model has been extensively used in different crop plants.

The mean number of grains/spike (Table 3) ranged from 30.09 grains to 43.40 grains. The highest number of grains/spike was observed for genotype DWL-5023 and minimum number was recorded by the genotype Kiran. Among the 50 genotypes, seven genotypes namely IDYT-CA 0548, NI-146, PDW-215, DWL-5023, MASA-35, Motia and DDW-06 recorded the higher mean number of grains/spike than the population mean (33.95±1.82). Considering high mean performance and stability parameters together, five genotypes namely NI–146, PDW–215, Motia, MASA-35 and DDW06were found to desirable and stable performance across the environments for number of grains/spike. The mean tiller number ranged from 5.88 to 8.89 over the four environments. The genotype WH-896 recorded the highest number of tillers and MACS-2856 recorded the lowest number of tillers/plant. Among the fifty genotypes, seven genotypes namely MASA-35, Meghdoot, EC-34, IDYN-46, IDYN-49, IDSN-236 and WH-896 recorded the higher number of tillers/plant than the population mean (7.20±1.00). Considering high mean performance and stability parameters together, seven genotypes i. e. MASA35, EC34, IDYN46, IDYN49, IDSN236, WH896 and Meghdoot were found desirable and have stable performance across the environment's fortiller number.

Table 3. Estimates of stability parameters in 50 genotypes of durum wheat

S.No.	Genotypes	Grains/spike			Tiller number		
		$\bar{X}$	b	S^2d	$\bar{X}$	b	S^2d
1	MACS-2856	31.12	0.79	-6.66	5.88	0.79	0.31
2	IDYT-CA-05-59	30.77	0.88	-10.26+	6.87	0.48**	0.32
3	IDYT-CA-05-40	32.10	0.84	-8.38	7.63	0.94	1.92+
4	IDYT-CA-05-48	37.67	1.40**	78.75++	7.49	1.32*	1.75
5	IDYT-CA-05-47	33.69	1.03	-11.23	7.73	1.66**	0.31
6	NI-146	36.01	1.14	-0.83	7.34	1.61**	1.13
7	PDW-215	36.25	1.15	2.29	7.06	0.61*	0.14
8	Behar Wheat	34.01	1.00	-2.76	7.50	1.27	1.89
9	Bejaga Yellow	33.97	1.06	-0.83	7.39	1.08	1.23
10	DWL-5023	43.40	0.54**	602.24++	7.58	1.02	2.36
11	NI-59	33.13	0.99	-4.73	7.00	0.88	1.83
12	Kiran	30.09	0.96	-8.74	6.07	1.23	0.48
13	MPO-215	31.55	0.80	15.42	6.90	1.22	0.17
14	MASA-35	36.67	1.03	-11.35	8.84	1.35	0.24
15	Malwa Raj	31.45	0.77	43.68+	6.01	1.46*	0.26
16	PKD-5	32.81	0.96	-0.92	7.09	1.08	1.81
17	JAI	30.98	0.72*	36.04	7.63	1.01	2.15+
18	HD-4502	32.26	0.97	-12.18	6.46	1.18	1.28
19	Meghdoot	31.55	0.85	1.80	8.30	1.05	0.19
20	JAI RAJ	33.43	1.01	-10.75	7.37	0.93	1.18
21	MOTIA	35.83	1.00	-7.75	7.81	1.80**	1.44+
22	PDW-254	31.99	0.86	-5.72	7.46	1.61**	1.14
23	VIJAY	32.55	0.89	1.07	6.24	0.95	0.16
24	HI 8381	33.79	0.96	-9.02	7.08	0.67*	0.39
25	EC-34	35.14	1.14	-10.86+	8.39	1.14	-0.10
26	EC-38	33.02	0.94	-0.17	7.51	1.41**	1.07
27	EC-39	34.48	1.06	-7.65	7.39	0.71	1.81
28	IDSN-72	34.53	1.09	-5.29	7.20	0.78	0.65
29	IDSN-148	33.73	1.08	-9.99	7.17	0.62**	1.36
30	IDSN-195	35.06	1.08	-7.23	6.88	1.24	-0.02
31	IDYN-46	33.83	1.06	-7.47	8.81	1.13	-0.01
32	IDYN-49	32.82	0.91	-1.81	8.65	1.04	1.28
33	IDYN-76	34.86	1.06	-4.85	6.86	0.76	1.17
34	EDUYT-54	33.36	1.02	0.36	6.40	1.17	0.19
35	DDW-01	32.11	0.97	-11.81	6.92	0.35**	0.07
36	DDW-06	36.07	1.11	-11.57	7.42	0.72	0.52
37	IDSN-76	34.83	1.06	-7.52	7.36	1.50**	0.61
38	IDYN-100	32.86	0.99	-9.90	7.10	1.01	0.69
39	IDSN-236	35.21	1.12	-2.52	8.86	0.96	2.15
40	EDUYT-64	33.81	1.04	9.63+	7.48	0.70*	2.22+
41	RAJ-1555	34.07	1.00	-9.04	6.72	0.71	0.69
42	PDW-233	34.35	1.04	-4.65	7.49	0.64*	0.45
43	WH-896	34.68	1.04	-2.92	8.89	0.74	0.72
44	NI-5749	34.90	1.02	0.01	7.29	0.98	1.97
45	NI-5749	33.92	1.05	-0.49	5.95	0.32**	0.25
46	IDYT-CA-0561	33.57	1.00	12.02+	7.16	1.06	1.04
47	IDYT-CA-0562	35.09	1.15	11.22+	7.40	0.36**	1.23
48	IDYT-CA-0563	34.77	1.11	-5.60	7.08	1.21	1.61
49	IA11SWID-D/ IDON 06-IRR-41	33.95	1.12	0.88	6.91	0.72*	2.04+
50	IA11SWID-D/ IDON 06-IRR-42	35.38	1.16	-5.88	7.20	0.84	1.99
	Population mean	33.95			7.20		
	S.E. of Mean	1.82			1.00		

*,**= Significantly deviating from unity at P=0.05 at P=0.01 level, respectively.
+,++= Significantly deviating from zero at P=0.05 at P=0.01 level, respectively.

Table 4. Estimates of stability parameters in 50 genotypes of durum wheat

S.No.	Genotypes	100-grain weight (g)			Grain yield (g)		
		$\overline{X}$	b	S^2d	$\overline{X}$	b	S^2d
1	MACS-2856	3. 56	0. 90	0. 21	29. 79	1. 18	4. 62
2	IDYT-CA-05-59	3. 46	0. 76*	0. 15	31. 13	1. 06	10. 95
3	IDYT-CA-05-40	3. 60	0. 93	0. 26	32. 11	1. 29*	15. 16
4	IDYT-CA-05-48	3. 57	0. 91	0. 01	34. 71	1. 01	23. 38
5	IDYT-CA-05-47	3. 61	0. 86	0. 13	37. 66	1. 19	15. 58
6	NI-146	3. 22	0. 63**	-0. 04	35. 82	0. 97	18. 72
7	PDW-215	3. 82	1. 00	0. 55	36. 54	1. 18	15. 73
8	Behar Wheat	3. 89	0. 91	0. 35	33. 03	0. 65*	27. 61^{+}
9	Bejaga Yellow	3. 47	0. 90	0. 15	33. 59	0. 67*	14. 42
10	DWL-5023	3. 83	0. 93	0. 36	34. 34	0. 48**	29. 41^{+}
11	NI-59	3. 79	1. 00	0. 66	33. 20	0. 60**	17. 51
12	Kiran	3. 24	0. 85	-0. 02	26. 86	1. 01	6. 44
13	MPO-215	3. 31	0. 70	0. 03	31. 04	1. 26	2. 27
14	MASA-35	3. 17	0. 55**	-0. 03	34. 61	1. 41*	11. 67
15	Malwa Raj	3. 30	0. 85	0. 18	35. 85	0. 38**	53. 50^{++}
16	PKD-5	3. 44	0. 86	-0. 13	31. 36	1. 10	5. 45
17	JAI	3. 52	1. 01	-0. 03	28. 89	1. 48**	18. 54
18	HD-4502	3. 44	0. 63**	-0. 12	34. 90	1. 22	10. 74
19	Meghdoot	3. 32	0. 59**	0. 01	35. 63	0. 99	43. 41^{+}
20	JAI RAJ	3. 45	0. 78	-0. 07	34. 98	1. 30*	20. 78
21	MOTIA	3. 59	0. 88	-0. 09	34. 13	0. 78	59. 09^{++}
22	PDW-254	3. 54	0. 88	-0. 07	33. 13	1. 04	34. 86^{+}
23	VIJAY	3. 58	1. 04	-0. 02	30. 96	0. 95	17. 68
24	HI8381	3. 36	0. 73*	0. 20	30. 88	1. 06	11. 59
25	EC34	3. 05	0. 50**	-0. 09	32. 83	1. 33*	5. 19
26	EC38	3. 47	0. 87	-0. 04	35. 84	1. 37*	6. 59
27	EC39	3. 28	0. 49**	-0. 02	33. 55	1. 28	5. 79
28	IDSN-72	3. 53	0. 99	8. 12^{+}	35. 54	1. 26	30. 39^{+}
29	IDSN-148	3. 30	0. 66*	0. 06	34. 53	0. 85	30. 76^{+}
30	IDSN-195	3. 38	0. 82	-0. 06	32. 41	1. 19	26. 74
31	IDYN-46	3. 53	0. 78	-0. 06	36. 84	1. 12	11. 71
32	IDYN-49	3. 68	0. 97	0. 09	36. 87	0. 98	39. 36
33	IDYN-76	3. 33	0. 56**	-0. 05	32. 92	0. 28**	19. 56
34	EDUYT-54	3. 53	1. 05	0. 07	30. 90	0. 90	5. 24
35	DDW-01	3. 53	0. 84	0. 10	27. 89	0. 80	15. 09
36	DDW-06	3. 65	1. 34*	0. 05	32. 43	1. 32*	12. 86
37	IDSN-76	3. 99	1. 60**	0. 09	32. 20	0. 89	8. 70
38	IDYN-100	3. 73	1. 39*	-0. 07	35. 13	1. 06	32. 74^{++}
39	IDSN-236	4. 21	1. 75**	0. 51^{+}	34. 43	1. 17	28. 22
40	EDUYT-64	4. 15	1. 62**	1. 26^{+}	33. 86	0. 84	13. 00
41	RAJ-1555	3. 89	1. 45*	0. 29	34. 35	0. 90	11. 83
42	PDW-233	3. 84	1. 13	0. 09	30. 79	0. 79	34. 32^{++}
43	WH-896	3. 83	1. 13	0. 11	33. 49	0. 98	55. 12^{++}
44	NI-5749	3. 96	1. 59**	0. 46	35. 13	1. 55**	24. 59
45	NI-5749	3. 52	1. 08	0. 13	30. 04	1. 16	1. 93
46	IDYT-CA-0561	3. 50	1. 01	0. 14	29. 59	1. 27	6. 61
47	IDYT-CA-0562	3. 73	1. 47**	0. 25	34. 98	0. 41**	13. 17
48	IDYT-CA-0563	3. 94	1. 51**	0. 02	32. 97	0. 78	36. 60^{+}
49	IA11SWID-D/ IDON 06-IRR-41	3. 91	1. 68**	0. 79^{+}	33. 33	1. 32*	22. 45
50	IA11SWID-D/ IDON 06-IRR-42	4. 01	1. 63**	0. 67^{+}	36. 51	1. 09	35. 03
	Population mean	3. 58			33. 20		
	S.E. of Mean	0. 20			1. 73		

*,**= Significantly deviating from unity at P=0. 05 at P=0. 01 level, respectively.
+,++= Significantly deviating from zero at P=0. 05 at P=0. 01 level, respectively.

Similarly for 100-grain weight, the mean ranged from 3.05 g to 4.21 g (Table 4) over the environments. Among the fifty genotypes, IDSN236 possessed the heaviest grain (4.21 g/100 grains) and genotype EC34 possessed the lightest grain (3.05 g/100 grains) and thirteen genotypes were having higher grain weight than the population mean (3.58±0. 20). Considering high mean performance and stability parameters together, five genotypes namely NI59, PDW233, Behar Wheat, PDW215 and DWL5023 were found desirable and have stable performance across the environments for 100 grain weight.

The mean grain yield ranged from 26.86 g/plot (Kiran) to 37.66 g/plot (IDYT-CA-05-47). Among the fifty genotypes, IDYT-CA-05-47, NI 146, PDW 215, Malwa Raj, Meghdoot, Jairaj, EC 38, IDSN 72, IDYN-46, IDYN-49, IDYN-100, NI 5749, IDYT-CA-0562 and IASWID-D/IDON 06-IRR-42 showed higher grain yield than the population mean (33. 20±1. 73). Considering high mean performance and stability parameters together, the genotypes IDYT-CA-05-47, NI 146, PDW 215, IDYN 46 and IDYN 49 were found to desirable and stable performance across the environments for grain yield (Table 4). Since performance *per se* and stability are two independent attributes and were considered by different set of gene systems (Finlay and Wilkinson, 1963; Bucio-Alanis *et al*., 1969; Verma *et al*., 1978 and Singh and Gupta, 1984). The genotypes Meghdoot, IDSN 72 and IDYN 100 had high mean grain yield with average response (b=1), but these genotypes were unstable as these had significant deviation from regression. Further, the genotypes Jairaj, EC38 and NI 5749 were having high mean grain yield than the population mean and regression coefficient significantly greater than unity (b>1) hence these genotypes are specifically adapted for favourable environments. Furthermore, the genotypes Malwa Raj and IDYT-CA-0562 having higher mean grain yield than the population mean and regression coefficient significantly lesser than unity (b<1) hence these genotypes are specifically adapted to poor environments. The genotypes MACS 2856, IDYT-CA-05-59, Kiran, MPO 215, PKD5, Vijay, HI 8381, EDUYT-54, DDW-01 and NI5749 having lower mean grain yield than the population mean and unit regression (b=1), hence these genotypes are poorly adapted to all the environments (Table 3 and 4). Further, considering high mean performance and stability parameters together, the genotypes NI146, PDW215, Motia, MASA35 and DDW 06 for grains/spike; MASA 35, EC34, IDYN-46, IDYN-49, IDSN-236, WH896 and Meghdoot for tiller number; NI59, PDW233, Behar Wheat, PDW-215 and DWL 5023 for 100 grain weight were screened as desirable and stable (Table 3 and 4). It is also evident from Table 5 that the linear component of G× E was pre-dominant for grains/spike and 100 grain weight while the non-linear component was pre-dominant for tiller number and grain yield. The result of the present study indicated that none of the genotypes studied were consistently superior for all the traits and the genotypes NI-146 and PDW-215 for grains/spike and grain yield; IDYN-46 and IDYN-49 for tiller number and grain yield; PDW 215 for 100 grain weight and grain yield showed stability together (Table 6). The stable genotypes identified for different traits may be used as parents in future breeding programmes for the development of new strains with combination of stable traits.

Table 5. Magnitude of linear and non linear portion of G × E interaction for different characters

S.No.	Characters	Linear component (%)	Non-linear component (%)
1.	Grains/spike	54. 20	45. 80
2.	Tiller number	41. 66	58. 34
3.	100-grain weight (g)	74. 35	25. 65
4.	Grain yield (g)	45. 63	54. 37

Table 6. Genotypes showing stable performance for different characters (high mean, b=1 and S^2 d=0)

Characters	Stable genotypes
Grains/spike	NI 146, PDW 215, Motia, MASA 35 and DDW 06
Tiller Number	MASA 35, EC 34, IDYN 46, IDYN 49, IDSN 236, WH 896 and Meghdoot
100-grain weight (g)	NI 59, PDW 233, Behar Wheat, PDW 215 and DWL 5023
Grain yield (g)	IDYT- CA- 05- 47, NI 146, PDW 215, IDYN 46 and IDYN 49

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SHORT COMMUNICATION

Promising High Yielding Genotypes of Jojoba (*Simmondsia chinensis*)

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Jojoba (*Simmondsia chinensis*) is an underutilized shrub grown for extracted oil from seeds for liquid wax. Number of crosses were attempted among the selected parents of exotic collections grown at field genebank at NBPGR, Regional Station, Jodhpur. EC33198-Sel.5 for bold seededness and high yielding F_1 hybrid EC33198-Sel.1×EC99692 was obtained with 3 seeds/capsuile with regular bearing and high seed yield.

Jojoba (*Simmondsia chinensis*) pronounced as *ho-ho-ba* – an underutilized shrub is native of Sonaran Deserts in North-western states of America and Mexico and Baja California (Gentry and Howard, 1958; Benzioni, 1995). Jojoba oil is the liquid wax produced in the seed of jojoba plant. The oil percentage in the seed by weight is approximately 50% (Kureel *et al*., 2008). Jojoba oil is used as a replacement for sperm whale oil and its derivatives such as acetyl alcohol (Miwa and Rothfus, 1979). Jojoba biodiesel has been explored as a cheap sustainable fuel that can serve as a substitute for petroleum diesel (Selim *et al*., 2003). Jojoba oil is relatively shelf stable than other oils like safflower, canola and almond oils as it does not contain triglycerides (Widyan and Al, 2010; Al, 2013). The oil may also be used as a fungicide to control mildew (Bream *et al*., 2001).

In many regards jojoba oil has been found to be superior to the sperm oil for application in the cosmetics, pharmaceuticals, plastic industries (Benzioni, 1995). This oil is found as an additive in many cosmetic products, especially those marketed as being made of natural ingredients. A number of accessions introduced in India time to time, and few of them were high yielding and adapted to the climatic conditions of western Rajasthan. However, some of the introductions were high yielding and adapted to the climatic conditions of western Rajasthan. The promising progenies of introduced jojoba and developed hybrids have been identified to be high yielding, adapted to hot and arid climate and having comparative oil content in their seeds. These promising jojoba can be propagated and conserved in field genebank and also following the protocols developed by Tyagi and Prakash (2004) under *in vitro* micropropagation and medium term conservation.

Promising bold-seeded high yielding jojoba: The most promising genotype EC33198-Sel.5 (Fig. 1) is a selection from progeny of jojoba identified in the jojoba field of NBPGR, Regional Station, Jodhpur. Plant flowers in the month of January and February and fruiting continues from February to May. The mature seeds are harvested during the month of May-June in 4-5 pickings at an interval of te10n days. It has very bold seed size (100 fully developed seed weight = 118.6 g) whereas the nearest bold seeded accession to this is EC272473 (100 seed weight = 84.4 g) (Fig. 2). Thus seed weight of EC33198 sel.5 is 40.64% higher than the closest bold seeded accession. The average yield of EC33198-Sel.5 is 7.5 kg/plant.

Promising hybrid of Jojoba: Most of the introduced jojoba were poor in yield and had irregular bearing of capsules. Therefore, a number of crosses were attempted among the selected parents with the objectives of genetic improvement and to develop desirable high yielding hybrids that should be adapted to the climatic conditions of arid and semi arid regions.

The crosses were attempted using the progeny EC33198-Sel.-1 of introduced accession EC33198 as female parent and accession EC52039, EC99690 and EC99692 as a male parents. The seeds of F_1s of theses crosses were grown in the pots and transplanted in the field after one year. The identified shrub of jojoba hybrid of cross of EC33198-Sel.-1 × EC99692 flowered within two years of initial sowing and male and female

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Colour Pix ?????

Fig. 1. Promising jojoba plant progeny EC-33198 sel. 5 (left) and lower two rows of its bold seed and upper two rows of seeds of another accessions EC272473 (right)

Colour Pix ?????

Fig. 2. Jojoba hybrid NBPGR-1 gives high yield, regular bearing (right) and 2-3 seeds/capsule (left)

Table 1. Traits of identified promising accessions of jojoba at NBPGR, Regional Station, Jodhpur

Accession	Seed size (mm.) (Length × breadth)		No. of seeds/ capsule (up to)	Seed bearing habit	Seed weight (g)	Oil (%)	Yield/tree (Kg)
EC 33198	16.365	09.254	2	alternate	69.84	**	5.86
EC 33198-sel.5	**19.652**	**11.880**	**2**	**alternate**	**118.60**	**45.13**	**7.50**
EC 342567	14.694	10.353	2	alternate	68.18	49.90	4.37
EC 342563	13.547	09.460	2	alternate	49.87	52.00	4.50
EC 342571	13.273	10.022	2	alternate	54.39	52.00	5.04
EC 342589	13.982	10.865	2	alternate	55.82	51.10	5.15
EC 342593	14.255	09.938	2	alternate	63.57	50.00	5.85
EC 33205	16.124	10.728	2	alternate	71.38	**	5.80
EC 99690	15.362	09.258	2	alternate	71.06	**	4.30
EC 99692	18.464	10.634	2	alternate	68.55	**	5.66
EC 134349	16.711	09.982	2	alternate	70.63	**	5.10
EC 52039	14.184	11.255	2	Alternate	71.38	**	5.62
EC 267781	18.454	10.468	2	alternate	81.55	**	6.05
EC 272472	15.970	12.011	2	alternate	80.26	**	5.50
EC 272473	15.948	11.486	2	alternate	84.40	**	4.90
EC 279586	14.562	11.638	2	alternate	76.48	**	6.60
EC 33198-sel.1 × EC 99692	**17.698**	**11.869**	**3**	**regular**	**82.95**	**50.60**	**8.00**
EC 33198-sel.1 × EC 99690	16.238	09.473	2	alternate	81.68	**	5.90
EC 33198-sel.1 × EC 52039	17.120	11.084	2	alternate	79.01	**	5.35

** not estimated.

flowers were observed. The seeds obtained from this F_1 (EC33198-sel.-1 × EC-99692) shrub were larger in size than the seed size of the parents. The developed F_1 plant yielded 8 kg seed on an average annually and exhibited regular seed bearing habit. The parents of this F_1 plant had irregular bearing of seed. Interestingly, number of seeds of this hybrid/capsule were up to 3 whereas, both parents had 1-2 seeds/capsule. The estimated oil content in the seed of this hybrid was high (50.60%).

Thus, genotype EC33198-sel.-5 and hybrid shrub of cross EC33198-sel.-1 × EC99692 have great potential to commercialize in the waste arid and semi-arid regions of Rajasthan.

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SHORT COMMUNICATION

Introduction, Evaluation and Adoption of an Exotic Banana (*Musa* AAB cv 'Popoulu') (EC320555) to Kerala, India

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Introduction, characterization and evaluation of exotic *Musa* germplasm has been undertaken at the Banana Research Station (BRS), Kannara, Kerala since 1994, under the aegis of All India Coordinated Research Project (AICRP) on Tropical Fruits, with the view to widen genetic base of this important crop. An exotic cultivar 'Popoulu' belonging to the Maia Maoli/Popoulu group of the AAB genomic group was characterized and evaluated under Kerala growing conditions. Results revealed that 'Popoulu' is a potential dessert and cooking exotic banana cultivar, highly suited for preparation of chips with a recovery of 33%, similar to 'Nendran'. The higher bunch weight of 'Popoulu' contributes to higher yield of chips. 'Popoulu' has great potential for popularization amongst farmers of Kerela, as a profitable cultivar to complement 'Nendran' ecotypes.

Key Words: Banana subgroup, Characterization, Introduction, 'Maoli', 'Popoulu'

Banana is the most widely cultivated and consumed fruit cum vegetable species in the southern Indian state of Kerala. Various cultivars of banana are consumed at the green or half-ripe stage as a cooked starchy vegetable or ripe as a fruit. Edible forms of banana have been selected by farmers from the progeny of either one or two wild seeded diploid parent species**,** *Musa acuminata* Colla (A genome) and *M. balbisiana* Colla (B genome) with a wide diversity of diploid, triploid and tetraploid hybrids with widely differing properties and composition. More than 1,000 recognizable *Musa* cultivars distributed pantropically have been identified by taxonomists (IPGRI, 2006). Fifty per cent of the banana production in Kerala is confined to homesteads where a wide range of cultivars are accommodated in different cropping systems. While the French plantain (AAB) cultivar 'Nendran' is grown on a commercial scale in Kerala, the other cultivars *viz.* 'Palayamkodan' (Mysore), 'Rasthali', 'Njalipoovan' and 'Kadali' are integrated in the polyclonal system unique to Kerala. In the highly variable genomic group AAB, Plantain, Mysore, Silk and Padathi are the major subgroups, with 'Nendran', 'Palayamkodan', 'Poovan' and 'Nendrapadathy', the popular cultivars, respectively (Menon, 2000).

The center of origin of the banana is South-east Asia and the Pacific Islands extending from India to Papua New Guinea and including Malaysia and Indonesia (Marin *et al.*, 1998). A diverse selection of cultivars of *Musa* is thought to have arisen in South-east Asia along with the earliest development of agriculture many thousands of years ago (Sharrock *et al*., 2001). It is thought that the subsequent dispersal of edible bananas outside Asia was brought about solely by humans (Simmonds, 1962). This early dispersal of banana cultivars resulted in the development of distinct sub-groups of varieties in different geographic locations. Secondary diversification within the major groups of cultivated bananas is thought to have been the result of somatic mutations rather than sexual reproduction (Valmayour *et al*., 2002). Mutations affecting traits of economic or horticultural interest have been selected by farmers over the years and multiplied by vegetative propagation to produce morphotypes. Movement eastwards resulted in the development of a distinct group of AAB bananas cultivated throughout the Pacific Islands (Sharrock *et al*., 2001; Valmayour *et al*., 2002). These are known as the Maia Maoli/Popoulu group, and the progenitors of these bananas are thought to have been carried eastwards by proto-Polynesians from an area in or near the Philippines more than 4,000

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years ago (De Langhe, 1996). Today, amongst the several exotic groups of bananas occurring worldwide, the cultivated bananas in the Pacific Islands are unique in their high-level diversity (Daniells 1995; Kennedy, 2008). The Maia Maoli/Popoulu group are named after the 'Maoli' and 'Popoulu' bananas and 'Maia' being the Hawaiian term for bananas (Ploetz *et al*., 2007; Kepler and Rust, 2011). The Popoulu bananas domesticated in the Pacific region, comprise traditional cooking cultivars and are often referred to as 'Pacific plantains' because of their relationship with African plantains, which also belong to the AAB genome group. The cultivars in the Maoli-Popoulu are typically recognized by their plump, sausage-shape fruits that are either straight or slightly curved with rounded tips. They are also known as 'Hawaiian banana Popoulu', 'Plantain Popoulou', 'Banane à chair rouge', 'Banane de Nouvelle Calédonie'. The fruit has a salmon pink flesh, with smooth texture, no fibers and with a slightly acidic apple-like flavor that can be cooked or eaten fresh when it is ripe (Englberger *et al*., 2003a). Some types of 'Popoulu' are in danger of extinction (Sharrock *et al*., 2001).

Introduction, characterization and evaluation of exotic *Musa* germplasm has been undertaken at the Banana Research Station (BRS), Kannara, Kerala since 1994, under the aegis of All India Coordinated Research Project (AICRP) on Tropical Fruits (Menon *et al*., 2005). The goal is to finally make available suitable selected material to the farming community, to widen its genetic basket of cultivars. Amongst one of the earliest exotic introductions, 'Popoulu' (accession EC320555) was obtained from the National Bureau of Plant Genetic Resources (NBPGR), New Delhi, for its characterization and evaluation. The germplasm was acquired by NBPGR during 1991 from the erstwhile International Network for Improvement of Banana and Plantain (INIBAP), now known as the *Musa* International Transit Centre (ITC), Leuven, Belgium (accession ITC1135). There were no previous records of its cultivation in any part of India, and evaluation was initiated at BRS for the first time. Preliminary evaluation indicated its acceptability in terms of yield and quality, combined with resistance to Sigatoka (*Mycosphaerella sp.*), in India (Menon, 2000). The present work was undertaken to systematically characterize growth and yield traits of 'Popoulu' in the field at BRS, Kannara, and to carry out multi-location evaluation for its agronomic performance and assessment of farmers' acceptability.

In vitro rooted plantlets of 'Popoulu' obtained from NBPGR were hardened and multiplied in the field at BRS, Kannara. Standard agronomic practices were followed for raising the crop (KAU, 2011). During 1997-2000, morphological characterization was undertaken using standard descriptors for banana (IPGRI-INIBAP/CIRAD, 1996). Subsequently in three growing seasons (2003-2006), experiments were conducted in a randomized block design to evaluate 'Popoulu', with four local check cultivars of various AAB subgroups, namely, 'Nendran', 'Palayamkodan', 'Poovan' and 'Nendrapadathy'. Three growth parameters [pseudostem height (cm), pseudostem girth (cm), number of leaves] at bunch emergence, and three yield parameters [bunch weight (kg), number of hands/bunch, number of fruits/hand] at harvest and crop duration were recorded. During 2009-10 and 2010-11, detailed evaluation was carried out to compare yield traits [bunch weight (kg), number of hands/bunch, number of fruits/hand, fruit length (cm), fruit girth (cm), fruit weight (g), pulp-peel ratio] along with recovery of chips (%) of 'Popoulu' with 'Nendran'. Data were also recorded on incidence of Sigatoka leaf spot and rhizome root rot under prevailing conditions of Kannara. All growth and yield data were analyzed statistically and t-test was performed to test the significance. Micropropagation protocol was applied for the large scale multiplication of 'Popoulu' using to facilitate field evaluation at large scale.

Under Kannara conditions, 'Popoulu' plants exhibited robust and luxuriant growth and some selected descriptor states recorded are shown in Table 1. Amongst the morphological characters (Table 2), pseudostem height was tall (mean 295.6 cm) and girth was recorded as medium (mean 51.6 cm). Pseudostem was typically medium green in colour, with small blotches. Red pigmentation was observed only on the outer leaf sheaths. Leaves had intermediate habit, with a length to width ratio of 2.8. The petiole canal of the third leaf was open with erect margins, and red coloration was observed on petiole margins. The bunch hangs vertically and had a compact appearance (Fig. 1). Peduncle was glabrous. The rachis was pendulous, with a lanceolate male bud degenerating at harvest. Bracts were dark purple brown outside and orange red inside. Bracts were revolute and left a prominent scar on the peduncle upon falling. 'Popoulu' had light yellow compound tepal in contrast to the yellow-orange compound tepal of plantains.

Table 1. Salient descriptor states of 'Popoulu' (AAB) (EC320555)

Descriptor	Descriptor state
Pseudostem	tall
Pseudostem color	medium green
Pseudostem appearance	shiny
Presence of blotches	small blotches
Leaf orientation	normal
Petiole canal leaf III	straight with erect margins
Colour of leaves	medium green
Position of suckers	close to parent (vertical growth)
Inflorescence	falling vertically
Male bud type	normal, degenerating at harvest
Bunch	compact
Fruits	straight with blunt apex
Transverse section of fruits	rounded, slightly ridged
Immature peel colour	medium green
Mature peel colour	bright yellow
Remains of flower relicts at fruit apex	persistent style
Flesh texture	firm
Flesh colour	orange yellow
Fruit fall	persistent
Taste	sweet and starchy

Fig. 1. Bunch of 'Popoulu' banana at the time of harvest

Ripe fruit pulp had a striking resemblance to that of French plantain cv 'Nendran'. The cross section of fruits of 'Popoulu' was slightly angular, with blunt apex bearing flower relicts in the form of persistent style. The peel was thick and medium green in young fruits and turned bright yellow when ripe. The pulp colour was light pink when raw and orange yellow when mature, with a firm texture. The fruits were not palatable when raw, and become sweet/starchy at maturity. Seeds were absent in the fruit. Studies have shown that yellow or orange coloration of the edible flesh is a good indication of high carotenoid content in bananas; high carotenoid types help protect against vitamin A deficiency, anaemia, diabetes, heart disease, and certain cancers (Englberger *et al*., 2003 a, b, 2006).

Table 2 gives the comparison of mean values of growth and yield traits between 'Popoulu' and four local AAB checks. Plant height was significantly lower in 'Popoulu' (295.6 cm) as compared to 'Poovan' (331.0 cm) and 'Nendrapadathy' (272.6 cm) but comparable to 'Nendran' and 'Palayamkodan'. In terms of pseudostem girth, again 'Popoulu' was comparable to 'Nendran'. However, number of leaves were significantly higher in 'Popoulu' as compared to 'Nendran' as well as 'Poovan' (Table 2). Importantly, crop duration of 'Popoulu' (298 days) was the shortest and significantly less compared to all the tested checks, which ranged from an average of 311 to 358 days. Also bunch weight (17.5 kg) recorded in 'Popoulu' was significantly higher than that in other local AAB cultivars, ranging from 10.4 to 13.7 kg (Table 2). Number of hands/bunch was comparable to 'Poovan' and 'Nendrapadathi', but significantly higher than 'Nendran'. 'Popoulu' bunch bore more number of fruits/bunch than 'Nendran', but registering fewer fruits than other checks.

Table 2. Preliminary evaluation of 'Popoulu' (EC320555) in comparison to popular AAB cultivars

Variety	Plant height (cm)	Pseudostem girth (cm)	No. of leaves	Crop duration (days)	Bunch weight (kg)	No. of hands/ bunch	No. of fruits/ bunch
'Popoulu'	295.6^{c}	51.6^{c}	12.4^{a}	298.0^{d}	17.5^{a}	7.2^{c}	76.8^{d}
'Nendran'	301.0^{c}	50.6^{c}	9.8^{b}	311.0^{c}	10.7^{c}	5.4^{b}	56.0^{e}
'Palayamkodan'	305.0^{c}	59.0^{b}	12.8^{a}	313.6^{c}	13.7^{b}	9.8^{a}	168.0^{a}
'Poovan'	331.0^{a}	64.6^{a}	9.6^{b}	358.6^{a}	10.6^{c}	7.4^{c}	115.6^{b}
'Nendrapadathy'	272.6^{b}	58.8^{b}	13.0^{a}	322.4^{b}	10.4^{c}	6.6^{c}	102.0^{c}
CV	7.17	10.29	14.63	7.21	23.96	21.54	37.81

Values in a column followed by the same letter are not significantly different ($P < 0.05$)

Table 3. Performance of 'Popoulu' (EC320555) in comparison to 'Nendran' (2009-11)

Parameters	'Popoulu'	'Nendran'
Growth characteristics		
Plant height (cm)*	299.8[b]	311.5[a]
Pseudostem girth (cm)*	51.6[a]	50.7[a]
No. of leaves*	12.2[a]	10.7[b]
Days to flowering*	227.2[a]	220.1[b]
Crop cycle (days)*	301.0[b]	310.2[a]
Yield characteristics		
Bunch weight (kg)*	19.45[a]	11.21[b]
Number of hands*	7.60[a]	5.40[b]
Number of fruits*	79.20[a]	57.00[b]
Fruit length(cm)*	15.60[b]	24.00[a]
Fruit girth (cm)*	20.50[a]	13.50[b]
Fruit weight (g)*	267.90[a]	190.10[b]
Pulp peel ratio	3.30	3.10
Recovery of chips (%)	33.0	32.0

* t value=2.101

Values in a row followed by the same letter are not significantly different ($P < 0.05$)

Data on comparative traits between 'Popoulu' and 'Nendran' showed significant variation during detailed evaluation (Table 3). In general, 'Popoulu' appeared short statured than 'Nendran' with a shorter crop cycle. Bunch weight recorded in 'Popoulu' was superior to 'Nendran'. Thus, fruit yield of 'Popoulu' was significantly higher as compared to 'Nendran' (10.68 kg and 56 fruits/bunch). Though 'Popoulu' fruits were shorter than 'Nendran', fruit girth and weight were significantly more. The variety also accounted for higher pulp to peel ratio and recovery of chips (33%, Fig. 2). While 'Popoulu' displayed slight tolerance to Sigatoka leaf spot in comparison to Nendran, susceptibility to rhizome rot was high. Since the intensity of rhizome rot is high during monsoon, planting during August conferred some protection, as the harvest could be done before the onset of rains. It also displayed susceptibility to stem borer which could be managed by prophylactic sprays. Unlike 'Nendran' it is not vulnerable to wind damage and no staking is required.

Micropropagtion technique was successfully applied for large scale multiplication of 'Popoulu' plants resulting in the production of over 5,000 plants. The variety now under multi-locational testing in 10 locations, is being deployed as a dessert and cooking cultivar highly suited for preparation of chips. It is also useful for the preparation of a variety of snack items as that of 'Nendran'.

To conclude, 'Popoulu' is a potential dessert and cooking exotic banana cultivar, highly suited for preparation of chips with a recovery of 33%, similar to 'Nendran'. The higher bunch weight of 'Popoulu' contributes to higher yield of chips. Since the crop cycle is completed within one year, it can be accommodated in the annual cropping pattern preferred for banana in Kerala. Propping is not needed which would account for reduced cultivation costs. Thus, 'Popoulu' needs to be popularized amongst farmers of Kerala as a profitable cultivar to complement 'Nendran' ecotypes.

Fig. 2. Banana chips made from 'Popoulu'

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXIXth meeting held on May 5th, 2014 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 18 germplasm lines out of 84 proposals considered. 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. AC-42091 Bhundi (JRS-9) (IC0575277; INGR 14025), a Rice (*Oryza sativa*) Germplasm with Elongation Ability of Shoot

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The rice germplasm namely "Bhundi" (IC0575277; INGR14025; AC42091), a landrace was collected from the farmer's field in Village-Sahu sahi, Block-Dhamnagar, District-Bhadrak, Odisha state. Rice, the only cereal crop is grown in flood prone ecosystem. Uncertainty of rainfall is a major factor affecting the rice yield in South and South-east Asia, sometimes flash flood affects the crop stand seriously depending on duration of submergence stress which is considered as the third most important constraint to high yield in India, particularly in the eastern Indian States (Sarkar *et al.,* 2006). Quiescence and elongation are two opposite strategies by which rice adapts to flood depending upon the nature of flooding (Sarkar and Bhattacharjee 2011). The ethylene response factor genes *Snorkel1* (*SK1*) and *Snorkel2* (*SK2*) allow rice to adapt to deep water whereas *Submergence1A-1* (*Sub1A-1*) allows rice to acclimatize under flash flooding. Both *SKs* genes and *Sub1A-1* are connected with gibberellin biosynthesis or signal transduction, yet deep water and submergence-tolerant rice seem to have opposite flooding response; namely, escape by elongation or remain stunted under water until flood recedes (Xu *et al.,* 2006; Hattori *et al.,* 2009; Sarkar and Panda, 2009). However, rice plants that exhibit only limited elongation during submergence often show tolerance to flash flooding. The ideotype is not suitable if water level increases and then (i) stays at that level (ii) recedes only partly or (iii) recedes but then rises again and continues for longer duration (Sarkar *et al.,* 2006). Analysis of flooding pattern in rainfed lowland of South-east Asia reveals that about 20 million ha falls under medium-deep to deep and very deep ecology based on water stagnation. Here the ideal response to flooding is submergence tolerance (survival under water) together with some elongating ability (Sarkar *et al.,* 2006, Sarkar and Bhattacharjee, 2011). Incidences of flooding have been increased in recent years due to the extreme weather events such as unexpected cyclonic heavy rains and outflows of rivers that have inundated wider areas across many regions in Asia. Rice is the only cereal crop that is well adapted to the conditions of water logging or partial flooding or complete submergence. In areas where plant experiences both complete submergence and waterlogging a perfect blend of elongation and tolerance is required. The genotype namely "Bhundi" (IC0575277; INGR14025; AC42091) with SUB1 QTL possesses greater elongation ability and re-emergence growth among the SUB1 lines (Sarkar and Bhattacharjee, 2011). It could be employed for developing varieties for the locations where both submergence and water logging tolerance are required.

The morpho-agronomic traits of the germplasm are described in Table1. Minimal descriptors for characterization and evaluation of rice germplasm

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Table 1. Morpho-agronomic traits of Bhundi (IC0575277)

Characteristics	AC 42091(IC0575277) Bhundi
Early plant vigour	Intermediate
Coleoptile: Anthocyanin colouration	Absent
Basal leaf sheath colour	Green
Leaf blade colour	Pale green
Leaf pubescence	Glabrous
Leaf length (cm)	65.3
Leaf width (cm)	0.73
Ligule length (cm)	2.67
Days to 50 % flowering	123 (highly photo-sensitive)
Panicle exsertion	Well exserted
Stigma colour	White
Apiculus colour	Green
Number of effective tillers	8.7
Culm diameter (cm)	0.37
Plant height (cm)	174
Panicle length (cm)	29.8
Panicle type	Horizontal
Awning	Absent
Days to maturity	153
Seed coat colour (kernel colour)	Light brown
Grain length-breadth ratio	2.3
100 grain weight (g)	3.34
Hull colour (husk colour)	Straw
Threshability	Easy
Aroma	Absent
Grain yield/plant (g)	22.5
Abiotic stress note	Moderately tolerant (SES score= 3-5) to salinity stress at seedling stage

"BHUNDI" (JRS-9, CRRI AC-42091) (As per AICRP data).

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2. AC-42087, Kalaketki (JRS-4) (IC575273; INGR 14026), a Rice (*Oryza sativa*) Germplasm with Submergence Tolerance (20 days)

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The rice germplasm namely "Kalaketaki" (IC0575273; INGR14026; AC42087), a landrace was collected from the farmer's field in Village- Baharbil, Block-Dhamnagar, District-Bhadrak, Odisha state. Excessive rains during monsoon season adversely affect agricultural productivity in large areas of South and Southeast Asia by causing complete submergence of rice plants. The extent of injury and subsequent survival under submergence are influenced by the depth of flood water, the concentration of oxygen dissolved in water, *pH*, pre- and post-submergence carbohydrate content of plant, the degree of turbidity and damage to the photosynthetic apparatus (Panda *et al.,* 2006; Das *et al.,* 2009). In areas where typical flash-floods occur (water recedes to lower levels after complete submergence for 1-2 weeks), reduced underwater elongation is beneficial for survival because the elongating plants exhaust their energy reserves and tend to lodge as soon as the water level recedes (Sarkar *et al.,* 2009). Cultivars with *SUB1* (*e.g.* Swarna-Sub1, IR64-Sub1, Samba Mahsuri-Sub1) tolerate complete submergence for over 2 weeks, depending on floodwater conditions (Das *et al.,* 2009; Sarkar and Bhattacharjee, 2011), whereas some other cultivars withstand 3 weeks of complete submergence with greater variations in plant height and elongation ability under submergence (Table 1). These cultivars maintain greater dry biomass

Table 1. Survey of rice germplasm with *SUB1A* and *SUB1C* specific primers SC3 and ART5, respectively, and plant height, elongation of shoot and survival percentage due to 14 and 20 days of submergence

Cultivars	Primers		Plant Height (cm)		Elongation (%)		Survival (%)	
	SC3	ART5	14 DS	20 DS	14 DS	20 DS	14 DS	20 DS
Swarna-Sub1	(+)	(+)	37 ± 0.8	39 ± 1.3	54 ± 7.4	64 ± 2.5	88 ± 9.0	12 ± 2.5
IR64-Sub1	(+)	(+)	42 ± 4.0	50 ± 3.7	52 ± 11.8	62 ± 1.7	90 ± 3.3	30 ± 8.5
SambaMahsuri-Sub1	(+)	(+)	45 ± 4.1	48 ± 3.0	57 ± 10.6	69 ± 12.1	66 ± 7.8	14 ± 5.0
AC42087	**(+)**	**(–)**	**63 ± 2.2**	**67 ± 2.6**	**78 ± 7.3**	**81 ± 9.4**	**96 ± 5.2**	**85 ± 6.9**
IR42 (Susceptible check)	(–)	(–)	58 ± 3.6	NB	113 ± 12.6	NB	5 ± 1.6	0
FR13A (Tolerant check)	(+)	(+)	56 ± 4.5	59 ± 0.7	61 ± 5.4	63 ± 4.8	93 ± 3.3	78 ± 4.6
LSD*p<0.05			5	6	20	16	10	9

at the end of submergence and re-growth occurs fast during re-emergence. Identification of non-elongating, submergence tolerant cultivars with better agronomic traits is desired to develop new varieties. "Kalaketaki" is one such variety which can withstand up to 20-days of complete submergence and also has good regeneration capacity. This genotype would be of immense use as a valuable gene source in breeding new cultivars tolerant to complete submergence for longer duration. Table 2 presents the agro-botanical traits of Kalaketaki DS, days after submergence; NB, not obtained; Data are presented as mean ± standard deviation based on two years replication average data; Numbers of replication, 3; (+), designates presence; (-), designates absent.

Table 2. Minimal descriptors for characterisations and evaluation of rice germplasm "Kalaketaki" (IC05752273)

Characteristics	JRS-4 (Kalaketaki)
Early plant vigour	Good
Coleoptile	Green
Basal leaf sheath colour	Purple
Leaf blade colour	Green
Leaf Pubescence	Pubescent
Leaf length (cm	55.66
Leaf width (cm)	1.54
Days to 50 % flowering	130
Panicle exsertion	Well exserted
Stigma colour	White
Apiculus colour	Straw
Number of effective tillers	6.2
Plant height (cm)	160.6
Panicle height (cm)	26.1
Panicle type	Intermediate
Awning	Nil
Days to maturity	160
Seed coat colour (kernel colour)	Light Brown
Grain length-breadth ratio (mm)	1.89
100 grain weight (g)	1.72
Hull colour (husk colour)	Brown furrows on straw
Threshability	Intermediate
Aroma	Absent
Grain yield/plant (g)	21.55
Abiotic stress note	Submergence tolerant, Elongation ability and re-generation growth

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3. UAS-334 (IC0599612; INGR 14027), a Wheat (*Triticum aestivum*) Germplasm with Resistance to Foot Rot

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Foot rot of wheat caused by *Sclerotium rolfsii* Sacc. is a serious problem mainly in the rainfed ecosystem (Kulkarni, 1979; Naragund, 1981; Reddy *et al.,* 1971). This disease can cause yield loss in the range of 10-30%. Control of soil-borne pathogens is one of the greatest challenges facing agriculture. Soil fumigants can be effective but the cost is prohibitive except with high-value crops. Breeding for host plant resistance is the best strategy in addressing this constraint. In this context, the genotype UAS 334 (SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC) identified from the International Bread Wheat Screening Nursery-2003 (Line No. 227). This genotype exhibited complete resistance to foot rot with only 1-5 percent disease incidence. Further, it exhibited resistance to karnal bunt. Apart from resistance to diseases, this genotype also found to be potential for high grain yield which widens its scope for utilization in breeding programme.

Table.1. Performance of UAS 334 under coordinated multi-location evaluation for yield and foot rot disease resistance

Year	Mean yield (q/ha)			CD at 5%	Foot Rot	
					HS	AV
	UAS 334	GW-322	MACS-6222		UAS 334	
2011	44.8	40.3		5.0	0.9	-
2012	47.7*	44.9	43.20	1.4	3.3	0.7
2013	45.7*	42.3	41.6	1.6	2.7	0.4
Mean	**46.1**	**42.5**	**42.4**			

HS-Highest Score; Av–Average score; **Significant at 5 % level*

Morhpo-agronomic characteristics: The genotype UAS 334 was evaluated along with the check varieties GW 322 and MACS 6222 in Peninsular zone of India over three years from 2010-11 to 2012-13 (Table 1). Based on yield potential, it exhibited significant yield superiority over check varieties and showed about 8.4% yield advantage over GW 322 and 8.7% over MACS 6222. It exhibited distinct features in terms of profused tillering, erect growth habit and green foliage; spikes are tapering with medium in waxiness as well as in density with medium beak length.

Associated characters and cultivation practices: UAS 334 exhibited resistance to stem rust. It possesses stem rust resistant gene *Sr 31*. It has high protein content, hectoliter weight, sedimentation value and better grain appearance than the best check GW 322.

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4. RG-2822 (IC0346626; INGR 14028), a Castor (*Ricinus communis*) Germplasm Resistance to Root Rot (*Macrophomina phaseolina* tassi Goid)

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5. Tukdah-383 (T-383) (IC0610184; INGR 14029), a Tea (*Camellia sinensis*) Clone with Very High Darjeeling Flavour (147:100)

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It is a China Hybrid tea plant (*Camellia sinensis* var. T383) released in 1980 for large scale commercial plantation in Darjeeling hills. The leaf is semi erect, widely spreading frame, large hairy tip with high flavour (Flavour Index 147:100). Ovate shaped leaf, acuminate leaf apex and attenuate leaf base are unique characters of the germplasm (Barman, 2013). The plant is multiplied exclusively by vegetative propagation and genetically a good rooter. The clone is resistant to drought and blister blight disease but susceptible to red spider mite (Singh, 1989).The clone is suitable for planting in mid and low elevation of Darjeeling hills. The variety has been conserved at TTRI Clonal Proving Station, Ging Tea Estate, Darjeeling (altitude of 1200 m.s.l.).

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6. Phoobsering-312 (P-312) (IC0610185; INGR 14030), a Tea (*Camellia sinensis*) Clone with High Darjeeling flavour (141:100)

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P312 – a China Hybrid tea plant (*Camellia sinensis* var. P312) was released in 1970 for large scale commercial plantation in Darjeeling hills (Ann. Sci. Rep., 1970-71). It is a China hybrid progeny and long term agricultural trial was conducted before release at TTRI Clonal Proving Station (CPS) at Ging tea estate (altitude of 1200 m.s.l.) of Darjeeling hills. Leaves are semi erect, dark green having pronounced serration and matty foliage (Sarkar *et al*., 1975). Leaf shape is lanceolate with acuminate apex and attenuate leaf base. Single leaf cuttings are good rooter in the nursery. The tender shoots are slender, densely haired (pubescence) producing golden tippy tea. Volatile flavour compounds like linalool and linalool oxides which produce sweetish flavour of tea liquor were found higher in Darjeeling cultivar P312 (Bhuyan *et al*., 2012). The orthodox made tea has high flavour (Flavour Index 141:100). The clone is conserved at TTRI Clonal Proving Station, Ging T.E., Darjeeling.

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7. Tukdah-246 (T-246) (IC0610186; INGR 14031), a Tea (*Camellia sinensis*) Clone with Unique Darjeeling flavour (138:100)

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Cultivar Tukdah 246 (*Camellia sinensis* var. T246) is a China Hybrid tea clone developed through progeny selection and released in 1973 to the tea industry for large scale plantation in Darjeeling hills (Grice and Bezbarua, 1973). Leaves are large and semi erect spreading frame with thin branching habit. The tender shoots are large in size with thick pubescence (Sarkar *et al*., 1975) and orthodox tea of high flavour (Flavour index 138:100) can be manufactured. The clone is a good rooter yet susceptible to drought (Singh, 1989). The leaf shape is ovate with acuminate leaf apex and obtuse base (Barman, 2013). The clone is susceptible to blister blight disease and red spider mite. It is a suitable clone for planting in both mid and low elevation of Darjeeling hills. The clone is conserved at TTRI Clonal Proving Station, Ging T.E., Darjeeling for further multiplication as and when required.

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8. Ambari Vallai-2 (AV-2) (IC0610187; INGR 14032), a Tea (*Camellia sinensis*) Clone with High Flavour Index (134:100), High Pubescence, Spreading and Dense Frame

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Variety Ambari Vallai 2 (*Camellia sinensis* var. AV2), a China Hybrid was developed through progeny selection and released to the tea industry of Darjeeling in 1973 (Grice and Bezbaruah, 1973). Semi erect leaf, less spreading frame of erect growing habit, high pubescence in the unopened apical buds, good rooting ability are the characteristic features of the clone (Sarkar *et al*., 1975).The leaf shape is lanceolate having acuminate apex and attenuate base (Barman, 2013). The clone has high Darjeeling flavour (Flavour index 134:100) but susceptible to drought and fairly resistant to Red spider mite and blister blight disease. It is a high yielding variety (Sarkar *et al*., 1975) and suitable for planting in mid elevation of Darjeeling hills. The clone is conserved in TTRI Clonal Proving Station, Ging T.E., Darjeeling for multiplication and other use in breeding programme.

References

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9. Bannockburn-157 (B-157) (IC0610188; INGR 14033), a Tea (*Camellia sinensis*) Clone with High Darjeeling Flavour (131:100)

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Bannockburn 157 (*Camellia sinensis* var. B157), a China Hybrid clone was developed through progeny selection and released in 1970 for large scale commercial cultivation in tea industry of Darjeeling hills (Sarkar *et al*.,1975). The plant has semi erect dark green elliptical leaves with down turn acute apex and obtuse leaf base (Barman, 2013). The bush frame is narrow and compact. The unopened buds and tender leaves bear thick pubescence contributing to the quality of made tea of high flavour (Flavour Index 131:100). The clone is susceptible to frost, mites and blister blight disease but tolerant to drought (Sarkar *et al*., 1975). The clone grows well in high and mid elevations of Darjeeling. The clone is conserved in TTRI Clonal Proving Station at Ging T.E., Darjeeling, for distribution of cuttings to the member estates and further use in research and development works.

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10. Kopati 1/1(K1/1) (IC0610189; INGR 14034), a Tea (*Camellia sinensis*) Clone with High Darjeeling Flavour (129:100) and Early Flusher

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Early flusher clone Kopati 1/1 (*Camellia sinensis* var. K 1/1) was developed through progeny selection and released in 1985 for large scale commercial cultivation in tea industry of Darjeeling hills (Singh, 1985). It is an Assam Hybrid quality cultivar with high Darjeeling flavour (Flavour Index 129:100). Concentrations of quality determining components of Darjeeling orthodox black tea like trans-2-hexanal, linalool oxide II, linalool, methyl salicylate, geraniol and 2-phenyl ethanol were found higher in cultivar K1/1 (Bhuyan *et al*., 2012). The bush frame is compact and moderately spreading. The lanceolate dark green, matte leaf has the acuminate leaf apex and obtuse leaf base. The drought tolerant variety prefers the agro climatic conditions of mid and low elevations of Darjeeling hills (Barman, 2013).The clone is susceptible to mites and blister blight disease (Singh,1985). The plants are conserved in TTRI Clonal Proving Station at Ging T.E., Darjeeling, for distribution of cuttings to the member estates and further use in research and development works.

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Singh ID (1985) Clones for Darjeeling. *Two Bud* **32**:53

11. Bannockburn-688 (B-688) (IC0610190; INGR 14035), a Tea (*Camellia sinensis*) good flavour Darjeeling clone (128:100) with high Geranial content (20.74)

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Cultivar Bannockburn 688 (*Camellia sinensis* var. B 688) was developed through progeny selection and released in 1975 for large scale commercial cultivation in tea industry of Darjeeling hills (Sharma *et al*., 1975). It is a drought tolerant Assam Hybrid variety having lanceolate leaf with down turn acuminate leaf apex and attenuate leaf base (Barman, 2013). The semi-erect leaf has deep leaf bulation which is a unique character of the clone. It has good rooting ability and grows well in mid and low elevations of Darjeeling hills. The clone is susceptible to both mites and blister blight disease (Singh, 1989). Geraniol, linalool, methyl salicylate, 2-phenyl ethanol, trans-2-hexanol, linalool oxide II are the determining component for quality of Darjeeling orthodox black tea which were considerably higher in B 688 (Bhuyan *et al*., 2012). The clone is well protected in TTRI Clonal Proving Station, Ging T.E., Darjeeling for future research on tea improvement programme in Darjeeling hills.

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12. Tukdah-78 (T-78) (IC0610191; INGR 14036), a Tea (*Camellia sinensis*) Clone with High Darjeeling Flavour (121:100). Suitable for Mid & Low Elevation of Darjeeling

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Tukdah 78 (*Camellia sinensis* var. T78)-a China Hybrid tea variety was developed through progeny selection and released in 1978 for large scale commercial cultivation in tea industry of Darjeeling hills (Bezbaruah and Awasthi, 1979). It is a drought tolerant China Hybrid clone which bears Lanceolate leaf with acuminate leaf apex and attenuate leaf base. The clone is very vigorous in growth with erect leaf of dark green colour, easy rooting ability, thick but almost smooth leaf lamina (Singh, 1989). The yield potential is 54 % higher than the Darjeeling seed stock Nandadevi TS378 (Bezbaruah and Awasthi, 1979) and flavour index is 121:100. It is fairly tolerant to blister blight disease and Red spider mite but resistant to pink mite (Singh, 1989).It grows well particularly in

the mid and low elevations of Darjeeling hills (Barman, 2013). The cultivar is conserved in TTRI Clonal Proving Station at Ging T.E., Darjeeling for distribution of cuttings among planters of Darjeeling who are keen to propagate for planting and future breeding program for cultivar development.

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13. Teesta Valley-1 (TTV-1) (IC0610192; INGR 14037), a Tea (*Camellia sinensis*) Clone with Good Darjeeling Flavour (117:100)

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Teesta Valley 1 (*Camellia sinensis* var. TTV1)-a China Hybrid tea variety was developed through progeny selection and released in 1987 for large scale commercial cultivation in tea industry of Darjeeling (Singh, 1987). It is a clone of erect growth habit of moderately spreading frame having semi erect, yellowish green, medium size leaf. The clone bears Lanceolate leaf with acuminate leaf apex and obtuse leaf base and suitable for planting in mid and low elevations of Darjeeling hills (Barman, 2013). It has a moderately spreading frame with semi erect medium size leaves (Singh, 1989). The drought tolerant clone having good Darjeeling flavour (Flavour Index 117:100) with good rooting ability grows well in mid and low elevations of Darjeeling hills. The clone is susceptible to red spider mite and Blister blight disease. The clone has been conserved in TTRI Clonal Proving Station at Ging T.E., Darjeeling for distribution and multiplication as and when required.

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Singh ID (1989) Tea Breeding in Darjeeling. Proc. Joint Area Scientific Committee Meeting. Tea Research Association, Darjeeling. Nov. 9-11, 1989, pp 9-14.

14. Tukdah-145 (T-145) (IC0610193; INGR 14038), a Tea (*Camellia sinensis*) Clone with Above Average (110:100) Darjeeling flavour

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Tukdah 145 (*Camellia sinensis* var. T145)-an Assam Hybrid tea variety was developed through progeny selection and released in 1970 for large scale commercial cultivation in tea industry of Darjeeling (Ann. Sci. Rep., 1970-71). Spreading frame, flat leaf, thin plucking point in the plucking surface of the bush, low pubescence, average yield, good rooting ability are some of the morphological features of the cultivar (Sarkar *et al*., 1975). Quality of the clone is above average and Flavour Index is 110:100. Higher concentrations of flavour compounds like hexanal and t-2-hexanal were reported in T145 (Bhuyan *et al*., 2012). Leaf shape is Lanceolate with acuminate leaf apex

and attenuate leaf base.The clone is tolerant to drought (Barman, 2013) but susceptible to red spider, scarlet mite and blister blight disease (Singh, 1989). The clone is extensively cultivated in both mid and low elevations of Darjeeling hills. The plants of the variety have been conserved at TTRI Clonal Proving Station, Darjeeling for multiplication through vegetative propagation and for future breeding program in tea research and development in Darjeeling.

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15. A-9/69 of IISR (IC0537218; INGR 14039), a Nutmeg (*Myristica fragrans*) Germplasm with Bold Nut a, High Sabinene and Myrecene Content

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Nutmeg (*Myristica fragrans* Houtt.) is an important tree spice, yielding two spices, namely, the nutmeg (dried seed) and the mace (dried aril surrounding the seed). It is an evergreen, conical tree reaching a height of 10 metres, belonging to the family Myristicaceae. Dried nutmeg and mace are used as spice and also for extracting oil and oleoresins. Nutmeg has a tremendous potential in the spice industry for flavouring food and beverages and in the manufacture of value added products. It has immense medicinal properties and is used by the pharmaceutical industry. It is also used by the perfume industry to a limited extent. Myristicin, elemicin, sabinene and safrole constitute 80% of both these oils. Myristicin, elemicin and safrole are hallucinogenic compounds in nutmeg and mace oils and sabinene imparts sweetness to the produce. A large extent of variability exists in the composition and proportion of the major components in both nutmeg and mace oil. Based on the proportion/quantity of these compounds they can be utilized in various industries. The major applications of nutmeg and mace oils are in the pharmaceutical, food and perfume industry.

The main mandate of Indian Institute of Spices Research (IISR), Calicut, is collection, conservation, cataloguing and evaluation of germplasm in spices. The institute has conserved 484 accessions of nutmeg germplasm in the field repository. Nutmeg accession IC0537218 (INGR14039) was registered with NBPGR, New Delhi, as an unique germplasm. This germplasm is a selection from open pollinated seedling progeny raised from seeds collected from an elite mother tree from Burliar, Nilgiris and Tamil Nadu and conserved and evaluated at IISR, Kozhikode. This nutmeg fruit has very thick, entire, dark red coloured mace and very bold nut. Besides, it also has an added advantage of high sabinene and myrcene in the mace and nut oils. The fresh weight of IC0537218 mace ranges from 4.5 to 6.0 g and seed weight from 13to16 g in. The mace and nut of IC0537218 is rich in sabinene and myrcene (35.4% in nut oil and 29.4 % in mace oil). The morphological and quality parameters of this accession are given in Table 1.

Table1. Characterization and evaluation of IC0537218 accession of nutmeg

Plant characters	
Plant height of graft	4.5 to 5.0 m at 10 years
Stem girth at 60 cm	25.00 cm
Leaf size	Medium
Leaf shape	Elliptic
Flowering	Profuse
Male flowers (%)	0
Female flowers (%)	100
Age at first flowering of graft	4 years after planting
Arrangement of flowers	Single, rarely seen in clusters of 2
Colour of ripe fruit	Yellow
Colour of aril	Dark red
Colour of seed	Brownish black
Shape of fruit	Elongate/oblong
Size of nut	Bold
Mace	Entire, thick, dark red
Yield characters	
Fresh weight of fruit	75-100 g
Fresh weight of nut	13-16 g
Dry recovery of nut	70%
Fresh weight of aril	4.5 to 6.0
Dry recovery of aril (mace)	35%
Mean yield/graft at 10 year after planting	2000 fruits
Essential oil in nut	5.9
Dry nut yield/graft at 10 th year after planting	21 kg
Mace yield/graft at 10 th year after planting	4.2 kg
Essential oil in nut (%)	5.9
Essential oil in mace (%)	7.5
Oleoresin in nut (%)	9.1
Myristicin in nut oil (%)	1.6
Myristicin in mace oil (%)	9.4
Elemicin in nut oil (%)	1.4
Elemicin in mace oil (%)	0.07
Total fat content (%)	24.9
α- Pinene in nut oil (%)	7.1
A-Pinene in mace oil (%)	4.7
Sabinene+ Myrcene in nut oil (%)	35.4
Sabinene+ Myrcene in mace oil (%)	29.4

16. PSRKK-11287 (IC0436231; INGR 14040), a Chilli (*Capsicum annuum*) Germplasm with Purple Phenotype as a Morphological Marker

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Chilli (*Capsicum annuum* L.) with long history of cultivation, natural selection pressure and adaptability to different environments led to the origin of a great diversity of forms. Many landraces of chilli have been recorded in India, varying in shape, colour, size and pungency. As such there is a large scope for selection and breeding from *Capsicum* genetic resources for developing varieties suitable to different climates in India (Pandravada *et al*., 2007). Systematic characterization and evaluation of germplasm collections facilitate estimation of genetic diversity, identification of promising accessions and elite material for utilization in crop improvement programmes (Chapman, 1989). A number of landraces/ primitive cultivars were utilized either directly as a pure line selection for release as a variety and/ or as parental material in chilli improvement after proper characterization and evaluation (Gupta and Rai, 1994).

While characterizing and evaluating chilli germplasm at NBPGR Regional Station, Rajendranagar, Hyderabad, an interesting accession IC0436231 which was completely purple was observed. This accession has purple pigmentation in whole/ stripes on stem, node, leaf, pedicel, corolla, style, calyx and fruit and is also characterized by its erect flowers and fruits as well (Anonymous, 2006a, 2006b and 2010). This particular accession PSRKK-11287 (IC0436231) was collected from Mopidevi Village and Mandal, Krishna District, Andhra Pradesh and appeared to be a naturally occurring landrace with purple pigmentation (Pandravada, 2004). This genotype was characterized/ evaluated for a total of 54 qualitative and quantitative descriptors/states developed by IPGRI and NBPGR (IPGRI, AVRDC and CATIE, 1995 and Srivastava *et al*., 2001).

The purple chilli landrace (IC0436231) identified will be very promising as a distinct morphological marker. The purple pigmentation which acts as a gene marker is a dominantly inherited trait in the segregating progeny (Ahmad Nazeer *et al*., 1992). Hence, this accession assumes importance in the wake of plant variety protection as a parental material for crossing, wherein uniqueness and distinctiveness has to be brought in to the phenotypic/ morphological traits of varieties for differentiation between varieties already released and proposed for release. This accession can also be used as an inbred line for developing new varieties with the purple morphological marker as a trait for distinctiveness, uniformity and stability. There are a total of 13 accessions of chilli Registered under ICAR/ NBPGR (*www.nbpgr.ernet.in/ inventory of Registered Crop Germplasm/ reports*) and 96 chilli/ *Capsicum* Varieties/ Hybrids released in India (*www.nbpgr.ernet.in/ norv/ reports*) and none of them have this trait of purple pigmentation in the phenotype.

Morpho-agronomic characteristics: The brief morpho-agronomic description of the chilli accession IC0436231 is as follows: stem cylindrical, sparsely pubescent, length 20.7 cm and diameter 1.0 cm; plants erect, height 59.8 cm and canopy width 42.2 cm; branches 5.2; leaf ovate-lanceolate, sparsely pubescent, margin undulate, length 6.7 cm and width 2.9 cm; calyx margin dentate, annular constriction absent and sepals 5; corolla rotate and petals 5; anther blue; stigma exserted; fruit set low, erect, singular, small conical thick/stout and dark red on maturity; fruit length 2.9 cm, width 1.5 cm, pedicel length 1.9 cm and fruit weight 1.8 g; fruit shape at pedicel attachment obtuse and blunt at blossom end with smooth fruit surface; neck at fruit base and fruit blossom end appendage absent; pedicel persistent with fruit and stem; days to flowering 89 and maturity 146; fruits 31.7 and yield 55.8 g/plant.

The other traits of potential value include, purple stem; dark purple node; purple leaf; erect and solitary flower; purple pedicel; pigmented calyx; white with purple margin corolla and purple spot colour; purple style; purple fruit with anthocyanin spots when immature. The reaction of the genotype to different biotic/abiotic stresses is moderate to tolerant.

This accession can be grown in all chilli cultivating areas by adapting the local recommended package of practices. The purple genotype IC0436231, identified through characterization and evaluation enables as a

parent the incorporation of genes for several phenotypic traits which are purple and highly heritable as morphological markers (stem colour; nodal anthocyanin; leaf colour; flower/ fruit position; pedicel pigmentation; corolla colour; style colour; fruit colour at intermediate stage etc.) to bring in distinctness in the phenotype by genetic enhancement.

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17. SBT-12549 (IC0570408; INGR 14041), a Chilli (*Capsicum annuum*) Germplasm immune to Anthracnose caused by *Colletotrichum capsici*

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Chilli (*Capsicum annuum* L.) is a tropical and sub-tropical vegetable-cum-spice crop and India contributes towards major share of the world's production. Anthracnose caused by *Colletotrichum capsici* is one of the most devastating diseases in chilli growing ecosystems. The disease can cause losses up to 50% in the form of pre and post-emergence damping-off, premature fruit drop, mummification of unripe green fruits and fruit rot (Pakdeevaraporn *et al*., 2005). As the crop has lot of export potential, effective disease management following eco-friendly approach by growing resistant cultivars is a good alternate strategy. Although research workers identified certain resistant sources earlier, commercial cultivars of *C. annuum* resistant to anthracnose are yet to be developed. Therefore, the present investigation was carried out to identify diversified sources of resistance for utilization in resistance breeding programmes.

Chilli germplasm consisting of *C. annuum* (22) and *C. frutescens* (3) was screened in the greenhouse of NBPGR Regional Station, Hyderabad, for sources of resistance against anthracnose disease with "Pusa Jwala" as the susceptible check. The accessions were grown up to one month in the greenhouse and spray inoculated with a high spore load (5 x 10^6 conidia/ml) in an isolated chamber. At the time of spraying, it was ensured that ten seedlings were present in each pot and three such replications were screened. The seedlings in control pots were sprayed with sterile water only. Optimum conditions required for disease development were maintained.

Observations were recorded at weekly intervals on symptom development and seedling mortality and each seedling was given a score based on 0-4 scale (Bansal and Grover, 1969). Disease symptoms were observed 7 days after inoculation and observations were recorded up to 30 days. The per cent disease index (PDI) was calculated per replication and the mean of three replications was taken as the final score. Grouping of accessions based on PDI was as given in Table 1. The PDI among the accessions ranged from 0.0 (IC570408/ SBT-12549) to

Table 1. Reaction of chilli accessions based on artificial screening with *C. capsici* inoculum in green house conditions

Scale	Per cent disease index (PDI)	Accessions*	Reaction
0	0	IC570408	Immune
1	1- 5	–	Resistant
2	6 - 25	CA-960, SNTV-87	Moderately resistant
3	26 - 50	IC572480, PBC-474, Pusa Jwala, EC391082, EC628901	Susceptible
4	> 50	EC390030, EC391083, EC399574, EC596920, EC596940, EC599969, EC599992, IC255896, IC436231, IC570369, IC572469, IC572472, IC572475, IC570484, IC572490, IC572498, SNTV-88	Highly susceptible

100 (EC399574, EC599969, SB-12693 and SR-6428) at the end of four weeks after inoculation. It was observed that in all the accessions disease progressed gradually with time except in IC570408, which was completely free from disease throughout the screening period inspite of the heavy inoculum load used. The highly susceptible accessions (EC391083, EC599969, SB-12693 and SR-6428) with PDI of 100 were completely defoliated and dried within one month after inoculation.

The present investigation resulted in identifying an accession SBT-12549 (IC570408) as a promising diversified donor for incorporating resistance against anthracnose in to the backgrounds of existing promising varieties/elite material of chilli (Narendra Varma *et al*., 2012), which are lacking.

Morpho-agronomic characteristics of chilli (*Capsicum annuum* L.) accession (INGR-14041) IC570408 (SBT-12549)

The distinguishing morpho-agronomic characters of the chilli accession IC570408 are as follows: Stem colour (Green with purple stripes); Stem shape (Cylindrical); Stem pubescence (Sparse); Nodal anthocyanin (Dark Purple); Plant growth habit (Erect); Plant height (59.7 cm); Plant canopy width (44.3 cm); Branches (4); Leaf colour (Dark green); Leaf shape (Ovate-lanceolate); Leaf pubescence (Sparse); Leaf density (Dense); Flowers/axil (1); Flower position (Pendent); Pedicel pigmentation (Green); Corolla colour (White); Corolla spot colour (White); Petals (5); Anther colour (Pale blue); Filament colour (White); Style colour (White); Stigma exsertion (Exserted); Calyx pigmentation (Absent); Anthocyanin spots/stripes on fruits (Absent); Fruit colour at intermediate stage (Green); Fruit set (High); Fruit position (Pendent); Fruits/axil (1); Fruit colour at mature stage (Red); Fruit shape (Medium long slender); Fruit length (9.3 cm); Fruit width (1.6 cm); Fruit pedicel length (3.5 cm); 10 Dry fruit weight (17.2 g); Fruit shape at pedicel attachment (Obtuse); Fruit shape at blossom end (Pointed); Fruit surface (Wrinkled); Days to flowering (77); Days to maturity (134); Fruits/plant (63.3); Fruit yield/plant (108.9 g); Reaction to Anthracnose (immune).

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18. CNA-5 (IC0597395; INGR 14005), a Cotton (*Gossypium arboreum*) Germplasm inter-racial pigmented arboreum

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CNA-5 (Pigmented arboreum) is an inter-racial cross developed through introgression breeding. It has been derived from progenies of the cross between *G. arboreum* race indicum and *G. arboreum* race burmanicum through single plant selection.

By virtue of being derivative of races of cultivated species of *Gossypium viz. G. arboreum*, it is highly stable and tolerant to jassids and bollworms which do not require chemical insecticidal sprays thereby apt for organic cultivation of cotton. The unique feature of this genotype is that it possesses pigmented plant body which forms a morphological marker for its identification and easily differentiation from other genotypes even at seedling stage. At flowering it could be very well identified with its red colour flower (Table 1).

Table 1. Characteristic features of *G.arboreum* (IC0597395; CNA -5):

Trait	Feature
Plant height (cm)	115
Seed cotton yield (kg/ha)	1950
Lint colour	white
Boll weight (g)	2.89
Fibre length (2.5% SL length mm)	26.7
Fibre strength (g/tex)	18.1
Uniformity ratio	54
Micronaire value (Fineness)	4.8
GOT (%)	38
Tolerant to jassids, bollworm, bacterial blight and grey mildew	

The unique feature of this genotype is that it possesses pigmented plant body which forms a morphological marker for its identification. Pigmented plant body can easily differentiate it from other genotypes even at seedling stage. At flowering it could be very well identified with its red colour flower.

AWARD FUNCTION
AND
GENERAL BODY MEETING OF ISPGR

An Award Function of the Indian Society of Plant Genetic Resources (ISPGR), New Delhi, and its General Body Meeting (GBM) has been scheduled to be held on March 5, 2015. All members of ISPGR and Awardees are cordially invited. The meeting shall be held at the National Bureau of Plant Genetic Resources, New Delhi. Details of the programme shall be communicated separately.

For further enquires please contact, General Secretary, ISPGR, New Delhi (email : ispgr@nbpgr.ernet.in).

ANNOUNCEMENT OF AWARDS (2013-2014)

The Indian Society of Plant Genetic Resources is pleased to announce the following awards:

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Professor HY Mohan Ram

Former Professor of Botany, Department of Botany, University of Delhi

Dr Harbhajan Singh Memorial Award

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Principal Scientist & Head, Genebank, ICRISAT, Patencheru, Andhra Pradesh

Dr R K Arora Best Paper Award (2013)

to

Drs D Mohan, RK Gupta and BS Tyagi

for their paper entitled

"Meddling Wheat Germplasm to Augment Grain Protein Content and Grain Yield" published in the Indian Journal of Plant Genetic Resources, Volume 26(3): 202-206

Dr K L Mehra Award (2013)

for the best M.Sc. (PGR) student from IARI PG School during the 52nd Convocation (2014) to

Mr Manish Kumar Mittal

Dr K L Mehra Award (2014)

for the best M.Sc. (PGR) student from IARI PG School during the 53rd Convocation (2015) to

Ms Padmavati G Gore

FELLOWS OF ISPGR (2013)

- **Dr SR Pandravada**, Principal Scientist, NBPGR, Regional Station, Rajendranagar, Hyderabad, Andhra Pradesh.
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- **Dr Mukesh Kumar Rana**, Principal Scientist, Division of Genomic Resources, NBPGR, Pusa Campus, New Delhi.
- **Dr M Elangovan**, Principal Scientist, Directorate of Sorghum Research, Rajendranagar, Hyderabad, Andhra Pradesh.
- **Dr DR Bhardwaj**, Principal Scientist, IIVR, Varanasi, Uttar Pradesh.

The Society extends congratulations to all the awardees for their contributions and accomplishments in the field of plant genetic resources.

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GENERAL

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