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Short Communication

Character association and genetic divergence in teasle gourd (*Momordica subangulata* subsp. *renigera*)

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Teasle gourd (*Momordica subangulata* subsp. *renigera*) is very nutritious fruit vegetable (Ram *et al.* 2001; Singh *et al.* 2009) but they are still regarded as minor/underutilized crops in India. Root cuttings from one year old matured female and male clones are collected separately after the senescence of the crop. The sprouted root cuttings of female and male clones are usually planted in separate plots at a ration of 8-10:1 during spring-summer over trellises by the farmers of West Bengal. Female clones are pollinated manually either in the morning hours (9 a.m. to 11 a.m.) or the pollens from male clones are collected in the morning and used to pollinate female buds in the afternoon (4.30 a.m. to 6 a.m.) to get cent percent fruit setting. Eleven genotypes of teasle gourd were collected from the Gangetic plains (Nadia, Murshidabad, and 24 Parganas Districts) of West Bengal, North-eastern states (Assam and Meghalaya), and evaluated in a Randomized Block Design during 2010 with three replications. The crop was raised over trellises, made up of bamboos and nylon strings. Pollination was done by hand in the morning hours (9.00 a.m. to 10 a.m.). The observations were recorded for nine quantitative traits viz., days to 50% flowering, days taken from anthesis to edible maturity, internode length (cm), fruit length (cm), fruit girth (cm), fruit weight (g), fruit number per plant, seed number per fruit, and fruit yield per plant (kg) from the six plants per replication. Data were subjected to analysis of variance (Panse and Sukhatme, 1984). The genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (P.C.V.) were calculated by the formula given by Burton (1952). For the estimation of heritability (broad sense) and genetic advance as percentage of mean, the method of Hanson *et al.* (1956) was followed. Later correlation coefficients at genotypic and phenotypic levels were calculated (Johnson *et al.*, 1955). Path coefficient was done as per Dewey and Lu (1959). D^2 statistic was used for assessing the genetic divergence between populations (Mahalanobis, 1936). The grouping of the populations was done by using Tocher's method as described by Rao (1952).

The variance analysis showed that genotypes differ significantly among themselves for all the characters under study. The co-efficient of variation (CV) were below 12% for all the characters studied confirming the reliability of the experiment and also suggesting less G x E interactions. Phenotypic co-efficient of variation (PCV) agreed closely with the genotypic co-efficient of variation (GCV) for all the characters except days taken from anthesis to edible maturity and number of seeds per fruit but the magnitude of PCV was higher than GCV for all cases (Table 1).

The GCV ranged from 3.45% to 33.17%, while PCV ranged from 5.41% to 33.97%. High proportion of GCV to PCV is desirable in selection process because it depicts that the traits are mainly under the genetic control rather than the environment (Kaushik *et al.*, 2007). High to moderate GCV and PCV values were found for number of fruits per plant and fruit yield per plant, indicating the potential of simple selection for the improvement of these characters. These observations find support from the previous workers (Ram *et al.* 2004) who observed moderate GCV and PCV values for number of fruits per plant. The proportion of GCV in PCV observed in this study was generally high, ranging from 63.77% in number of seeds per fruit to 99.55% in fruit length. However, in this study, the proportion of genetic contribution to the overall phenotypic expression of most of the traits was very high. These traits are reliable for selection in genetic improvement of the teasle gourd genotypes. Traits whose expressions are environmentally dependent may not be

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reliable descriptors for morphological characterization (Samaee *et al.* 2003, Pandey *et al.* 2008). Therefore, their use as important discriminatory variable for teasle gourd classification studies seems relatively reliable.

Traits with high broad sense heritability estimates suggest that they have high genetic potential; the effect of the environment in determining them is low. Higher estimates of broad sense heritability (more than 90%) coupled with the higher genetic advance (more than 55%) for number of fruits per plant and fruit yield per plant is indicative of additive gene action and selection based on these parameters would be more reliable. These observations corroborate the findings of previous workers (Singh *et al.*, 2009; Ram *et al.*, 2004). On the contrary, moderate heritability and low genetic advance for number of seeds per fruit has been observed. High heritability accompanied (more than 80%) with low genetic advance (less than 24%) for days to 50% flowering, internode length, fruit length, fruit diameter and fruit weight indicated advancement of non-additive gene action and the high heritability is being exhibited due to favourable influence of the environment rather than genotypes. This result corroborates earlier observations of Ram *et al.* (2004).Low heritability and low genetic advance for number of seeds per fruit and days taken from anthesis to edible maturity indicated that selection based on this character will be less effective. Johnson *et al.* (1955) suggested that high GCV along with high heritability and genetic advance gave better picture for the selection of the genotypes than heritability values alone. The disparities of some results might due to use of genotypes belonging to mixture of species under different environmental conditions by previous workers.

Mutual association of traits is often expressed by phenotypic, genotypic and environmental correlations (Akinyele and Osekita, 2006). In the present study, genotypic correlation coefficients were higher than corresponding phenotypic correlation coefficients, indicating greater contribution of genotypic factor in the growth and development of these traits association (Table 2). Significantly (Pd”0.01) positive genotypic relationships were found for number of fruits per plant (r = 0.958) and internode length (r = 0.823) with fruit yield per plant. Traits (days to 50% flowering, days taken from anthesis to edible maturity and fruit length) with negative genotypic correlations imply that a lot of breeding programmes are needed to improve such traits.

Positive and significant (Pd”0.01) phenotypic correlations were observed for number of fruits per plant (r = 0.954) and internode length (r = 0.764) with fruit yield per plant. Significant phenotypic association between fruit number per plant and fruit yield per plant has been observed by previous workers (Saha *et al.*, 1991; Singh *et al.*, 2009) in *Momordica dioica*. Fruit yield per plant also exerted positive but insignificant phenotypic correlations with fruit weight, fruit diameter and number of seeds per fruit. On the other hand, significantly (Pd”0.01) negative correlations were exhibited for days to 50% flowering (r = -0.688) and

Table 2: Genotypic and phenotypic correlations and direct effects (phenotypic level) of eight characters on fruit yield of teasle gourd

Characters	rg with fruit yield per plant	rp with fruit yield per plant	Direct effects on fruit yield per plant at phenotypic level
Days to 50% flowering	-0.805**	-0.688*	0.079
Days taken from anthesis to edible maturity	-0.932**	-0.676*	0.230
Internode length (cm)	0.823**	0.764**	-0.203
Fruit length (cm)	-0.297	-0.291	-0.024
Fruit diameter (cm)	0.418	0.400	0.059
Fruit weight (g)	0.535	0.526	0.396
Fruit number/plant	0.958**	0.954**	1.263
Number of seeds/fruit	0.118	0.159	-0.028

* Significant at 5% level; ** Significant at 1% level; rg = Genotypic correlation coefficient; rp = Phenotypic correlation coefficient; Residual effect at phenotypic path = 0.069

Table 1: Mean, range and estimates of genetic parameters of teasle gourd genotypes

Characters	Mean	Range	GCV (%)	PCV (%)	GCV : PCV	Heritability (%) in b.s.	Genetic advance as (%) of mean
Days to 50% flowering	75.39	62.66 -81.66	7.15	7.87	90.85	82.49	13.37
Days taken from anthesis to edible maturity	17.58	15.00 - 19.33	6.68	8.66	77.13	59.55	10.62
Internode length (cm)	5.58	4.73 - 6.03	6.71	7.14	93.97	88.19	12.98
Fruit length (cm)	6.96	6.62 - 9.08	11.24	11.29	99.55	99.09	23.04
Fruit diameter (cm)	5.38	4.71 - 5.95	8.15	8.28	98.42	96.76	16.50
Fruit weight (g)	64.14	49.66 - 69.00	10.44	10.75	97.11	94.37	20.89
Fruit number/plant	20.09	12.33 - 32.33	27.70	28.76	96.31	92.78	54.97
Number of seeds/fruit	28.58	27.00 - 30.33	3.45	5.41	63.77	40.63	4.53
Fruit yield/plant (kg)	1.30	0.78 - 2.21	33.17	33.97	97.64	95.32	66.70

days taken from anthesis to edible maturity (r = -0.676) with fruit yield per plant. It could be implied that teasle gourd genotypes which flowered early would produce more fruit yield. Negative insignificant correlation between fruit length and fruit yield per plant has also been observed.

In the present study, the phenotypic correlations were partitioned into direct and indirect effects to identify relative importance of yield component towards fruit yield of teasle gourd. Fruit yield in teasle gourd is important as this is utilized as vegetable in India and abroad. Hence, the direct effect and positive association with fruit yield per plant was considered essential. Among the eight yield component traits, number of fruits per plant followed by fruit weight showed high positive direct effects on fruit yield per plant (Table 2). The direct selection for these two characters could be beneficial for yield improvement of teasle gourd since these characters also showed positive correlation with pod yield per plant. Though internode length, fruit diameter and number of seeds per fruit had significant positive correlation with fruit yield per plant but their direct effects were negative/negligible because of high positive indirect effects via fruit weight. In such case, direct selection based on these characters will not be very effective. Residual effect was very low (0.069) suggesting inclusion of maximum pod yield influencing characters of vegetable cowpea in the present analysis.

Based on the determination of divergence, all the eleven genotypes could meaningfully be grouped into two clusters (Table 3). Cluster I had the maximum of ten genotypes, Cluster II had only one genotype. In general, the pattern of distribution of genotypes from diverse geographical region into different clusters was random. It might be due to free and frequent exchange of genetic materials among the farmers of different regions. Differential selection pressure according to regional preference also produced greater uniformity in the germplasm. Formation of relatively small number of clusters in the present study indicated either common character constellation or mutual balancing of characters among the genotypes. Bharathi *et al.* (2010) also categorized twenty-six accessions of spine gourd (*Momardica dioica*) into three distinct groups. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as exchange of genetic stock, genetic drift, spontaneous mutation, natural and artificial selection are responsible for genetic diversity. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Environmental influence on the composition of cluster was also recorded earlier (Bharathi *et al.*, 2010) in *Momardica dioica*.

The intra-and inter-cluster distance among eleven genotypes revealed that Cluster I showed the maximum intra-cluster value (43.46) indicating that genotypes belonging in this cluster are diverse (Table 4). On the other hand, Cluster II had the minimum intra-cluster value (0.02). The maximum inter-cluster value was observed between cluster I and II (43.46) which indicated that the genotypes included in these clusters had the maximum divergence. Hence, intermating between the genotypes included in these clusters was expected to give transgressive segregates in the advanced generation. Kalloo *et al.* (1980) suggested that the crosses between selected varieties from widely separated clusters were most likely to give desirable recombinants. The top four characters which contributed most towards the genetic divergence (Table 5) were fruit yield per plant (34.54%) followed by fruit diameter (21.81%), average fruit weight (20.00%) and number of fruits per plant (20.00%).These characters may be used in selecting genetically diverse parents for

Table 3: Cluster classification and source of collection of eleven genotypes of teasle gourd

Cluster Number	Name of the genotype/Source
I	BCTG-1 (Nadia,W.B), BCTG- 2 (North 24 Parganas, W.B.), BCTG- 3 (Murshidabad, W.B.), BCTG-4 (Nadia, W.B.) , BCTG- 5 (Nadia, W.B.), BCTG-6 (North 24 Parganas, W.B.), BCTG-7 (Assam), BCTG-8 (Hooghly, W.B.), BCTG-9 (Meghalaya), BCTG-10 (Assam)
II	BCTG-11 (Nadia, W.B.)

Table 4: Inter- and intra-cluster distances of eleven genotypes of teasle gourd

Cluster Number	I	II
I	18.38	43.46
II		0.02

Table 5: Contribution of different characters (%) towards divergence.

Characters	Number of first rank	(%) contribution
Days to 50% flowering	0	0.00
Days taken from anthesis to edible maturity	0	0.00
Internode length (cm)	1	1.81
Fruit length (cm)	1	1.81
Fruit diameter (cm)	12	21.81
Fruit weight (g)	11	20.00
Fruit number/plant	11	20.00
Number of seeds/fruit	0	0.00
Fruit yield/plant (kg)	19	34.54

Table 6: Cluster means of nine characters of teasle gourd

Cluster/ Characters	Days to 50% flowering	Days taken from anthesis to edible maturity	Internode length (cm)	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruit number/ plant	Number of seeds/fruit	Fruit yield/plant (kg)
I	74.76	17.43	5.66	6.74	5.44	64.21	20.86	28.73	1.35
II	81.66	19.00	4.73	9.08	4.71	63.33	12.33	27.00	0.78

hybridization programme to exploit either maximum heterosis or to execute efficient selection in the segregating generation.The cluster means of eleven genotypes (Table 6) showed that the mean values of the clusters varied in magnitude for all the 9 characters. Considerable distances in cluster mean were observed for the characters like days to 50% flowering, fruit yield per plant. Cluster I was the highest pod yielder followed by Clusters II. Internode length, fruit diameter, fruit weight, fruit number per plant and number of seeds per fruit was found highest in Cluster I, whereas fruit length was highest in Cluster II. Thus, the maximum cluster mean was observed in Cluster I for fruit yield per plant, internode length, fruit diameter, fruit weight, fruit number per plant and number of seeds per fruit. Genotypes belonging to these clusters could be regarded as useful sources of gene for improving fruit yield of teasle gourd. Moreover, genotypes belonging to Cluster I had taken the earliest days to reaching 50% flowering and edible maturity which could be helpful for breeding an early plant type. Hybridization between genotypes belonging to Cluster I and Cluster II could combine higher fruit productivity with longer fruit.

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