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STUDIES ON GENETIC DIVERSITY OF BITTER GOURD (*MOMORDICA CHARANTIA* L.) GENOTYPES

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I. INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is one of the most important vegetable grown throughout the country. The origin of this crop is probably India with secondary centre of diversity in China. Among the cucurbits, it is considered a prized vegetable because of its high nutritive value and medicinal properties. India is endowed with large amount of genetic diversity based on morphological and agronomic characters. Analysis of genetic diversity and relatedness between species and among genotypes is useful in plant breeding programmes because it provides a tool for acurate organization of germplasm. Multivariate analysis (D^2 statistics and principle component analysis) helps in quantification of degree of divergence among the biological populations and assessing the relative contribution of different characters to the total divergence. Mahalanobis (1936) generalized distance estimated by D^2 statistics has been used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in plant breeding programme.The present study was therefore undertaken for assessement of genetic diversity among bitter gourd germplasm.

II. MATERIALS AND METHODS

The investigation on assessment of genetic diversity in bitter gourd was carried out at the experimental area of the Department of Vegetable Science, Punjab Agricultural University, Ludhiana, India during 2013. The experimental plant material comprised of 36 germplasm lines of bitter gourd originating from different agro-ecological regions of the country. These lines were evaluated in a simple lattice design of 6x6 with two replications. Ten plants were grown on raised beds of width 1.5 m at plant to plant spacing of 45 cm.

Data on five random competitive plants per treatment per replication were recorded. The recommended NPK fertilizer doses and cultural practices along with plant protection measures were followed to rise an ideal crop. Observations for the quantitative and biochemical were recorded on indiviual plant basis and the average was computed.

III. RESULTS AND DISCUSSION

The D^2 values of each pair of varieties were estimated after confirming that the varietal differences are highly significant for all the 20 quantitative characters including yield. The 36 genotypes were grouped according to Tochers method (Rao 1952) into 4 clusters (Table 1) depending on their genetic divergence. Group III had the highest number of genotypes (15) followed by group IV and group I with 12 and 6 genotypes respectively. Group II had only 3 genotypes.

Table 1 Clustering pattern based on horticultural traits

Cluster	Genotypes	No. of genotypes
I	Punjab Kareli-1, PBBG-2, PBBG-7, PBBG-11, PBBG-13, PBBG-31	6
II	PBBG-20, CO-1, Coimbatore long	3
III	Arka Harit, DBG-35, DBG-3, DBG-45, DBG-41, DBG- 44, DBG-40, Janupuri long, PBBG-3, PBBG-6, PBBG-9, PBBG-8, PBBG-40, Hirkani, PBIG-56	15
IV	Punjab-14, Pant Kareli -2, Solan Hara, Pusa Do Mausmi, Pusa Visesh, WBBG-6, WBBG- 48, WBBG-5, DBG-18, PBBG-1, PBBG-10, PBBG-14	12

The cluster means of 36 genotypes (Table 2) showed that the mean values of the clusters varied in magnitude for all the 20 characters. Cluster I showed the highest days to first male flower (66.67), days to first female flower (72.92), node to first male flower (5.83), node to first female flower (10.58), fruit length (13.58) and average fruit weight (35.39) and it is important to note that cluster I showed second highest yield per plant (1512.92) and lowest values for fruit width (2.46), number of seeds per fruit (1.58), moisture content (7.25) and vitamin C (93.31). The cluster II showed the lowest values for the traits like days to last harvest (132.17), number of fruits/plant (22.83), total yield per plant (582) and moisture content (89.27) and highest values for days to first fruit maturity (89.17), vine length at final harvest (215.17), vitamin C (118.84) and carotene content (0.82). The cluster III showed highest values for number of fruits per plant (67.63),number of seeds/fruit (10.03),moisture (92.45), total sugars (3.87),reducing sugars (1.93), non reducing sugars (1.92) and lowest values for anthesis of first female flower (65.97), node at which the first male flower appears (4.73), node at which the first female flower appears (9.03), days to first fruit maturity (75.87),fruit length (9.10), carotene (0.71). Cluster IV showed highest values for days to last harvest (156.38),fruit width (3.47),total yield per plant (1640.42), fruit cavity (2.43) and lowest values for anthesis of first male flower (55.29),vine length at final harvest (180.08), total sugars (2.31), reducing sugars (1.17), non reducing sugars (1.14). Fruit yield showed highest (1640.42) value in cluster IV and lowest (582) in cluster II.

Relative contribution of different characters towards total genetic divergence is given in Table 3 It is evident from that vitamin C (44.60%) contributed maximum towards total divergence followed by non reducing sugars (18.25%), moisture content (11.75%) and number of seeds per fruit (11.11%). These were potential traits which could be recognized as parameters, whereas node to first male flower (0%), days to last harvest (0%), yield/plant (0%),node at which the first female flower appears (0.16%),fruit length (0.16%),fruit cavity (0.16%) showed lower contribution toward total divergence.

Cluster analysis of 36 genotypes based on 20 horticultural traits were performed and a dendogram was prepared as shown in Figure 1. It was observed that all the genotypes were resolved into four major clusters. In one cluster the genotype Punjab Kareli-1 was quire diverse from rest of the genotypes in the same cluster. In the second cluster there were only three genotypes namely PBBG-20, CO-1 and Coimbatore long.This indicated that these genotypes are quite different from other genotypes and these may be originated from closely related genotypes. Third cluster was further subdivided into two clusters first subgroup has eight genotypes and second subgroup has seven genotypes. Some of the very closely related genotypes in this cluster are DBG-45 and DBG-40, PBBG-40 and DBG-3.

Table 2 Cluster mean across various characters

Cluster No./Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
I	66.67	72.92	5.83	10.58	81.25	154.00	13.58	2.46	41.75	35.39	1512.92	185.67	1.58	7.25	91.76	3.13	1.53	1.63	93.31	1.30
II	64.50	68.83	5.33	8.50	89.17	132.17	9.22	2.48	22.83	28.52	582.00	215.17	1.97	7.83	89.27	3.48	1.60	1.73	118.84	0.82
III	57.03	65.97	4.73	9.03	75.87	154.73	9.10	3.21	67.63	27.65	1427.47	184.20	2.35	10.03	92.45	3.87	1.93	1.92	107.78	0.71
IV	55.29	67.25	5.46	9.58	77.08	156.38	11.10	3.47	47.92	33.48	1640.42	180.08	2.43	8.67	91.38	2.31	1.17	1.14	99.12	0.81

1: Anthesis of 1st male flower
2: Anthesis of 1st female flower
3: Node at which 1st male flower appears
4: Node no at which 1st female flower appears
5: Days to 1st fruit maturity
6: Days to last harvest
7: Fruit length (cm)
8: Fruit width (cm)
9: No of fruits/plant
10: Average fruit weight (g)
11: Total yield/plant (g)
12: Vine length (cm)
13: Fruit cavity (cm)
14: No of seeds/fruit
15: Moisture content (g/100g)
16: Total soluble sugars (g/100g)
17: Reducing sugar (g/100g)
18: Non reducing sugar (g/100g)
19: Vitamin C (mg /100g)
20: Carotene (mg/100g)

Cluster I: Punjab Kareli1, PBBG-2, PBBG-7, PBBG-11, PBBG-13, PBBG-31
Cluster II: PBBG-20, CO-1 and Coimbatore long
Cluster III: Arka Harit, DBG-35, DBG-3, DBG-45, DBG-41, DBG-44, BDG-40, Jaunpuri long, PBBG-3, PBBG-6, PBBG-9, PBBG-8, PBBG-40, Hirkani, PBIG-56
Cluster IV: Punjab-14, Pant Kareli -2, Solan Hara, Pusa Do Mausmi, Pusa visesh, WBBG-6, WBBG- 48, WBBG-5, DBG- 18, PBBG-1, PBBG-10, PBBG-14

Cluster fourth comprises of 12 genotypes with seven genotypes in subgroup first and remaining five genotypes in subgroup second.

Table 3 Contribution of each character for genetic divergence

Character	%age
Anthesis of first male flower	1.43
Anthesis of first female flower	0.32
Node at which first male flower appears	0.00
Node at which first female flower appears	0.16
Days to first fruit maturity	0.63
Days to last harvest	0.00
Fruit length (cm)	0.16
Fruit width (cm)	0.63
No of fruits/Plant	2.70
Average fruit weight (g)	1.11
Total yield/Plant (g)	0.00
Vine length (cm)	2.22
Fruit cavity (cm)	0.16
No. of seeds/Fruit	11.11
Moisture content (g/100g)	11.75
Total soluble sugars (g/100g)	1.75
Reducing sugar (g/100g)	0.32
Non reducing sugar (g/100g)	18.25
Vitamin C (mg /100g)	44.60
Carotene (mg/100g)	2.70

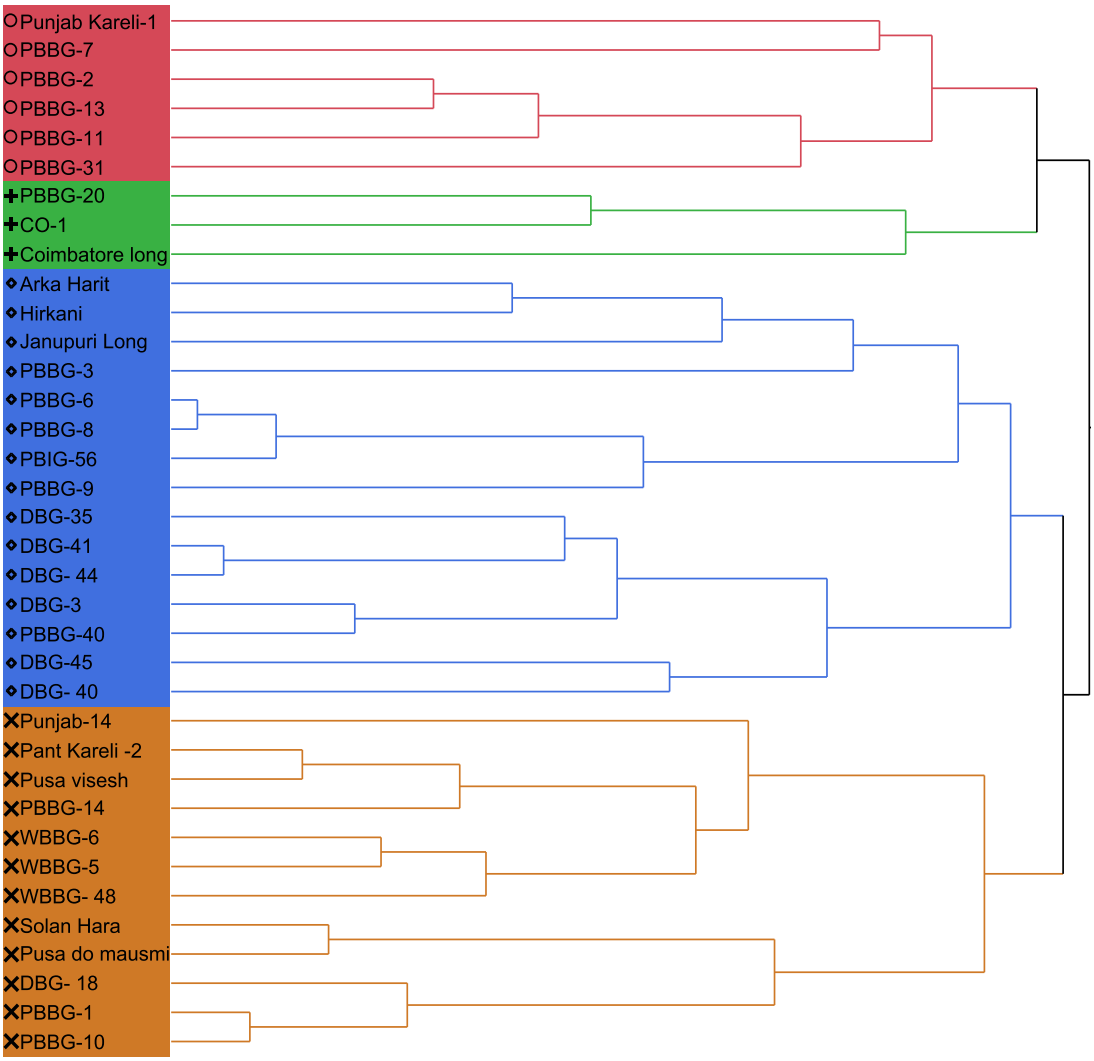
In general, the pattern of distribution of genotypes from different regions into different clusters was random. Similar observation was also reported by Waheb and Gopalakrishan(1993), Parthi *et al* (1993) and Joseph (2005) in bitter gourd. Kalloo*et al* (1983), Singh and Lal (2000) and More and Sheshadri (2002) in muskmelon. Reddy (2004), Knerr *et al* (1989) and Meglic *et al* (1996) in snapmelon. Mliki *et al* (2003) in cucumber and Levi *et al* (2001) in watermelon. One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of genetic material among the farmers and breeders in the country makes it very difficult to maintain the real identity of the genotype. 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 variation, natural and artificial selection are responsible for genetic diversity. It may also be possible that causes of clustering pattern were much influenced by environment and genotype x environment interaction resulting in different expression. Another possibility may be that estimates of diversity based on the characters used in the present investigation might not have been sufficient to account for the variability caused by some other traits of physiological or biochemical nature which might have been important in depicting the total genetic diversity in the population. Most of the commercially cultivated varieties came under cluster I and IV. It may be inferred from this result that almost all the commercially cultivated genotypes of our country originated from closely related sources.

The best cluster with respect to yield and other component characters represented by cluster I followed by cluster IV. It is also evident that except cluster II and cluster III (represented by small fruited genotypes) all the clusters showed higher yield potential than cluster IV which containing most of the commercially cultivated varieties. So, it may be concluded in bitter gourd, there is a vast scope to develop new varieties with more yield potential and other attributes of economic

importance by using the elite germplasm. To develop early varieties with more yield, selection from cluster IV will be more effective as it showed higher yield with early maturity. To breed good varieties in small fruited group, selection from cluster III will be highly useful and to breed long fruited varieties having some demand in specific region of our country, selection from cluster I and II will be useful.

The genotypes of different divergent clusters may be utilized in a dialled or line x tester fashion for effective exploitation of heterosis.

Fig 1 Dendrogram for bitter gourd germplasm lines based on horticultural traits



IV. CONCLUSIONS

The 36 genotypes were grouped according to Tochers method into 4 clusters depending on their genetic divergence. Group III had the highest number of genotypes (15) followed by group IV and group I with 12 and 6 genotypes respectively. Group II had only 3 genotypes which exhibited no association between geographical distributions of the genotypes.The cluster means of 36 genotypes showed that the mean values of the clusters varied in magnitude for all the 20 characters. Cluster I showed the highest days to first male flower (66.67), days to first female flower (72.92), node to first male flower (5.83), node to first female flower (10.58), fruit length (13.58) and average fruit weight (35.39) and it is important to note that

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