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Evaluation of Genetic Diversity in Bitter Gourd (*Momordica charantia* L.) under Subtropical Conditions of Garhwal Himalaya

Vivek Singh, D.K. Rana and K.N. Shah

Department of Horticulture, H.N.B. Garhwal University,
Srinagar (Garhwal), Uttarakhand, India

Abstract

In the family cucurbitaceae, bitter gourd (*Momordica charantia* L.) is one of the most important commercial crops in the point of economic and medicinal value. The experiment was conducted during summer season 2015, at Horticultural Research Centre, Chauras Campus and Department of Horticulture, H.N.B. Garhwal University, Srinagar (Garhwal), Uttarakhand, to assess the genetic diversity among the genotypes. The results indicated that there is large genetic diversity between the genotypes use in present study. The genotypes were grouped into 5 clusters based on Mahalanobis D^2 statistics using Tocher's method. The grouping pattern of genotypes revealed that among the 5 clusters, maximum numbers of genotypes were found in cluster III which comprises 6 genotypes, while clusters I and II comprises two genotypes each. The maximum intra clusters distance was observed in cluster IV and lowest intra cluster distance was recorded in cluster I. The cluster IV and V were strikingly diverse from rest of the clusters, the divergence between these two clusters was high as evident from their high inter cluster D^2 value. Therefore, the genotypes falling in these clusters were genetically more divergent. The results obtained in present investigation indicate that considerable diversity was available in the experimental material for converting the elite allelic resources though a systemic breeding. Therefore, selection of parents for hybridization should be done form different clusters having wider inter-cluster distance.

Key words: *Bitter gourd, Genetic, Diversity, Mahalanobis, Tocher's and Cluster.*

1. Introduction

Bitter gourd (*Momordica charantia* L.) one of the most important and popular cucurbitaceous crop grown in all parts of India for various purposes. It is highly rich in nutrients, medical properties and adoptable in various agro climatic conditions. Bitter gourd is use in different way like, boiled, curried, stuffed or sliced and also pickled. The fruit acts as an anthelmintic, stomachic, purgative, antibilious, carminative, anti-diabetic and laxative. A decoction of the root extract is helpful in abortion, hemorrhoids and also in biliaesness (**Khulakpam *et al.*, 2015**). India is a place of vast genetic variability of bitter gourd; mostly it is showed their variability in the morphological and also their fruit traits. The choice of any strains totally depends on the quality production and disease resistance. The selection of the strains is one of the most important factors in bitter gourd breeding and production. The different strains of bitter gourd have different yield potential, disease and pest resistance and are breed for various agro climatic conditions. Therefore, it is necessary to grow the defined variety in a defined area for good and quality yield. Basically, the selection of parental strains in bitter gourd breeding programs has been cleared on the basis of horticultural traits. There is scarcity of gene level data and the insufficient identification of the strains and also lack of proper estimation of the genetic diversity among bitter gourd lines. In addition, the continuous selection for the same traits like, yield in improvement programs has caused a reduction in diversity in bitter gourd strains. Through the estimation of genotypic and phenotypic correlations among yield and related traits has paved the basis for selection of superior genotypes from the diverse breeding populations. Genetic diversity arise due to geographical differences or due to genetic barriers to cross ability or due to different patterns of evolution be measured following D^2 statistics that measure group distance based on multiple characters (**Mahalanobis, 1928**) and it has become one of the important technique to assess genetic divergence on the basis of multiple traits. With the help of this technique, one can

easily predict strains which have high index scores and fell into different clusters can be crossed to have maximum variability of good combinations of different traits. **Rao (1952)** suggested the application of these techniques for the assessment of genetic diversity in plant breeding. Divergence analysis is being a powerful tool in quantifying the degree of divergence present at genotypic level based on phenotypic observations in different crops. The objective of this study was to establish genetic diversity within a collection of selected bitter gourd strains with important contrasting features under subtropical conditions.

2. Materials and Methods

The present investigation was conducted at Horticultural Research Centre, Chauras Campus, Department of Horticulture, H.N.B. University Srinagar, Garhwal, Uttarakhand (India). The experimental materials comprised of 20 strains of bitter gourd *viz.*, GP-1, HP-1, HP-2, JP-1, KVS-7, MN-1, MP-1, PDM, PSPB-14, RAJ- 1, RAJ-2, VRBTG-1, VRBTG-2, VRBTG-3, VRBTG- 4, VRBTG-5, VRBTG-6, VRBTG-7, VRBTG-8 and VRBTG-9 collected from different parts of India. The seeds were sown in the nursery bed on February and transplanting was done in March 2015. These plants are raised in randomized block design (RBD) which was replicated thrice with twelve plants in each treatments following a spacing of 1.5 x .50 m. Recommended package of practices for growing a healthy crop was followed to grow a successful crop of bitter gourd. The observation were recorded on five randomly selected plants per treatment from each replication for twenty growth, yield, quality and seed characters *viz.*, length of vine, diameter of vine, number of primary branches per vine, number of nodes per vine, days to opening of first male and female flower, number of nodes bearing first male and female flower, days to first fruit harvest, number of fruit per vine, fruit length (cm), fruit diameter (cm), fruit weight (g), fruit yield per vine (kg), fruit yield per plot (kg), number of locules per fruit, carbohydrate (g/100g), ascorbic acid (mg/100g), total soluble solids (^{o}Brix) and number of seeds per fruit. Genetic diversity was estimated by calculating **Mahalanobis (1936)** D^2 statistic. The genotypes were further grouped into different clusters as per Tocher's method **(Rao, 1952)**.

3. Result and Discussion

The analysis of variance revealed significant differences among the genotypes for almost for all the traits except number of nodes per vine and fruit length, that indicating adequate genetic variability present in the experimental material used for this research work. On the basis of D^2 values, twenty genotypes were grouped into five clusters which indicated a large genetic diversity between the strains use in present research work. The cluster III include six strains *viz.*, VRBTG-4, VRBTG-5, PSPB-14, VRBTG-6, GP-1 and VRBTG-8, cluster IV (VRBTG-9, MP-1, KVS-7, HP-1 and HP-2) and V (VRBTG-7, RAJ-1, RAJ-2, MN-1 and JP-1) includes five strains each and cluster I (PDM and VRBTG-1) and II (VRBTG-2 and VRBTG-3) included two strains each (Table 1).

Table 1. Distribution of 20 strains of bitter gourd in different clusters on the basis of D^2 statistic

Cluster	Number of genotype	Genotypes
I	2	PDM and VRBTG-1
II	2	VRBTG-2 and VRBTG-3
III	6	VRBTG-4, VRBTG-5, PSPB-14, VRBTG-6, GP-1 and VRBTG-8
IV	5	VRBTG-9, MP-1, KVS-7, HP-1 and HP-2
V	5	VRBTG-7, RAJ-1, RAJ-2, MN-1 and JP-1

Genotypes from different geographical regions were grouped in the same cluster indicating no relationship between geographic distribution and genetic divergence, while genotypes collected from same location were grouped into different clusters, showing great genetic diversity. Similar results were also obtained by **Rao *et. al.* (2003)** in cucumber; **Khan (2006)** in pointed gourd. The intra cluster distance was observed in the all clusters. This finding is in conformity with the findings of **Birari and Ghanekar (1992), Biju *et al*. (2001)** and **Ganesh *et al*. (2007)**. The intra cluster distance was observed in the clusters I, II, III, IV and V. Intra clusters distance was maximum in IV (54.165) followed by cluster III (53.882) and lowest in cluster I (41.721). The inter cluster D^2 values were maximum between cluster I and IV (111.041). The minimum distance was observed between cluster II and III (67.34), cluster IV and V was the most diverse as many clusters showed high inter cluster distances with it (Table 2.). Therefore, the genotypes falling in these clusters were genetically more divergent. Intercrossing the genotypes from these two clusters may generate wider variability and is expected to throw high yielding transgressive segregants in a population.

Table 2: Average intra and inter cluster D² values of bitter gourd genotypes based on 37 traits

Cluster	I	II	III	IV	V
I	**41.721**	67.801	99.594	111.041	111.002
II		**49.462**	67.34	68.219	88.346
III			**53.882**	68.001	81.249
IV				**54.165**	76.945
V					**53.727**

The minimum inter cluster D² value was observed between cluster II and III indicating high genetic relationship between genotypes of these two clusters. In heterosis breeding genotypes of diverse clusters are known to play an important role of potential parents and they are likely to produce heterotic combinations. In general, less intra-cluster distance than inter cluster distance suggested homogenous and heterogeneous nature of the genotypes within and between the clusters, respectively.

The mean values of 20 traits for five clusters are summarized in Table 3. The maximum vine length (323.25 cm) was reported in cluster IV, while the minimum (211.97 cm) in cluster I. The highest vine diameter (4.70 mm) was observed in cluster III, whereas lowest in cluster I (3.10 mm). The strains of cluster V showed maximum primary branches per vine (9.54), while minimum in cluster I (6.40). The number of nodes per vine was minimum (35.02) in the cluster I, whereas it was maximum (55.84) in the cluster IV. The days to first male flower (57.26 days) and female flower opening (61.37 days) was early in the strains of cluster III, whereas it was late (71.09 days) and (75.75 days) in the strains of cluster V respectively. The strains of cluster I showed minimum number of nodes at which first male flowers (7.26) appeared and it was maximum (9.21) in IV cluster. The strains of cluster II showed less number of nodes at which the first female flowers (11.82) appeared and it was maximum (14.16) in IV cluster.

The days to first fruit harvest was early (87.60 days) in III cluster strains, whereas late in (92.10 days) of cluster V. The cluster III showed maximum number of fruits per vine (42.70) and fruit length (19.01 cm), whereas (32.62) number of fruits per vine and fruit length (9.02 cm) minimum in cluster I. The maximum fruit yield per vine (3.37 kg) and fruit weight (89.51 g) was recorded in cluster IV and minimum in cluster I for fruit yield per vine (1.30 kg) and fruit weight (39.48 g). The strains of cluster V showed highest fruit diameter (4.35 cm) and it was less in cluster III for fruit diameter (3.30 cm). The cluster I showed maximum number of locules per fruit (4.00), while minimum (3.20) number of locules per fruit reported in cluster V. The strains of cluster IV showed highest fruit yield per plot (33.06 kg), whereas cluster I showed the lowest fruit yield per plot (15.52 kg). The strains of cluster III showed highest carbohydrate content (8.12 g/100g), whereas cluster V showed lowest carbohydrate content (4.95 g/100g). The cluster V showed highest vitamin C (91.82 g/100g), whereas cluster IV showed minimum (77.32 mg/100g) for vitamin C content. The maximum T.S.S (5.55 ^{0}Brix) was recorded in cluster II, while minimum in cluster I for T.S.S (5.25 ^{0}Brix). The highest number of seeds per fruit was recorded in cluster V (19.84), while cluster I showed (11.65) lowest.

4. Conclusion

On the basis of above results, it can be concluded that more emphasis should be given to improve number of nodes per vine, number of fruit per vine, number of primary branches per vine, days taken to opening of first male and female flower and fruit length, while making selection of high yielding lines in bitter gourd. Moreover, it will be effective to intercross genotypes belonging to more diverse clusters like clusters IV and III, while inter cluster D² values were maximum between cluster I and IV to create wide spectrum of variability and to produce transgressive segregants for fruit yield and yield contributing characters.

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Table 3: Cluster mean values of 20 characters in bitter gourd genotypes

Cluster	Length of vine (cm)	Diameter of vine (mm)	Number primary branches per vine	Number of nodes per vine	Days taken to opening first male flower	Number nodes bearing first male flower	Days taken to opening first female flower	Number nodes bearing first female flower	Days first fruit harvest	Number of fruits per vine	Fruit yield per vine (kg)
I	211.97	0.42	6.40	35.02	65.35	7.26	71.55	12.07	86.89	32.62	1.30
II	219.59	0.31	8.11	41.30	58.38	7.88	62.05	11.82	78.36	40.98	2.77
III	288.50	0.47	9.22	47.54	57.26	8.90	61.37	13.83	72.20	42.79	2.27
IV	323.25	0.41	8.32	55.84	59.67	9.21	64.06	14.16	77.72	37.81	3.37
V	295.08	0.44	9.54	50.44	71.09	8.91	75.75	13.71	92.10	42.49	2.57

Cont…..

Cluster	Length of fruit (cm)	Weight of fruit (g)	Diameter of fruit (cm)	Number of locules per fruit	Fruit yield per plot (kg)	Carbohydrate (g/ 100g)	Vit. C (mg/ 100g)	T.S.S (^{0}Brix)	Number of seeds per fruit
I	9.02	39.48	3.89	4.00	15.52	5.65	85.19	5.25	11.65
II	12.11	66.64	3.30	3.33	30.83	7.80	83.98	5.55	16.08
III	19.01	72.37	4.25	3.38	22.97	8.12	91.76	5.40	14.97
IV	18.98	89.51	4.15	3.46	33.06	5.55	77.32	5.27	15.03
V	18.91	74.55	4.35	3.20	29.38	4.95	91.82	5.45	19.84