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Analysis of Genetic Diversity among F_4 segregating population of bitter gourd (*Momordica charantia* L.)

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Abstract

Seventeen breeding lines (ten F_4 segregants and seven parents) of bitter gourd were evaluated at Department of Vegetable Science, OUAT, Bhubaneswar, during late kharif, 2022. These genotypes were used for evaluation of 13 quantitative characters which were grouped into five different clusters through Tocher's method of genetic divergence analysis. Cluster I consists of ten genotypes, Cluster II, III and IV comprising of two genotypes each, while cluster V included only one genotype. Highest intra cluster distance was found in cluster IV (17.14) while lowest in cluster II (8.70). The highest inter cluster distance was observed between cluster III and V (26.18), followed by clusters I and V (25.06). For future breeding programme in bitter gourd, genotype of Cluster V should be selected for better vegetative growth, earliness in appearance of 1st female flower and giving yield for longer duration. Similarly, Cluster III for earliness in appearance of 1st male flower and more number of fruits vine^{-1} while that of cluster II should be considered for getting high yield with less number of seeds fruits^{-1}. Seeds fruit^{-1} (61.03%) contributed maximum towards divergence followed by fruits vine^{-1} (12.50%).

Keywords: *Cluster Analysis, Genetic Divergence, Momordica Charantia*

1. Introduction

Bitter gourd (*Momordica charantia* L.) is an important monoecious cucurbitaceous vegetable crop extensively grown throughout the country. It is locally known as Bitter Melon, Karela, Maiden apple and Balsam pear etc. In terms of both nutrition and commercial point of view it is an important crop. The plant is mainly grown for immature fruits although the young leaves and tips are edible (Aruna and Swaminathan, 2012). The fruits can also be dried and pickled (Vinning, 1995). The fruit juice is very useful for diabetic patients due to its potent oxygen free radical scavenging activity (Sreejayan and Rao, 1991)

India annually produces 10,83,000 MT of bitter gourd from an area of 96,000 ha with a productivity of 11.28 tha^{-1} (NHB, 2021). This low productivity leads to decrease in farmer's income. Being an important vegetable crop, there is a need to develop varieties and hybrids suitable to specific agro-ecological conditions and also tolerant to different biotic stresses. Genetically diverse parents upon hybridization can result in productive hybrids and transgressive segregants with high heterotic effects. One of the present techniques of measuring genetic divergence is by Mahalanobis's D^2 statistic. The very purpose of D^2 analysis in the present investigation was grouping of all the 17 breeding lines of bitter gourd in order to assess the nature and extent of genetic divergence among them for further crop improvement programme.

2. Materials And Methods

The present study material was comprised of 17 genotypes (ten F_4 segregants and seven parents). This investigation was conducted at Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India during late *kharif* season, 2018. The experiment was laid out in Randomized Block Design (RBD) with three replications. The spacing

adopted was 1.75 m between rows and 1.25 m between pits. All the recommended package of practices were adopted uniformly to all the 17 genotypes in order to raise a good crop stand. All the observations were recorded from randomly selected four plants per replication for 13 traits *viz.*, vine length (cm), primary branches vine^{-1}, internodal length (cm), days to 1st male flower, days to 1st female flower, sex ratio (male:female), days to final harvest, fruit length (cm), fruit girth (cm), average fruit weight (g), fruits vine^{-1}, total green fruit yield (kg) and seeds fruit^{-1}. Mahalanobis generalized distance (D^2) was used to determine the degree of divergence and the genotype were grouped into clusters following Tocher's method (Rao, 1952).

3. Results and Discussion

Group constellation using D^2 statistics

The cluster derived using Tocher's method are presented in Table 1. The 17 breeding lines of F_4 segregants and parents used in the study were grouped on the basis of genetic closeness or divergence by D^2 into five Clusters. Cluster I was found to be the largest with ten genotypes that were PGG X NL, PGG X Priya, IK X Priya, IK X PDM, HL X Tushi, NL X Tushi, NL X Priya, NL X PDM, Tushi X PDM, Priya X PDM indicating the lack of significant genetic differences among them. Cluster II comprising of two genotypes such as PGG and IK. The parent NL and Tushi were grouped together in cluster III. Cluster IV includes PDM and HL. Cluster V include the single genotype *i.e.* Priya. The results clearly indicated that genotype of different geographical origin were grouped into a single cluster, indicating closeness genetically. The study also showed that selection of superior genotypes through hybridization programme should be based on their genetic diversity rather on the basis of geographical diversity. Similar results were also reported by Islam *et al*. (2010), Kundu *et al*. (2012), Reshmi *et al*. (2012) and Singh *et al*. (2014) in bitter gourd.

Table 1 Composition of D^2 based on clusters

Clusters	No. of breeding lines	F4 Segregants / Parents
I	**10**	Phule green gold X Nakhara Local Phule green gold X Priya Improved Kathi X Priya Improved Kathi X Pusa Do Mousumi Hirkani Local X Tushi Nakhara Local X Tushi Nakhara Local X Priya Nakhara Local X Pusa Do Mousumi Tushi X Pusa Do Mousumi Priya X Pusa Do Mousumi
II	**2**	Phule green gold (PGG) Improved Kathi (IK)
III	**2**	Nakhara Local (NL) Tushi
IV	**2**	Pusa Do Mousumi (PDM) Hirkani Local (HL)
V	**1**	Priya

Table 2 Average intra-cluster (diagonal) and inter- cluster distance (D^2 value) of 17 breeding lines (F_4 segregants and parents) of bitter gourd

Cluster	I	II	III	IV	V
I	12.26	19.88	14.27	21.36	25.06
II		8.70	21.11	11.65	21.55
III			15.27	22.91	26.18
IV				17.14	24.54
V					0.000

Table 3 Cluster means of 17 breeding lines (F_4 segregants and parents) of bitter gourd for 13 quantitative characters

Clusters	1	2	3	4	5	6	7	8	9	10	11	12	13
I	4.15	15.93	6.10	42.55	51.74	0.11	138.7	9.41	10.68	56.07	42.14	2.49	16.44
II	4.76	13.18	4.60	48.08	56.97	0.12	137.8	13.53	12.33	46.31	26.83	1.64	23.53
III	3.66	15.53	6.05	42.53	51.80	0.13	134.5	7.50	9.86	35.07	43.99	1.68	18.52
IV	3.85	14.88	3.90	45.25	56.60	0.15	133.6	10.36	13.06	53.55	30.80	1.66	22.83
V	5.05	17.00	5.26	44.66	49.70	0.26	139.9	16.03	9.66	53.61	21.86	1.88	18.24

1.Vine length 2. Primary branches vine-1 3.Internodal length 4.Days to 1st male flower 5.Days to 1st female flower 6.Sex ratio 7.Days to final harvest 8. Fruit length 9. Fruit girth 10. Average fruit weight 11. Fruits vine^{-1} 12. Seeds fruit^{-1} 13. Total green fruit yield

Table 4 Percentage contribution of each character towards total genetic divergence in 17 breeding lines (F_4 segregants and parents) of bitter gourd

Character	No. of first rank	% contribution
Vine length at the time of final harvest	2	1.47
Primary branches vine^{-1}	4	2.94
Internodal length	9	6.62
Days to 1st male flower	2	1.47
Days to 1st female flower	5	3.68
Sex ratio (M:F)	0	0.00
Days to final harvest	0	0.00
Fruit length	0	0.00
Fruit girth	12	8.82
Average fruit weight	1	0.74
Fruits vine^{-1}	17	12.50
Seeds fruit^{-1}	83	61.03
Total green fruit yield	1	0.74
Total	**136**	**100**

Intra and inter cluster divergence

Inter cluster distances were greater than intra cluster distances, revealing a considerable amount of genetic diversity among the genotypes studied (Table 2). These findings were in agreement with Kundu *et al*. (2012), Kumari *et al*. (2017) and Tyagi *et al*. (2017). Highest intra cluster distance was found in cluster IV (17.14), followed by cluster III (15.27) and cluster I (12.26). The least intra cluster distance was observed by cluster II (8.70) which consisted of two genotypes.

Similarly, inter cluster distance ranged from 11.65 (cluster II and IV) to 26.18 (cluster III and V). The results clearly indicated that the breeding lines included in these clusters were distinctly and distantly related to each other due to the presence of high inter cluster distance between cluster III and V (26.18). In general, the magnitude of heterosis primarily depends on the degree of genetic diversity between the parental lines. The greater the genetic divergence between two clusters, the higher is the difference between the genotypes. Therefore, hybridization between two diverse genotypes which differs distantly and distinctly produced more variability in subsequent segregating generations. It can be concluded that crosses involving cluster III (Nakhara Local and Tushi) with cluster V (Priya) can give desirable recombinants with maximum hybrid vigour in future study.

Characterization of D^2 based on cluster

Regarding characterisation of D^2 based on clusters, the results presented in table 3 indicated that Cluster I comprised of ten breeding lines and was found superior in sex ratio (0.11) and average fruit weight (56.07). The characters like seeds fruit^{-1} (1.64) and total green fruit yield (23.53) were reported superior in cluster II which comprising of two genotypes. Similarly, cluster III which include the genotypes Nakhara Local and Tushi was found superior for the traits days to 1st male flower (42.53) and fruits vine^{-1} (43.99). Internodal length (3.90) and fruit girth (13.07) were identified as superior in cluster IV (Pusa Do Mousumi and Hirkani Local). However, cluster V comprising of one genotype (Priya) was found superior in vine length at the time of final harvest (5.05), number of primary branches vine^{-1} (17.00), days to 1st female flower (49.70), days to final fruit harvest (139.90) and fruit length (16.03).

Contribution of each character towards divergence

The proportional contribution of characters towards the total D^2 statistics was different, which is represented in table 4. Seeds fruit^{-1} (61.03%) was the maximum contributors towards total divergence followed by fruits vine^{-1} (12.50%), fruit girth (8.82%), internodal length (6.62%) and days to 1st female flower (3.68%). This agreed with the findings of Kundu *et al*. (2012), Kumari *et al*. (2017) and Tyagi *et al*. (2017). Therefore, more emphasis should be given to improve these characters while making selection of high yielding genotypes of bitter gourd.

4. Conclusion

From the present study, it can be concluded that for future breeding programme in bitter gourd, genotype of Cluster V should be selected for better vegetative growth, earliness in appearance of 1st female flower and giving yield for longer duration. Similarly, Cluster III for earliness in appearance of 1st male flower and more number of fruits vine^{-1} while that of cluster II should be considered for getting high yield with less number of seeds fruits^{-1}.

References:

Aruna P and Swaminathan V. 2012. Evaluation of hybrids with high yield and yield attributes in bitter gourd (*Momordica charantia* L.), *The Asian journal of Horticulture*, **7(**2): 624-625.

Islam MR, Hossain MS, Bhuiyan MSR, Husna A and Syed MA. 2010. Multivariate analysis in bitter gourd (*Momordica charantia* L.), *Middle-east journal of scientific research*, **5**(2): 86-90.

Kumari P, Kumari R, Rani N, Verma RB and Verma RK. 2017. Genetic divergence of bitter gourd (*Momordica charantia* L.) for sixteen important yield attributing traits, *Current journal of applied Science and technology*, **23**(2): 1-11.

Kundu BC, Hossain MA, Main K and Main IH. 2012. Genetic divergence in bitter gourd (*Momordica charantia* L.), *Journal of Asiatic society of Bangladesh Science*, **38**(2): 125-134.

National Horticulture Board (nhb.gov.in).

Rao CR. 1952. Advanced statistical methods in biometrical research, 390pp, John Wiley Sons, Newyork.

Reshmi J and Sreelathakumary I. 2012. Studies on genetic divergence in bitter gourd (*Momordica charantia* L.), *Journal of Horticultural Sciences*, **7**(2): 152-155.

Singh HK, Singh VB, Kumar R, Barnawal DK and Ray PK. 2014. Assessment of genetic diversity based on cluster and principal components analysis for yield and its contributing charecters in bitter gourd, *Indian Journal of Horticulture*, **71**(1): 55-60.

Sreejayan and Rao M N A. 1991. Oxygen free radical scavenging activity of *Momordica charantia* fruits, *Fitoterpeda*, **62**: 344-346.

Tyagi N, Singh VB and Tripathi V. 2017. Studies on genetic divergence in bitter gourd (*Momordica charantia* L.), *Indian journal of Ecology*, **5**(3): 607-609.

Vinning G. 1995. Market Compendium of Asian Vegetables: a report for RIRDC Res. **95** (12): 386.