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# Studies on genetic divergence in bitter gourd (*Momordica charantia* L.)

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## ABSTRACT

**Genetic divergence study was conducted on 33 bitter gourd genotypes for twenty characters. These genotypes were grouped into five clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. Cluster-I was the largest comprising 11 genotypes, followed by Clusters-III and V with 10 genotypes each. Clusters-II and IV comprised one genotype each. As regards cluster means, Clusters-II and IV performed better in most of the biometric characters studied. Maximum inter-cluster distance was observed in Clusters-III and IV, followed by Clusters-II and III, and clusters-I and IV. Intra-cluster distance was highest in Cluster I.**

**Key words:** Bitter gourd, genetic divergence, $D^2$ Statistics

## INTRODUCTION

Bitter gourd is an important cucurbitaceous vegetable. Diverse morphological characters of *M. charantia* provide a relatively broad phenotypic species-variation. Bitter gourd crop improvement programmes need an understanding of the nature and degree of genetic divergence available in the germplasm. Mahalanobis's $D^2$ statistics is a powerful tool for determining degree of divergence between populations, and relative contribution of different components to the total divergence, in isolation of suitable parents. This technique provides a basis for selection of genetically divergent parents in a hybridization programme. Therefore, the present investigation was carried out to examine the nature and magnitude of genetic divergence in 33 bitter gourd genotypes with different geographical origins and distribution.

## MATERIAL AND METHODS

Thirty three genotypes of bitter gourd having diverse origin were evaluated at the College of Agriculture, Thiruvananthapuram, during the period August – November, 2009. Genotypes were evaluated using Randomized Block Design, with two replications. Plants were grown at a spacing of 2.0m × 2.0m adopting the package of practices recommended by Kerala Agricultural University (KAU, 2007). Observations were recorded on four randomly selected plants of each genotype in each replication for eleven characters, viz., days to seedling emergence, vine length (cm), internodal length (cm), number of primary branches, number of secondary branches, days to first male flower emergence, days to first female flower emergence, location of the node where first male flower or first female flower appeared, sex ratio, days to first fruit harvest, fruit length (cm), fruit girth (cm), number of fruits per plant, average fruit weight (g), yield per plant (kg), number of seeds per fruit, 100-seed weight (g), incidence of fruit fly infestation (%) and mosaic incidence (%). Genetic divergence was estimated using $D^2$ statistics of Mahalanobis (1928) and the populations were grouped into clusters as per Rao (1952).

## RESULTS AND DISCUSSION

Analysis of variance indicated that the genotypes differed significantly in all the characters studied except fruit fly infestation percentage. Having computed $D^2$ values for all possible pairs, the thirty three genotypes were classified into five groups of gene constellations. These indicated a large genetic diversity (Table 1). Maximum number of genotypes (11) grouped under Cluster-I, followed by Clusters-III and V, with 10 genotypes each. Clusters-II and IV comprised one genotype each. Commercially cultivated varieties like CO-1, Preethi, Konkan Tara and Priya grouped under Cluster-I, while Pusa Do Mousami and

**Table 1. Grouping of 33 bittergourd genotypes into clusters**

| Cluster No. | Number of genotypes | Treatment |
|---|---|---|
| I | 11 | MC 1 (Thiruvalla, Pathanamthitta, Kerala) |
| | | MC 2 (CO-1, TNAU, Coimbatore) |
| | | MC 4 (Preethi, KAU, Thrissur) |
| | | MC 12 (Konkan Tara, KKV, Dapoli) |
| | | MC 15 (Priya, KAU, Thrissur) |
| | | MC 21 (Vellathuval, Idukki, Kerala) |
| | | MC 22 (Chathamangalam, Kozhikode, Kerala) |
| | | MC 26 (Thripunithara, Ernakulam, Kerala) |
| | | MC 27 (Charuplasseri, Palakkad, Kerala) |
| | | MC 29 (IC 68326, NBPGR, Thrissur) |
| | | MC 32 (IC 85612, NBPGR, Thrissur) |
| II | 1 | MC 20 ( Priyanka, KAU, Thiruvalla ) |
| III | 10 | MC 3 (IC 68314, NBPGR, Thrissur) |
| | | MC 6 (Pusa Do Mausami, IARI, New Delhi) |
| | | MC 7 (Kuzhipalam, Thiruvananthapuram, Kerala) |
| | | MC 8 (IC 85632, NBPGR, Thrissur) |
| | | MC 9 (Anchal, Kollam, Kerala) |
| | | MC 11(Arka Harit, IIHR, Bangalore) |
| | | MC 14 (IC 85603, NBPGR, Thrissur) |
| | | MC 17(IC 85627, NBPGR, Thrissur) |
| | | MC 28 (Kadakkal, Thiruvananthapuram, Kerala) |
| | | MC 33 (Pala, Kottayam, Kerala) |
| IV | 1 | MC 10 (MDU-1, TNAU, Madurai) |
| V | 10 | MC 5 (Kalpetta, Wayanad, Kerala) |
| | | MC 13 (IC 85650, NBPGR, Thrissur) |
| | | MC 16 (Haripad, Alappuzha, Kerala) |
| | | MC 18(IC 50523, NBPGR, Thrissur), |
| | | MC 19 (Kattakada, Thiruvananthapuram, Kerala) |
| | | MC 23 (IC 113878, NBPGR, Thrissur) |
| | | MC 24 (IC 85636, NBPGR, Thrissur) |
| | | MC 25 (IC 470569, NBPGR, Thrissur) |
| | | MC 30 (Chennai, Tamil Nadu) |
| | | MC 31(IC 85642, NBPGR, Thrissur) |

**Table 2. Average inter- and intra-cluster distance in thirty three genotypes of *M. charantia***

| Cluster | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | 1197.78 | 1570.86 | 1566.15 | 1856.82 | 1022.33 |
| II | | 0.00 | 2088.12 | 1545.21 | 1595.39 |
| III | | | 1149.66 | 2515.57 | 1167.00 |
| IV | | | | 0.00 | 1822.31 |
| V | | | | | 903.03 |

Diagonal elements: Intra-cluster values; Off -diagonal elements: Inter-cluster values

Arka Harit figured under Cluster-III. This result showed that almost all commercially cultivated varieties of bitter gourd in our country may have originated from closely related sources. Commercially released cultivars from Southern part of the country like Priyanka and MDU-1 grouped singly in Clusters-II and IV respectively, indicating that these genotypes were distinctly different from the rest of the germplasm studied.

Intra- and inter-cluster distances are an index of genetic diversity among clusters as shown in Table 2. Inter-cluster distances were greater than intra-cluster distances, revealing a considerable amount of genetic diversity among the genotypes studied. Intra-cluster distance was highest in Cluster-I (1197.78), followed by Clusters-III and V (1149.66 and 903.03, respectively). Highest inter-cluster distance was observed in Clusters-III and IV (2515.57), followed by Clusters-II and III (2088.12) and Clusters-I and IV (1856.82). Genetic distance ($D^2$) between Clusters-I, III and V was larger than in Cluster-IV. Minimum inter cluster distance was observed between Clusters-I and V (1022.33) indicating close relationship among genotypes. Data clearly indicated that the genotypes did not cluster according to their geographical distribution. In general, the pattern of distribution of genotypes from various regions into different clusters was seen to be random. Similar observations were also reported by Lovely (2001) in ash gourd, Kale *et al* (2002) and Lakshmi *et al* (2003) in pumpkin, Kandasamy (2004) in melon, Maharana *et al* (2006) in ivy gourd, and by Devmore *et al* (2007) and Dey *et al* (2007) in bitter gourd. One possible reason may be that it is very difficult to establish the actual place of origin of a genotype. Free and frequent exchange of genetic material among breeders in the country makes it very difficult to maintain the real identity of a genotype. Absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin (such as exchange of genetic stock, genetic drift, natural mutation, spontaneous variation or natural and artificial selection) may be responsible for the genetic diversity. Another possibility may be that estimates of diversity based on characters used in the present investigation may not be sufficient to account for variability caused by some other traits of physiological / biochemical nature (which could be important in depicting the total genetic diversity in a population). Therefore, selection of genotypes for hybridization should be based on genetic diversity other than geographic divergence.

Cluster means of 33 genotypes (Table 3) showed that mean values of clusters varied in magnitude for all the 20 characters studied. As regards cluster means, Clusters-II and IV performed better for most of the biometric characters studied. Among the clusters studied, Clusters-III was

**Table 3. Cluster means of eleven quantitative traits in bitter gourd**

| Cluster No. | Days to seedling emergence | Vine length (cm) | Internode length (cm) | Number of primary branches | Number of secondary branches | Days to first male flower emergence | Days to first female flower emergence | Node Number where first male flower appeared | Node Number where first female flower appeared | Sex ratio |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 8.59 | 358.59 | 2.92 | 20.02 | 35.64 | 38.18 | 42.18 | 13.05 | 15.77 | 18.65 |
| II | 7.75 | 468.75 | 5.58 | 13.25 | 19.50 | 44.25 | 51.00 | 16.50 | 23.25 | 17.17 |
| III | 8.33 | 240.38 | 2.99 | 10.70 | 18.95 | 39.23 | 43.23 | 14.08 | 17.15 | 21.99 |
| IV | 11.75 | 572.50 | 3.28 | 21.00 | 26.50 | 51.00 | 54.50 | 17.75 | 20.00 | 17.19 |
| V | 10.08 | 348.25 | 2.99 | 19.00 | 32.50 | 41.88 | 30.38 | 19.05 | 24.20 | 22.18 |

**Table 3 (contd.) Cluster means of eleven quantitative traits in bitter gourd**

| Cluster No. | Days to first fruit harvest | Fruit length (cm) | Fruit girth (cm) | No. of fruits per plant | Average fruit weight (g) | Yield per plant (kg) | No. of seeds per fruit | 100-seed weight (g) | Incidence of fruit fly infestation (%) | Mosaic incidence (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 52.06 | 24.56 | 16.90 | 22.16 | 189.95 | 2.97 | 20.45 | 20.15 | 5.84 | 21.68 |
| II | 59.55 | 38.83 | 25.53 | 14.75 | 578.75 | 5.89 | 33.00 | 21.60 | 8.75 | 41.00 |
| III | 55.03 | 15.82 | 14.23 | 14.33 | 116.01 | 1.33 | 15.65 | 15.00 | 4.62 | 46.45 |
| IV | 56.50 | 33.66 | 8.48 | 34.25 | 183.05 | 4.41 | 16.00 | 25.10 | 4.57 | 38.00 |
| V | 53.33 | 16.75 | 15.62 | 17.58 | 125.72 | 1.32 | 17.95 | 18.73 | 5.45 | 34.05 |

generally poor, and Clusters-I and V were found to be intermediate. It is also evident that except Clusters-III and V (represented by small fruited genotypes), all other clusters showed higher yield potential than Cluster-I, represented by most of the commercially cultivated varieties.

Cluster-I consisted of 11 genotypes with medium-sized fruits and shortest internode, male and female flowers at lower nodes, earliness in fruit harvest, and highest mosaic resistance. Cluster-II (MC 20) had a single genotype, with earliness in seedling germination, longest internode, lowest sex ratio as well as highest fruit length, fruit girth, average fruit weight, yield per plant and number of seeds per fruit. Cluster-III comprised genotypes with smallest fruits, shorter vine-length and less number of branches, with lower fruit yield. Cluster-IV consisted of a single genotype (MC 10) with medium-sized fruits, longest vine-length, highest number of primary and secondary branches, number of fruits per plant and 100-seed weight, along with lowest fruit fly infestation. Cluster-V comprised 10 genotypes of small-sized fruits, with lowest fruit yield**.** The best cluster with yield and other component characters was represented by Cluster-II followed by Cluster-IV.

Based on these results, Mahalanobis's $D^2$ was found to be a useful tool in grouping genotypes phenotypically and geographically. Findings revealed that in bitter gourd, there is a vast scope for developing new varieties with greater yield potential and to better other attributes of economic importance, using this elite germplasm. In crop improvement programmes, intercrossing among genotypes with outstanding mean performance for these characters would prove to be effective. To develop early varieties with higher yield, selection from Cluster-I would be effective, as, it showed higher yield with early maturity. It is clear that for attaining maximum yield with highest number of fruits from an early crop, Cluster-II would be a good candidate. To breed good varieties from the small-fruited group, selection from Cluster-V will prove to be highly useful and selection from cluster-IV will be useful for breeding long, slender-fruited varieties with higher demand in specific regions of our country.

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