Divergence analysis of Bitter gourd genotypes for yield and yield attributes

Abstract

Genetic divergence for yield and yield attributes were evaluated in 33 bitter gourd genotypes for 17 characters. Characters such as, days to first male flower appearance, days to first female flower appearance, node of first male flower appearance, node of first female flower appearance, number of male flowers per vine, number of female flowers per vine, days to first harvest, number of harvests, fruit length (cm), fruit girth (cm), individual fruit weight (g), vine length (cm), number of primary branches per vine, number of fruits per vine, sex ratio, number of seeds per fruit and yield of fruits per vine (g) were used for analysing the divergence among the genotypes. Genotypes were grouped into five clusters using D^2 statistics, and a dendrogram was created using Ward's approach. Out of the five clusters, cluster I was the largest comprising of 14 genotypes. Maximum inter cluster distance was observed between cluster III and cluster V, hence diverse parents for hybridization can be selected from these two clusters.

Key words: Bitter gourd, *Momordica charantia* L., divergence, cluster

Introduction

Bitter gourd often known as bitter melon (*Momordica charantia* L.) is one of Kerala's major cucurbitaceous vegetable crops. Bitter gourd is thought to have first appeared in the Old World tropics, specifically in eastern India and southern China [1]. Since bitter gourd flowering is monoecious in nature, it is a crop that is highly cross pollinated. The crop is in a diploid state with chromosome number 2n= 22. The fruits have a great nutritional and therapeutic value and are utilised in a range of culinary recipes. The fruits contain alkaloid compounds with potential medical value such as momordicine, saponine, and albuminoides and are high in vitamin C and folate. It is rich in minerals such as zinc, iron, magnesium, and calcium, and is also an excellent source of fibre. [2].In addition to being used for consumption, fruits are said to have a variety of pharmacological qualities, including antioxidants, anti-diabetes, antibacterial, anti-cancer, and others. [3].

In spite of these much economic and medicinal significance of the crop, due attention has not been given towards a need-based crop improvement programme. However, in recent

years, bitter gourd cultivation has become more and more popular due to consumer awareness of its anti-diabetic and nutritional benefits. A significant increase in yield has been made possible by the work of several vegetable breeders, and a significant number of new varieties and hybrids have also been created. Assessing the available genetic variability and partitioning it into heritable and non-heritable components is a basic step to the planning of any breeding programme. In order to select appropriate parental lines for hybridization, it will be helpful to group genotypes based on D^2 analysis. Studying the genetic divergence at a specific level can aid in the effective use of the germplasm. It is crucial to conduct evaluation programs to identify genotypes for hybridization programs and develop advanced breeding lines. Mahalanobis D^2 distance, which calculates the multivariate distance between two operation taxonomic units (OUTs), can be used to analyse genetic diversity. By grouping genotypes into distinct clusters, this method minimizes the need for comparing each one individually. D^2 values are calculated through a process of converting correlated variables into uncorrelated ones via the pivotal condensation method [4].When it comes to clustering bitter gourd genotypes based on yield and its component traits, hierarchical clustering techniques like Ward's minimum variance method (introduced by Ward in 1963) are the most commonly employed. Ward's method provides an accurate number of clusters for various traits, and it also helps identify the genotype pairs that show the least diversity, as well as those with the most diversity, which can differ for different pairs of genotypes.

Considering the above mentioned facts, the current study was proposed with the main objective of assessing the available genetic divergence for yield and yield attributes which can be further utilized in crop improvement programmes.

Materials and methods

Thirty three genotypes consisting of released varieties, NBPGR accessions and local collections of bitter gourd were evaluated at Farming Systems Research Station, Sadananadapuram, Kottarakara, Kerala. The genotypes include both *M. Charantia var. charantia* and *M. charantia var. muricata,* which are included in the Table 1. Experiment was in Randomized Block Design with three replications during June 2021– September 2021. The package of practices recommended by Kerala Agricultural University was followed in adopting cultural and management practices. The evaluation was based on 17 characters such as days to first male flower appearance (DFMF), days to first female flower appearance (DFFF), node of first male flower appearance (NFMF), node of first female flower

appearance (NFFF), number of male flowers per vine (NMF), number of female flowers per vine (NFF), days to first harvest (DFH), number of harvests (NH), fruit length (FL) (cm), fruit girth (FG) (cm), individual fruit weight (IFW) (g), vine length (VL) (cm), number of primary branches per vine (NPB), number of fruits per vine (NFV), sex ratio (SR), number of seeds per fruit (NSF) and yield of fruits per vine (YFV) (g). D^2 is a statistical measure used to determine the degree of divergence between two populations based on their genotypes. It is calculated by summing the squares of the differences between the populations for each uncorrelated variable obtained through a method called pivotal condensation. The square root of the resulting D2 value represents the general distance between the populations. To group the genotypes based on their degree of divergence, the Tocher's method was used [5]. The model was originally developed by Mahalanobis [6] to determine the generalized group distance between populations. D^2 statistics was computed using INDOSTAT software programmes.

Results and Discussion

Divergence analysis

Thirty-three genotypes were grouped into five clusters based on D^2 values which is depicted in table 2 and figure 1. Among them, four clusters are poly-genotypic, i.e., Cluster I, Cluster II, Cluster III and Cluster IV, while Cluster V was mono-genotypic. Perhaps the reason for the emergence of separate, solitary clusters is either due to the fact that the ancestors of these clusters were geographically separated, which prevented the exchange of genes, or because natural and human selection favoured the development of diverse and adaptable gene complexes, resulting in genetic diversity. A Similar revelation of existence of solitary clusters was also studied by Prakash et al.[7]. Cluster I was the largest comprising of 14 genotypes followed by cluster II with nine genotypes, cluster IV with five genotypes, cluster III with four genotypes and cluster V was smallest with one genotype. The Mahalanobis D^2 metric has been utilized by numerous researchers to conduct multivariate analysis, such as investigating the degree of variation in crop germplasm collections. Nithinkumar et al. [8] and Singh et al. [9] has reported the success of this model for studying genetic divergence in rice genotypes. Nithinkumar et al. [8] studied genetic divergence of forty bitter gourd genotypes for sixteen different parameters by adopting Mahalanobis D^2 statistics and genotypes were grouped into six clusters irrespective of geographic divergence.

In the study conducted by Singh et al. [9], cluster analysis grouped 32 bitter gourd genotypes into 6 clusters and extreme genetic divergence was assessed among clusters

The average intra and inter cluster D^2 values were presented in table 3 and figure 2. The D^2 values of intra clusters are lesser than that of inter clusters, indicating lesser divergence within the cluster than among the clusters. This finding is agreement with the results reported by Jatav [10] Islam et al. [11] and Khosa and Dhatt [12]. In this study, it was noticed that the number of genotypes in a cluster did not always correspond to the magnitude of the intra-cluster distances. For instance, although Cluster I consisted of 14 genotypes, its intra-cluster distance was not necessarily the highest. This finding was in line with the earlier reports of Kundu et al. [13]. Intra-cluster D^2 values ranged from zero (cluster V) to 5.07 (cluster IV). Maximum intra cluster distance was observed in cluster IV (5.07), followed by cluster II (4.42), cluster III (4.33), cluster I (3.91), and cluster V (0.00). The highest intra-cluster distance may be attributed to limited gene exchange between genotypes within the cluster. Maximum inter cluster distance (10.05) was recorded between cluster III and V followed by cluster I and V (8.93) while minimum distance was between cluster I and II (4.89). Cluster V was the most diverse as more clusters exhibited maximum inter cluster distance with it. Similar observations were also reported by Maurya *et al*. [14], Dey *et al*., [15] Resmi and Sreelathakumari [16] The genotypes belonging to different clusters parted by high statistical distance could be used in hybridization programmes for attaining a wide spectrum of variation among the segregates. In this context genotypes from clusters III and V may result into heterotic combinations.

The cluster averages of 33 genotypes revealed that the average values differed in magnitude for each of the 17 traits (Table 4). Days to first male flower, days to first female flower and days to first harvest were detected at crest in cluster I. Cluster II had highest values for node of first female flower. Mean values of vine length, fruit length, fruit girth, individual fruit weight, number of seeds per fruit and yield of fruits per vine were highest in cluster III. Number of male flowers were more in cluster IV. The genotypes in cluster V exhibited the peak mean value for node of first male flower, number of female flowers, number of fruits per vine, number of harvest and number of primary branches.

Conclusion

The present study found that maximum inter cluster distance was between cluster III and cluster V, hence diverse parents for hybridization can be selected from these clusters. Since

no cluster was observed to record all the desirable characters, selecting individuals directly for immediate use was not considered possible. To enhance a specific trait in a hybridization programme, it is suggested to choose genotypes from clusters that have high average values for that trait. Furthermore, to obtain a combination of all the desired traits, it is recommended to hybridize genotypes from clusters that are genetically diverse.

References

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Table 1: List of genotypes used in the study

No.	Genotype	Source
T1	Saidabad local	Saidabad
T2	JP Nagar local	JP Nagar
T3	Ariadaha local	Kolkata
T4	Lodhi local	New Delhi
T5	Onkar Nagar local	New Delhi
T6	Vellayani local	Vellayani
T7	Telangana local	Telangana
T8	Jaya nagar local	Bangalore
T9	Vyasarpadi local	Tamil Nadu
T10	Andhra Pradesh local	Andhra Pradesh
T11	Bangalore local	Bangalore
T12	Palappur local	Trivandrum
T13	Udayagiri local	Udayagiri
T14	Idukki local	Idukki
T15	Preethi	Kerala Agricultural University
T16	Priyanka	Kerala Agricultural University
T17	Alacode local	Alacode
T18	Therthali local	Therthali
T19	Iritty local	Iritty
T20	Thrissur local	Thrissur
T21	IC 85636	National Bureau of Plant Genetic Resources, New Delhi
T22	IC 45346	National Bureau of Plant Genetic Resources, New Delhi
T23	IC 44413	National Bureau of Plant Genetic Resources, New Delhi
T24	IC 68335	National Bureau of Plant Genetic Resources, New Delhi
T25	IC 50527	National Bureau of Plant Genetic Resources, New Delhi

T26	IC 596980	National Bureau of Plant Genetic Resources, New Delhi
T27	IC 68309	National Bureau of Plant Genetic Resources, New Delhi
T28	IC 113875	National Bureau of Plant Genetic Resources, New Delhi
T29	IC 68272	National Bureau of Plant Genetic Resources, New Delhi
T30	IC 68275	National Bureau of Plant Genetic Resources, New Delhi
T31	IC 85634	National Bureau of Plant Genetic Resources, New Delhi
T32	IC 85626	National Bureau of Plant Genetic Resources, New Delhi
T33	IC 33275	National Bureau of Plant Genetic Resources, New Delhi

Table 2: Grouping of genotypes into five cluster

Cluster No	No of genotypes	Name of genotypes
I	14	T2,T21,T20,T22,T23,T24,T28,T5,T6,T10,T26,T27,T9,T12
II	9	T8,T11,T25,T33,T1,T29,T30,T32,T3
III	4	T4,T31,T15,T16
IV	5	T7,T14,T18,T19,T17
V	1	T13

Table 3: Average intra and inter cluster distance among five clusters formed in bitter gourd

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	3.91	4.89	6.12	6.38	8.93
Cluster II		4.42	7.01	6.99	7.88
Cluster III			4.33	7.69	10.05
Cluster IV				5.07	7.84
Cluster V					0.00

Table 4: Mean values of five clusters

	VL	DFMF	DFFF	NFMF	NFFF	NMF	NFF	DFH
Cluster I	442.69	50.11	51.57	21.86	27.88	278.86	19.24	79.10
Cluster II	352.63	45.81	46.26	19.44	28.30	240.74	18.81	78.74
Cluster III	461.08	48.92	50.5	19.42	23.25	257.00	19.33	79.00
Cluster IV	421.27	48.87	50.40	18.87	27.00	578.8	25.47	78.27
Cluster V	363.67	38.00	35.33	24.00	26.67	435.00	27.00	68.00

Table 4 contd…

	FL	FG	IFW	NFV	NSF	NH	SR	NPB	YFV
Cluster I	13.33	13.57	64.98	15.86	19.02	6.95	14.73	13.17	1019.83
Cluster II	13.34	12.02	61.50	14.37	14.30	6.70	12.89	15.63	853.31
Cluster III	17.89	16.2	166.1	16.08	26.92	8.42	13.45	19.50	2708.52
Cluster IV	11.29	11.62	47.13	22.73	24.20	10.53	23.34	19.13	1089.42
Cluster V	10.6	11.07	41.47	25.67	12.33	13.33	16.13	21.67	1067.07

Figure 1: Dendrogram showing clustering of bitter gourd genotypes by Ward's method

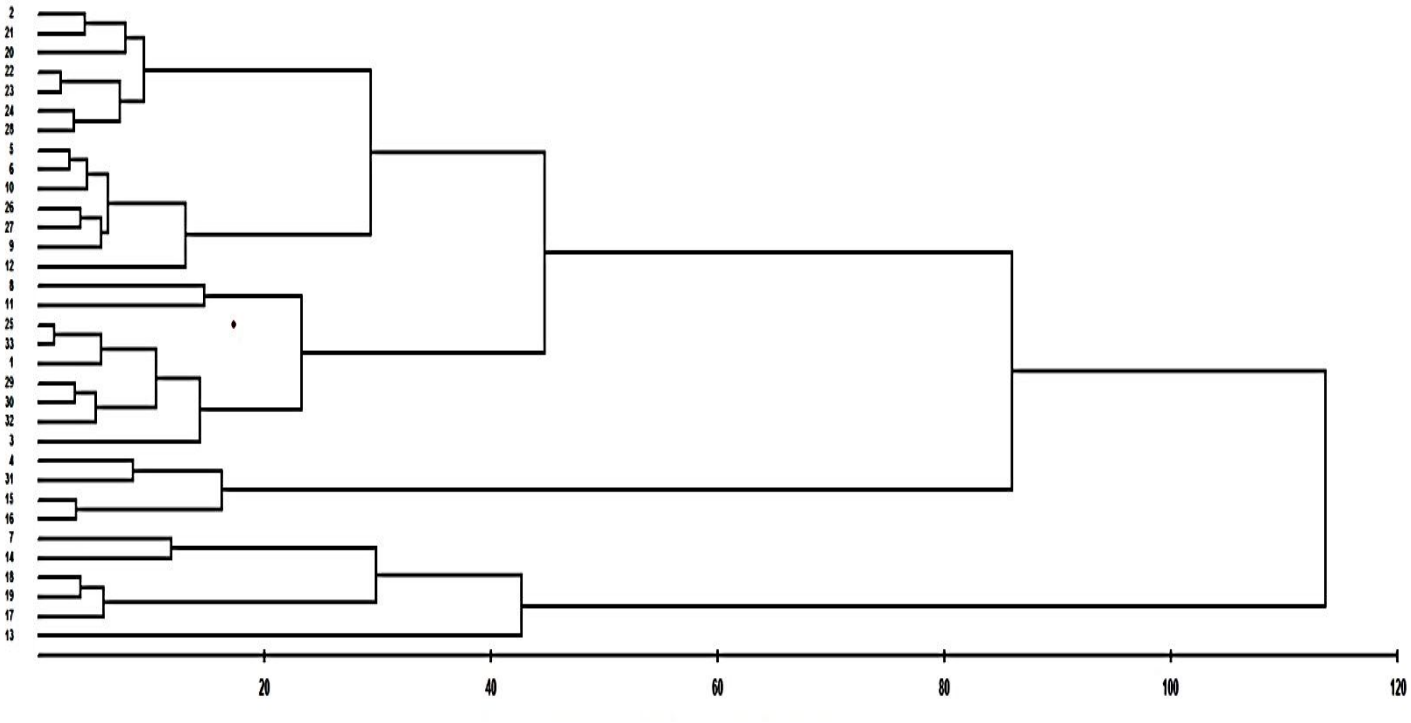

Figure 2: Intra-cluster and inter-cluster distance of bitter gourd genotypes