

GENETIC DIVERGENCE IN BHINDI (*ABELMOSCHUS ESCULENTUS* [L.] MOENCH)

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Abstract: Seventy genotypes of bhindi were subjected to D^2 analysis based on 14 economic characters in order to classify them into group constellations. The 70 genotypes were found to fall into six clusters with 57 genotypes in cluster I, four in cluster II, three in cluster III, two in cluster IV, three in cluster V and one in cluster VI. The distribution of the genotypes into six different clusters was not according to their places of origin showing that the genotypes forming one group were geographically diverse, while those obtained from the same region were genetically different. Cluster V showed high mean values for yield and major yield attributes indicating that it is superior to the rest of the clusters. Cluster I and IV were genetically closer while cluster II and VI were wider. Selection of parents from cluster II and VI for hybridisation is likely to give heterotic hybrids.

Key words: *Abelmoschus esculentus*, bhindi, genetic divergence

INTRODUCTION

Bhindi (*Abelmoschus esculentus* [L.] Moench) is an annual vegetable crop grown extensively throughout India. Due to its high adaptability, it can be cultivated under a wide range of environmental conditions. Bhindi is also a crop of significant nutritional as well as medicinal value. Heterosis is exploited in bhindi for many characters like earliness, dwarfness and high yield. As a preliminary step of heterosis breeding, it is desirable to investigate the nature and degree of divergence in a population of different groups. Multivariate analysis can be successfully used in this crop for the estimation of genetic divergence. It helps in choosing parents in the hybridization programme for achieving specific breeding objectives. With this objective, the present investigation was undertaken to estimate the genetic divergence among several genotypes and to group them into clusters according to the magnitude of genetic distance.

MATERIALS AND METHODS

The present investigation was undertaken in the Department of Plant Breeding, College of Agriculture, Vellayani during the period 1992-93 with 70 bhindi genotypes of diverse origin collected from the different agroclimatic regions of Kerala. These types were selfed to attain homozygosity. They were grown in a RBD with three replications. Observations on 14 economic characters were recorded for

estimating genetic divergence. Mahalanobis D^2 analysis (Rao, 1957) was used to compute the genetic distances and to cluster the genotypes into distant groups.

RESULTS AND DISCUSSION

The analysis of variance revealed significant difference for all the characters studied except leaf axil bearing the first flower and fruiting phase suggesting considerable variability and divergence between them. The 70 genotypes included in the study were subjected to D^2 analysis based on the 14 characters in order to classify them into group constellations. The 70 genotypes were found to fall into six clusters, with varying number of genotypes in each cluster. Cluster I, II, III, IV, V and VI contained 57, four, three, two, three and one genotypes respectively. The genotypes which exhibited minimum divergence got clustered together. The distribution of genotypes into six different clusters was not according to their places of origin showing that the genotypes forming one group were geographically diverse, while genotypes obtained from the same region were genetically different. This was also observed by Singh and Bain (1968), Gupta and Singh (1970), Ariyo *et al.* (1987), Henry and Krishna (1990) and Varalakshmi and Haribabu (1991).

The cluster means estimated for 14 characters in bhindi (Table 1) revealed that among the six clusters studied cluster V showed high mean

Table 1. Cluster means of fourteen characters

Characters	Cluster					
	I	II	III	IV	V	VI
Days to first flowering	46.82	45.58	47.44	47.33	48.55	42.37
Leaf axil bearing first flower	4.40	4.25	4.23	4.17	4.22	4.34
Number of leaves per plant	23.98	34.24	15.86	25.18	30.44	15.00
Leaf area	140.16	143.32	124.44	214.27	158.95	211.11
Number of branches per plant	2.49	2.74	2.56	2.16	3.33	2.67
Number of flowers per plant	8.42	7.83	9.39	10.00	9.00	5.33
Number of fruits per plant	6.11	6.33	7.67	7.50	6.45	3.67
Length of fruit (cm)	16.96	14.58	15.33	15.66	20.22	15.00
Girth of fruit (cm)	7.11	7.33	7.12	7.17	7.89	10.87
Weight of single fruit (g)	21.63	16.71	14.33	15.54	27.68	17.60
Weight of fruits per plant (g)	136.17	106.29	109.98	116.72	185.38	98.50
Number of seeds per fruit	77.07	81.25	76.44	81.00	66.89	89.00
Fruiting phase	52.13	49.38	52.22	53.50	52.55	52.00
Height of the plant (cm)	67.15	72.58	79.88	74.83	86.77	51.00

Table 2. Average intra and inter-cluster distances

Cluster	I	II	III	IV	V	VI
I	117.82	224.72	209.96	180.16	202.75	289.39
II		103.34	396.58	258.82	205.70	450.88
III			195.22	289.39	343.15	234.39
IV				89.88	263.44	230.27
V					134.98	425.14
VI						0

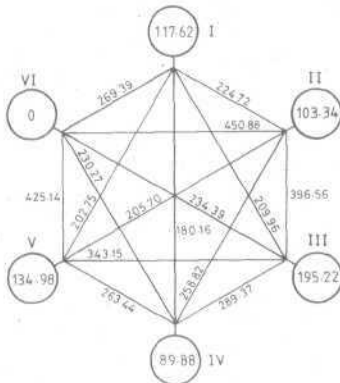


Fig 1. Cluster diagram (values on lines are inter-cluster D values and values in circles are intra-cluster D values)

values for yield, height of the plant, weight of single fruit, day to first flowering, length of fruit and number of branches indicating that cluster V is superior to the rest of the clusters

in respect to desirable attributes. Cluster IV was superior for characters like fruiting phase, number of flowers per plant and leaf area. Cluster III is superior for the character number of fruits per plant, cluster II for number of leaves and cluster I for leaf axil bearing the first flower. Cluster VI had low mean values for majority of the characters showing that it is highly inferior compared to the other clusters.

High intra-cluster distance within a cluster indicated high degree of variability within that cluster offering scope for improvement by various selection methods. The maximum intra-cluster distance was shown by cluster III (195.22), followed by cluster V (134.98), cluster I (117.62), cluster II (103.34) and cluster IV (89.88) thereby indicating highest degree of variability in cluster III.

The inter-cluster relationships are represented diagrammatically in Fig 1, the square root of average D^2 between the clusters being used to represent the relative disposition of clusters.

Studies on genetic divergence revealed that clusters I and IV were genetically closer while cluster II and VI were wider. It has been suggested that crossing among divergent parents is likely to yield heterotic hybrids. In future breeding programme, selection of parents from cluster II and cluster VI for

hybridization is likely to give heterotic hybrids.

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