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GENETIC DIVERGENCE STUDIES IN BHENDI [*ABLEMOSCHUS ESCULENTUS* (L.) MOENCH]

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Abstract

An experiment was conducted with 98 genotypes to assess the genetic divergence for 12 characters. Ninety eight genotypes were grouped into seven clusters. Cluster VII had the highest number of genotypes (51) followed by cluster I (37) genotypes and cluster II, III, IV, V and VI comprised two genotypes each. The maximum intra cluster distance was exhibited by VII (17.63) followed by cluster I (13.34). The maximum inter cluster distance was found between cluster V and cluster VII (18.52) followed by cluster I and cluster V (16.43) and cluster I and cluster VII (16.42). Analysis of contribution of the characters to genetic diversity revealed that characters *viz.,* leaf area (35.75%), contributes highest to divergence followed by yield plant^{-1} (16.54 %). On the basis of inter cluster distance value, cluster V and cluster VII were identified as more divergent clusters and genotypes of these clusters could be selected as parents for future hybridization programme in okra.

Key words : Okra, Fruit yield, Mean performance, Genetic divergence and D^2 analysis.

Introduction

Bhendi [*Ablemoschus esculentus* (L.) Moench] is an important vegetable crop widely grown in the tropical and subtropical regions of the world. Cultivated okra has significant variations in the chromosome numbers but most frequently observed chromosome number is 2n = 130 (Balai *et al*., 2015) and it belongs to the family Malvaceae. Being a day neutral plant, it is cultivated in every season in one or other parts of the country. Being a multipurpose crop, okra is valued for its tender delicious pods. Dry seeds are rich source of iodine, carbohydrate, protein, oil and vegetable curd. Seeds are also used as coffee additive or substitute. Roots are used to clean sugarcane juice to make jaggery. Bhendi is praised for its medicinal values, as its fruits are useful in genito-urinary disorders, spermatorrhoea and chronic dysentery. It is often cross pollinated crop, heterosis is being exploited in form of development of hybrids. Hence, genetic divergence is an important tool while selecting the parents for hybrid breeding. Genetic divergence analysis is more authentic and powerful tool for systematic identification of the diverse genotypes for hybridization purposes (Balai *et al*., 2015).

To develop high yielding varieties, genetic diversity is an important tool to select genetically diverse parents with high yield and wider adaptability in breeding programme, progress of any breeding programmes depends to a great extent on the availability of genetic variability for desirable traits in genotypes (Balai *et al*., 2014). Genetic diversity helps the breeders in deciding the most appropriate breeding method to increase the genetic potentialities as well as to surpass the yield barrier. Use of genetically diverse parents in recombination breeding supposed to give maximum heterosis in F_1's and also getting broad spectrum of variability for quantitative traits in segregating generations to select desirable recombinant. Therefore, genetic diversity is prerequisites for any successful breeding programme.

Materials and Methods

The experimental material comprised of 98 genotypes of okra. These genotypes were raised with a spacing of 60 × 45 cm in randomized block design with three replications at the Horticulture Farm, Department of Horticulture, Faculty of Agriculture, Annamalai University, Chidambaram, Tamil Nadu, India. The recommended

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agronomic package of practices and plant protection measures were followed to raise a healthy crop. The observations were recorded on five randomly selected plants in each replication for each genotype on 12 traits *viz*., chlorophyll, relative water content (RWC), leaf area, days to first flowering, node at which first flowering, internodal length, plant height, fruit length, fruit weight, fruit girth, number of fruits plant^{-1} and yield plant^{-1}. The data were statistically analyzed as per Mahalanobis D^2 (Mahalanobis, 1936) analysis as the measure of genetic divergence among 98 genotypes. Grouping of genotypes into different clusters was carried out following Tocher's methods (Rao, 1952) and the relative contribution of different characters towards total divergence was calculated as per Singh and Choudhary (1985).

Results and Discussion

The analysis of variance indicated significant variation among the 98 okra genotypes for each of twelve characters. Genetic divergence among 98 genotypes for 12 traits was analysed by using Mahalanobis D^2 and according to the analysis, 98 genotypes were grouped into seven clusters (table 1). Among sever of the seven cluster, cluster VII contains maximum number of 51 genotypes followed by cluster I, which contains 37 genotypes and cluster II, III, IV, V and VI comprised two genotypes each.

Average intra and inter cluster D^2 are values presented in table 2, indicating nature of genetic divergence at intra and inter cluster levels, respectively. In general, inter cluster distance was much more than intra cluster distance. This suggesting that within cluster genotypes have same genetic constitution *ie*., homogeneous are less divergent than those occurred in a different cluster. The information on the degree of genetic divergence would be helpful in selection of parents for hybridization programme (Balai, 2015).

The intra and inter cluster distances among the seven were computed and presented in table 2. The intra cluster distance ranged from 3.17 to 17.63. The cluster II showed the minimum intra cluster distance (3.17) and the maximum intra cluster distance was exhibited by VII (17.63). The maximum inter cluster distance was found between cluster V and cluster VII (18.52) followed by cluster I and cluster V (16.43) and cluster I and cluster VII (16.42). The minimum inter cluster distance was observed between cluster IV and cluster VI (5.81).

Cluster mean indicated the variation for the quantitative traits among the cluster (table 3). The maximum cluster mean value was noted for chlorophyll content in the cluster VI (36.37) followed by the cluster VII (33.42) and cluster IV (31.95) and minimum cluster mean was observed in cluster V (18.65) followed by cluster III (26.42). For RWC the maximum cluster mean value was observed in the cluster V (93.99) followed by cluster III (93.20) and the minimum cluster mean was found in cluster IV (80.67). The maximum leaf area was recorded in cluster I (33.43) followed by cluster III (33. 08) and minimum leaf area was observed in cluster V (14.02).

For the trait days to first flowering, minimum cluster mean was recorded in cluster V (37.67) followed by cluster VII (40.46) and maximum cluster mean was noted in cluster III (42.75). For the trait node at which first flowering cluster mean value was found to be minimum in the cluster IV (2.75) and maximum cluster mean in cluster III and VI (3.33). The minimum cluster mean value for inter nodal length was recorded by the cluster

Table 1 : Composition of D^2 cluster in bhendi.

S. no.	Cluster	Number of genotypes	Genotypes
1.	**I**	37	AE 1, AE 2, AE 3, AE 4, AE 5, AE 6, AE 7, AE 8,AE 9, AE 10, AE 11, AE 12, AE 13, AE 14, AE 15, AE 16, AE 17, AE 18, AE 19, AE 20, AE 21, AE 22, AE 23, AE 24, AE 25, AE 26, AE 27, AE 28, AE 29, AE 30, AE 31, AE 32, AE 33, AE 34, AE 35, AE 66, AE 67
2.	**II**	2	AE 82, AE 87
3.	**III**	2	AE 65, AE 68
4.	**IV**	2	AE 40, AE 51
5.	**V**	2	AE 75, AE 78
6.	**VI**	2	AE 44, AE 57
7.	**VII**	51	AE 36, AE 37, AE 38, AE 39, AE 41, AE 42, AE 43, AE 45, AE 46, AE 47, AE 48, AE 49, AE 50, AE 52, AE 53, AE 54, AE 55, AE 56, AE 58, AE 59, AE 60, AE 61, AE 62, AE 63, AE 64, AE 69, AE 70, AE 71, AE 72, AE 73, AE 74, AE 76, AE 77, AE 79, AE 80, AE 81, AE 83, AE 84, AE 85, AE 86, AE 88, AE 89, AE 90, AE 91, AE 92, AE 93, AE 94,AE 95, AE 96, AE 97, AE 98

Table 2 : Average intra (diagonal) and inter cluster D^2 values and distance (in parenthesis) in okra.

Cluster	I	II	III	IV	V	VI	VII
I	178.04(13.34)	188.85(13.74)	118.94(10.91)	143.69(11.99)	270.00 (16.43)	146.52(12.10)	269.65(16.42)
II		10.07(3.17)	111.83(10.58)	58.77(7.67)	90.34(9.51)	84.33(9.18)	218.35(14.78)
III			10.12(3.18)	97.78(9.89)	138.79(11.78)	58.53(7.65)	222.28(14.91)
IV				14.17(3.76)	192.29(13.87)	33.76(5.81)	172.06(13.12)
V					14.64(3.83)	185.60(13.62)	342.91(18.52)
VI						14.87(3.86)	183.79(13.56)
VII							310.97(17.63)

Table 3 : Cluster mean of 98 bhendi genotypes for various characters.

Traits \ Cluster	I	II	III	IV	V	VI	VII
Chlorophyll (µmol/m^2)	26.43	26.95	26.42	31.95	18.65	36.37	33.42
RWC (%)	85.34	83.67	93.20	80.67	93.99	88.05	81.35
Leaf area (cm^2)	33.43	14.63	31.08	25.27	14.02	26.06	28.24
Days to first flowering	41.15	40.83	42.75	40.83	37.67	42.08	40.46
Node at which first flowering	3.32	2.83	3.33	2.75	2.92	3.33	3.04
Inter nodal length (cm)	8.79	3.79	4.61	8.40	5.14	6.90	6.34
Plant height (cm)	79.95	83.58	85.42	66.32	45.04	68.33	69.97
Fruit length (cm)	10.67	11.47	9.28	11.92	9.98	9.95	10.34
Fruit weight (g)	15.74	17.08	16.13	11.73	17.24	11.87	15.17
Fruit girth (cm)	5.96	5.58	5.70	5.18	6.50	5.13	5.85
Number fruits plant^{-1}	12.59	10.33	10.25	7.833	5.75	7.50	9.16
Yield plant^{-1} (g)	185.40	139.29	144.03	78.45	66.78	87.63	114.07

II (3.67) and maximum inter nodal length was recorded in cluster I (8.79 cm) followed by cluster IV (8.40 cm).

The maximum cluster mean value for plant height was recorded by the cluster III (85.42 cm) followed by cluster II (83.58 cm). For the trait plant height, minimum cluster mean was noted in the cluster V (45.04 cm). The maximum cluster mean value for fruit length was noted in the cluster IV (11.92 cm) followed by cluster II (11.47 cm) and minimum cluster mean was present in cluster III (9.28 cm). For the trait fruit weight, cluster mean value was found to be maximum in the cluster V (17.24 g) followed by cluster II (17.08g) and minimum cluster mean value in the cluster IV (11.73 g). For fruit girth, maximum mean value was recorded in I (5.96 cm) followed by cluster VII (5.85 cm), while the minimum cluster mean value was found in the cluster VI (5.13 cm). The maximum cluster mean value for number of fruits per plant was found in cluster I (12.59) followed by cluster II (10.33), while the minimum cluster mean was found in cluster V (5.75). The maximum cluster mean value for yield per plant was recorded by cluster I (185.40g) followed by cluster III (144.03g) and minimum cluster mean was found in cluster V (66.78g).

Analysis of contribution of the characters to genetic diversity (table 4) revealed that the trait *viz*., leaf area (35.75%), contributed highest percentage of divergence followed by the characters *viz*., yield plant^{-1} (16.54%), RWC (14.35%), chlorophyll (11.09%), fruit girth (5.55%), number of fruits (4.97%), inter nodal length (3.79%), fruit weight (3.39%), fruit length (1.81%), plant height (1.33%), day to first flowering (1.24%) and node at which first flowering (0.21%), in the order.

Thus, the characters like fruit yield per plant and number of fruits per plant will offer a good scope for improvement through selection. De *et al*. (1988) proposed that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the cluster to be taken for further selection and choice of parents for hybridization. Moll *et al*. (1974) and Ramgiry and Singh (2017) also observed similar level of contribution of fruit yield per plant. On the basis of inter cluster distance value, cluster V and cluster VII were identified as more divergent clusters and genotypes of these clusters could be selected as parents for future hybridization programme in okra.

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