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Genetic Divergence in Fababean

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Fababean germplasm including 84 exotic lines from West Germany and 9 indigenous lines, were evaluated for ten metric traits of economic importance. The lines could be grouped into six clusters using D^2 and metroglyph analysis. The grouping parttern revealed by the metroglyph analysis and D^2 analysis had 55.9% resemblance. The comparative efficiency of these two methods to classify the germplasm collection has been discussed.

Fababean (*Vicia faba* L.), a winter food legume grown sporadically as a minor vegetable crop in Himalayan region possesses high genetic potential to produce seed yield greater than cereal crops (Bean, 1967). Considering its exceptional high productivity, it is necessary to undertake breeding work is order to develop high yielding varieties. For a successful hybridization programme, the parents need to be selected from the diverse groups so as to generate greater variability. Many of the lines might be similar to each other with respect to their genetic constitution. However, only the crosses of genetically divergent parents give highly heterotic F_1 and broad-spectrum variability in segregating generations (Arunachalam, 1981). Therefore, it becomes imperative to classify the germplasm into various groups so as to select diverse parents from these groups for hybridization programme. Keeping this in view, the present investigation was planned to evaluate 93 fababean germplasm lines and classify them into various distinct groups using metroglyph analysis (Anderson, 1957) and D^2 statistic (Mahalanobis, 1949).

MATERIALS AND METHODS

The experimental material comprised 84 exotic lines from West Germany and 9 indigenous lines of fababean. These were sown in randomized block design with three replications. Each genotype was grown in single, 3 m long rows. The spacing between rows and between plants was 50cm and 20cm, respectively. Observations on ten randomly chosen plants per row were recorded for days to flowering, days to maturity, plant height, branches/plant, internode length, clusters/plant, pods/plant, seeds/pod, 100-seed weight and seed yield/plant.

The mean values were used for metroglyph analysis as suggested by Anderson (1957) and branches/plant and seed yield were used as x- and y-coordinates, respectively. For D^2-analysis. the original mean values were transformed to standardized uncorrelated variables by Pivtol Condensation method (Rao, 1952).

Genetic distances between genotypes were assessed using Mahalanobis's (1949) D^2-statistic and the material was grouped into clusters according to Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance of means revealed significant differences amongst the genotypes for all the characters. The phenotypic coefficient of variation for branches/plant (47 per cent), clusters/plant (87 per cent), seed yield/plant (104 per cent) and pods/plant (108 per cent) revealed that three traits were highly variable.

Based on metroglyph analysis the germplasm was classified in six clusters (Table 1). All exotic lines except three were grouped in cluster I and were low yielding with poor branching. However, the differences among the genotypes within cluster were noted for days to flowering, days to maturity, clusters/plant, pods/plant and seed weight. Cluster II had two exotic and one indigenous genotypes which were characterized by tall stature medium-branching and low expression for other characters. Clusters III and IV possessed 3 and 4 genotypes,

TABLE 1. CLUSTERING PATTERN OF 93 FABABEAN LINES.

Cluster No.	Metroplyph method		Tocher method	
	Number of accessions	Genotypes	Number of accessions	Genotypes
I	81	2, 3, 4, 6, 7, 8, 10, 12, 13, 15, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 36, 37, 39, 42, 44, 45, 46, 47, 48, 49, 50, 51, 52, 54, 55, 56, 57, 59, 60, 63, 64, 65, 66, 67, 68, 70, 71, 72, 73, 74, 80, 83, 89, 91, 92, 93, 94, 95, 96, 98, 100, 101, 103, 106, 107, 108, 109, 110, 111, 112, 116, 117, 118, 119, 121, 123, 128	55	2, 3, 6, 7, 8, 10, 12, 13, 15, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 36, 37, 39, 42, 55, 70, 71, 80, 83, 89, 91, 92, 95, 96, 100, 101, 109, 110, 111, 112, 113, 116, 117, 118, 119, 121, 123, 129*, 130*
II	3	7, 113, ML*	27	45, 46, 47, 48, 49, 50, 51, 52, 54, 56, 57, 59, 60, 63, 64, 65, 66, 67, 68, 73, 74, 93, 94, 98, 106, 107, 128
III	3	129*, 130*, 134*	7	5, 44, 131*, 132*, 133*, 134*, DM-I*
IV	4	131*, 132*, 133*, DM-1*	2	72, 108
V	1	5	1	ML*
VI	1	HL*	1	HL*

Resemblance (%) 55.9% of metroglyph method

*Indicates indigenous genotypes.

respectively, which were indigenous and had medium seed yield, early maturity, number of high clusters and pods per plant. There was only one exotic line in cluster V and one indigenous line in cluster VI. Both these genotypes showed high manifestation for clusters/plant, pods/plant, seeds/pod and seed yield.

Based on generalized distance (D), 93 lines were grouped in six clusters (Table 1). The intra-cluster distance varied from 0 to 5.26, while inter-cluster distance ranged from 8.09 to 20.55 (Table 2). Intra-cluster distances were smaller than the inter-cluster distances which revealed that the genotypes within clusters had greater similarity. High inter-cluster distances between cluster I and III, I and VI, and IV and VI indicated greater divergence between the genotypes belonging to these clusters. Cluster I accounted for about 87 per cent of total germplasm and about 96 per cent of exotic lines. This showed that the exotic lines had greater similarity amongst themselves presumably due to being from the same source.

TABLE 2. INTRA- AND INTER-CLUSTER DISTANCES (D)

Cluster	I	II	III	IV	V	VI
I	4.85	14.22	18.43	9.30	11.61	20.55
II		5.00	9.19	8.09	9.84	11.43
III			5.26	12.15	9.83	8.21
IV				4.53	8.38	15.11
V					0.00	12.82
VI						0.00

Cluster means (Table 3) showed appreciable variation among the six clusters grouped according to D^2 analysis. The differences among cluster means, though observed for all characters, were more pronounced for days to maturity, plant height, branches/plant, clusters/plant, pods/plant, seeds/pod and seed yield/plant. The cluster II showed the highest mean seed weight. The genotypes in cluster III had higher number of branches, clusters and pods, seed weight and seed yield.

The utility of classifying germplasm for selection of diverse parents for hybridization has long been appreciated (Bhatt, 1970; Arunachalam, 1981). However, choice of method for classification continues to be an inportant issue. In the present study, the clustering pattern obtained with metroglyph analysis revealed 55.9 per cent resemblence with that of D^2 analysis. Of six clusters, only cluster I and II, in both approaches, seemed to possess some similar genotypes. The precise classification based on metroglyph technique is possible only when the maximum variability is explained by the two characters plotted as x- and y-coordinates. Obviously, these two characters should be chosen judiciously. The results of the present investigation revealed that this technique had been quite useful in grouping the material. Although D^2 statistic is quantitative measure of divergence, yet grouping pattern is arbitrary, subjective and changeable under the influence of environment (Singh and Gupta, 1979).

TABLE 3. CLUSTERS MEANS FOR VARIOUS CHARACTERS

Clusters	Days to flowering	Days to maturity	Plant height (cm)	Branches/ plant	Inter-node length (cm)	Clusters/ plant	Pods/ plant	Seeds/ pod	100-seed weight (g)	Seed yield (g/plant)
I	84.9	165.5	77.3	2.0	2.1	8.8	11.2	2.4	32.9	5.9
II	85.5	146.2	74.6	1.9	2.0	8.3	10.0	2.3	33.8	6.0
III	78.4	128.1	57.1	4.8	3.0	36.4	55.9	2.8	33.0	25.4
IV	84.5	158.5	67.8	1.7	1.7	5.8	11.4	2.0	29.8	3.4
V*	75.0	123.0	44.1	3.0	2.7	20.7	31.3	2.3	27.0	13.5
VI*	91.0	127.0	62.4	3.0	2.8	34.0	65.3	3.0	26.8	49.9

*Clusters with single genotypes

It was noticed that the lines of the clusters I and VI (D = 20.55) I and III (D = 18.43) and IV and VI (D = 15.11) showed the maximum distances. Obviously, the crosses between genotypes in these clusters might be useful for fixing transgressive segregants. However, the selection of more than one genotype from large clusters such as cluster I poses specific problems. In that context apart from high genetic divergence, the performance of genotypes for characters such as plant type, disease resistance etc. should be given due consideration. In the present study, genotypes, VH5, VH7, VH72, VH129, HL, LM-I and ML appeared to be desirable for further fababean improvement programme. Inclusion of these parents in multiple crossing programme of diallel selective mating is expected to prove more rewarding.

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