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GENETIC DIVERGENCE FOR YIELD CONTRIBUTING TRAITS AND PROTEIN CONTENT IN FABA BEAN (*VICIA FABA* L.)

R. P. KATIYAR AND A. K. SINGH

Chandra Shekhar Azad University of Agriculture & Technology, Kanpur 208002

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ABSTRACT

Genetic divergence measured by Mahalanobis D^2 statistic was studied for days to flower, plant height, branches/plant, pods/plant, pod length, grains/pod, grain yield/plant, 100-seed weight, harvest index, and protein content in 40 indigenous and exotic strains of faba bean (*Vicia faba* L.). The strains were grouped into 12 different clusters. The clustering pattern of the strains usually did not exhibit geographical distribution. Pods/plant and 100-seed weight showed important divergence.

Key words: Genetic divergence, cluster, geographic distance, *Vicia faba*.

Faba bean has been a neglected crop of India and no systematic efforts have been made till date for the genetic amelioration of this crop. Genetic manipulation can be employed to remove the genes responsible for some antinutritional constituents in the seeds. The available literature on this crop does not provide sufficient information on the morphological parameters to be used for selecting high yieding agronomically desirable ideotypes. Information on divergence for the characters determining yield provides the basis for a successful programme of hybridization and selection. The present study aims to analyse genetic divergence of 40 indigenous and exotic strains of faba bean (*Vicia faba* L.) using D^2 analysis.

MATERIALS AND METHODS

The material comprised 40 strains of indigenous and exotic (Afghanistan, Holland, West Germany, England, Syria, Egypt, Canada, Ethiopia, Jordan, Lebanon, Turkey) faba bean, grown in randomized complete block design with three replications. The plot was a single row of 5 m length with inter- and intrarow spacings of 40 and 10 cm, respectively. Detailed observations were recorded on 10 competitive plants taken at random for quantitative traits.

Following the analysis of variance, the data were subjected to multivariate analysis. The diversity in characters was studied using D^2 technique [1].

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among the strains for all the characters, indicating the existence of genetic variability among the strains. The dispersion between the variables was also highly significant as tested by Wilk's criterion.

The D^2 values varied from 0.0 to 399.9, showing high divergence among the strains. On the basis of relative magnitude of D^2 values, the strains were grouped into 12 clusters with the assumption that those within the cluster have smaller D^2 values among themselves than those belonging to two different clusters. Four strains each were accommodated in clusters I, II and III, five each in clusters IV and VIII, three each in clusters VI, VIII, IX, X and XI, two in cluster V, and one in cluster XII. The maximum genetic divergence was observed between strains of clusters III and XI (289.3), followed by 286.8 between those of clusters III and X (Table 1). Least divergence was recorded between clusters I and XII (12.4). The intracluster divergence ranged from 5.2 to 64.1, the lowest being in cluster V and the highest in cluster IX (Table 2). Cluster IV had high mean values for plant height and 100-grain weight; cluster V for grains/pod and harvest index; cluster VIII for days to flower and grain yield/plant; cluster XI for pods/plant, grains/pod, and protein content; and cluster XII for branches/plant (Table 3). The clustering pattern showed that the strains usually did not cluster according to their geographical distribution. Murty and Arunachalam [2] stated that genetic drift and selection in different environments could cause greater diversity than geographic distance. Further, there was a free exchange of seed material among the different regions. Consequently, character constellations that might be associated with a particular region in nature lose their individuality under human interference. Sindhu [3] also did not find parallelism between genetic diversity and geographic distribution in faba bean.

Table 1. Composition of clusters in *Vicia faba*

Cluster No.	No. of strains	Strains included in the cluster
I	4	ILB 227 (Afghanistan), FB-82-46 (Egypt), 76-3446 (W. Germany), Sevilla Giant (unknown)
II	4	Bianka (Holland), Lattakia (Syria), Jordan local (Jordan), Giza-3 (Egypt)
III	4	K 1 (Kanpur), FLIP 83-4 (Canada), Turkish Local (Turkey), FB 82-54 (Egypt)
IV	5	76-56297 (W. Germany), Elegant 5 MCI (Syria), FLIP 82-26 (Ethiopia), 77-8831 (W. Germany), Giza-4 (Egypt)
V	2	805-80026 (England), 80-S 84464 (England)
VI	3	K2 (Kanpur), FB 82-53 (Egypt), FLIP 83-6 (Canada)
VII	5	KF 4 (Kanpur), 795 546 (England), KF 2 (Kanpur), VH-5 (Hissar), Syrian Local Small (Syria)
VIII	3	KF-3 (Kanpur), VH-131 (Hissar), KF-6 (Kanpur)
IX	3	80 S 44178 (Egland), K5 (Kanpur, Syrian Local Large (Syria)
X	3	FB 82-39 (Egypt), 80 S 8002 (England, Lebanese Local (Lebanon)
XI	3	79 S 79180 (England), KF-1 (Kanpur), VH 130 (Hissar)
XII	1	FLIP 83-5 (Canada)

Timothy [4] examined about 12,000 genetic stocks of maize (*Zea mays* L.), but could not establish any direct association between geographic distribution and genetic diversity. However, in some cases the effect of geographic origin influenced clustering. Cluster VIII had all the strains from India, two out of three strains in cluster XI and three out of five strains in cluster VII were from India, indicating that although geographic distribution was not the sole criterion of genetic diversity, the importance of the former was still undisputable.

Free clustering of the strains indicated dependence on the directional selection pressure applied for realizing maximum yield in different regions, and thus, the well-evolved homeostatic devices will favour constancy of the associated characters and will therefore show indiscriminate clustering. Apparently, it is not necessary to choose diverse parents from diverse geographic regions for hybridization.

Table 2. Average intracluster (diagonal) in bold and intercluster D^2 and D values

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**10.6** **(3.2)**	20.7 (4.5)	190.2 (13.8)	96.1 (9.8)	33.0 (5.7)	115.7 (10.7)	14.5 (3.8)	34.9 (5.9)	60.1 (7.7)	24.2 (4.9)	28.3 (5.3)	12.4 (3.52)
II		**13.8** **(3.71)**	115.7 (10.75)	85.1 (9.2)	35.1 (5.9)	64.7 (8.0)	35.3 (5.9)	29.9 (5.5)	45.5 (6.74)	61.2 (7.8)	72.5 (8.5)	35.2 (5.9)
III			**20.3** **(4.50)**	44.4 (6.7)	89.5 (9.4)	22.9 (4.8)	188.9 (13.7)	110.8 (10.5)	99.4 (10.0)	286.8 (16.9)	289.3 (17.0)	224.1 (15.0)
IV				**9.6** **(3.1)**	41.5 (6.4)	22.9 (4.8)	94.7 (9.7)	54.1 (7.3)	51.3 (7.2)	147.2 (12.1)	165.4 (12.9)	102.26 (10.1)
V					**5.2** **(2.3)**	40.9 (6.4)	28.4 (5.3)	16.4 (4.0)	28.1 (5.3)	75.6 (8.7)	71.7 (8.5)	48.6 (7.0)
VI						**8.4** **(2.9)**	115.6 (10.7)	60.0 (97.7)	52.6 (7.2)	193.8 (13.9)	199.0 (14.1)	138.8 (11.8)
VII							**7.3** **(2.7)**	27.7 (5.3)	58.3 (7.6)	26.7 (5.2)	18.7 (4.3)	18.6 (4.3)
VIII								**20.9** **(4.6)**	43.9 (6.6)	71.4 (8.4)	63.5 (8.0)	53.3 (7.3)
IX									**64.1** **(8.0)**	102.2 (10.1)	111.2 (10.5)	72.21 (8.5)
X										**12.7** **(3.6)**	24.1 (4.9)	19.1 (4.4)
XI											**9.2** **(3.0)**	29.0 (5.4)
XII												**12.4** **(3.5)**

Figures in parentheses are D values.

Table 3. Cluster means for different characters

Cluster No.	Days to flower	Plant height, cm	No. of branches	Pods per plant	Pod length, cm	Seeds per pod	Grain yield per plant, g	100-grain wt., g	Harvest index, %	Protein content, %
I	38.3	71.8	7.0	10.7	5.50	2.43	9.7	41.1	28.7	27.9
II	40.7	75.0	6.1	10.3	5.76*	2.42	11.9	50.8	26.9	25.9
III	40.8	70.5	6.7	17.5	4.79	2.58	8.6	28.9	30.7	21.2*
IV	39.9	75.4**	5.8	8.7	5.60	2.12*	8.5	52.7**	21.8**	23.4
V	38.5	64.5*	6.3	18.2	3.96*	2.85**	8.5	20.7*	38.3**	25.9
VI	40.2	71.4	6.1	14.1	4.13	2.45	11.3	25.2	35.4	22.7
VII	42.1	72.3	5.5	19.6	4.37	2.79	9.9	23.3	36.1	28.3
VIII	43.3**	65.5	5.8	20.4	4.42	2.49	13.4**	21.5	36.4	26.3
IX	38.7	70.6	4.8	9.6	4.49	2.67	9.0	27.3	34.7	25.3
X	42.5	69.5	4.8*	7.0*	5.14	2.24	7.1*	42.3	22.9	29.5
XI	20.9	72.6	6.2	20.1**	4.54	2.85**	10.7	22.8	37.0	30.0**
XII	42.7	81.2	6.9**	9.5	4.60	2.46	8.7	20.3	30.3	28.2

*Indicates lowest, and **indicates highest mean value.

The strains which evolved in a common habitat also had ample genetic diversity and fell into different clusters. K 1 fell in cluster III, whereas K 2 was placed in cluster VI and K 5 in IX; FB 82-54 was in cluster III but FB 82-53 was in VI; and VH 131 found place in cluster VIII and VH 130 in XI. Substantial variability among the genotypes that evolved in the same habitat could be due to (i) some degree of heterogeneity either through marginal outcrossing or through balanced polymorphic system, (ii) directional selection for some agronomic characters under domestication, (iii) genetically diverse nature of the parents used in the evolution of genotypes, or (iv) genetic drift due to selection under diverse environments. Number of pods per plant and 100-grain weight made a predominant contribution to interstrain diversity. These traits are important yield contributing attributes and should be more useful for further consideration in hybridization and improvement of faba bean.

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