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GENETIC DIVERSITY AND RELATIONSHIP STUDY IN FABA BEAN (*VICIAFABA* L.) GENOTYPES OF INDIAN AND EXOTIC ORIGIN

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ABSTRACT
Estimation of genetic diversity is important to utilize it into the crop improvement programmes. Genetic divergence studies help to identify the parents which can give better performing hybrids or transgressive segregants upon crossing. The cluster analysis technique based on Mahalanobis's D^2 Statistics was used as a tool of analysis of genetic diversity in 65 faba bean genotypes of Indian and exotic origin which grouped into 9 clusters.Three out of the total nine clusters incorporated genotypes originating from different geographic locations of the world including India and hence a definite relationship between geographic origin of the genotypes and genetic divergence could not be established.The intra-cluster distances ranged from 0 to 3.59 with an average of 2.38.The inter-cluster D^2 values ranged from 2.67 to 8.77 with an average of 6.12. The number of clusters and the inter-cluster distances indicated presence of significant genetic diversity in the genotypes under study. The study helped in the identification of superior faba bean genotypes for further among crossing for yield enhancement.

INTRODUCTION

Faba bean (*Viciafaba* L.),widely cultivated for human food, animal feed and fodder, is the world's fourth most important legume crop after pea, chickpea and lentil (Kaur *et al*., 2014). It is gaining importance as a grain legume for protein security of demographically expanding and climatically changing world (Bishnoi *et al.,* 2012). Faba bean plays an important role in world agriculture because of its high seed protein content which ranges from 20 to 40% depending upon the genotype and the environmental conditions in which it has been grown (Negash *et al*., 2015). However, in India it has been categorized as an underutilized potential legume crop. It was introduced into India through Mesopotamia probably after the advent of the Arabian spice trade route which came in to existence around 3000B.C. (Bishnoi, 2016).The global faba bean germplasm has quite large genetic variability. Based on differences in seed weight, shape and size, two subspecies *Viciafaba*s sp paucijuga and *Vicia faba*s speu faba have been recognized. The subspecies eufaba is further divided in to three types viz. minor, equina and major(Oliveira *et al*., 2016).Over the years the faba bean germplasm have naturalized under Indian agro-climatic conditions and have developed area specific adaptive traits. The faba bean germplasm from India is reported to exhibit considerably high diversity in morphological and agronomic traitswhich is attributed to its wider distribution and partially all ogamous pollination biology.The degree of genetic diversity and its evaluation can reflect the level of genetic progress in future breeding (Hou *et al*., 2015). The genetic divergence studies are of great help in selecting parents for developing varieties especially the hybrids. Effective hybridization program between genetically divergent parents will lead to considerable amount of heterotic responsein F_1hybrids and broad spectrum of variability in segregating generations (Johnson *et al.,* 2015). The genetically characterized genotypes are a necessary requisite to identify desirable characters and genes from unadaptedgenotypes that cannot be used directly in breeding programmes for producing new varieties with desired attributes. The increased yield caused by heterozygosity due to outcrossing has been well documented in faba bean. Thus, heterosis, resulting from the combined action and interaction of allelic and interallelic genes is effective in faba bean and improved yield can be obtained by hybrid combinations (Bishnoi *et al.,* 2015, Bishnoi, 2016).The present study involved faba bean genotypes of Indian and exotic origin and was carried out with the objective to estimate genetic divergence and relationship to identify superior and diverse genotypes for further use in the hybrid or transgressive breeding programme aimed at realization of yield potential in this important pulse crop.

MATERIALS AND METHODS

A total of 65faba bean genotypes originating from different geographic origins of the world were evaluated in randomized block design with three replications during 2015-16 at the experimental farm of Medicinal, Aromatic and Potential Crops Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The row length was kept 3 meter with 3 rows per replication and a spacing of 30×10 cm. The data was recorded on five randomly selected

characters on days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, 100 seed weight and seed yield. The analysis of data was carried out using the online version of OPSTAT of CCS Haryana Agricultural University, Hisar. Mahalanobis D^2 statistics (Mahalanobis, 1936) was used for estimation of genetic divergence among the genotypes and clustering was done based on Tocher's method as described by Rao, 1952. The average intra-cluster and inter-cluster distances and percent contribution of the traits towards genetic divergence were estimated as per Singh and Chaudhary, (1979).

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) showed significant differences for all the studied traits which indicated the presence of significant genetic variability in the set of genotypes under study. The 65 genotypes under study were grouped into nine different non-overlapping clusters. (Table 1). Clusters I and III were the largest with 20 genotypes each, followed by cluster IV with 11 genotypes, clusters VIII and IX with 4 and I genotypes respectively, cluster II, VI and VII with 2 genotypes each and cluster V with only one genotype.The number of clusters and the inter-cluster distances indicated presence of considerably high genetic diversity in the genotypes under study. The cluster IV included genotypes of Indian origin only while clustersVII and VIII had genotypes of exotic origin only. On the other hand, cluster I, III and IV incorporated genotypes originating from different geographic locations of the world including India and thus a definite relationship between geographic origin of the genotypes and genetic divergence could not be established. Similar findings were reported by Katiyar and Singh (1990),Keneni*et al.,* (2005),Keneni*et. al.,* (2007) and Bishnoi (2016). The average inter-cluster distances were greater as compared to the intra-cluster distance revealing that considerable amount of genetic diversity existed among the genotypes (Table 2).Fikreselassie and Sekoba (2012) reported similar results in Ethiopian genotypes and Sharifi and Aminpana (2014) reported similar findings in Iranian genotypes.

The intra-cluster distances ranged from 0 to 3.585 with an average of 2.38 Cluster V was having only one genotype thereforethe intra - cluster distance waszero. Among the clusters having more than one genotypes, cluster VI had minimum intra-clusterdistance (1.98) indicating clustering together of genetically closely related genotypes.While cluster IX had maximum intra-cluster distance (3.58) indicating clustering together of genotypes which were not significantly related. The inter cluster D^2 values ranged from 2.67 (cluster III and V) to 8.77(cluster IV and VII) with an average of 6.12indicative of the presence of high genetic variability among the genotypes**.**The cluster mean values for different characters are very helpful in identification of a genotype with desired value of the desired trait for inclusion in a hybridization programme as parent. The cluster mean values for different characters under study are presented in table 3. The cluster IX was having genotypes with highest mean values for days to 50% flowering, 100 seed weight, seed yield while cluster VIIwas having highest mean value for plant height and seeds per pod, cluster VI was having highest mean values for cluster per plant, pods per plant and pod length and cluster V showed highest mean value for number of branches per plant.

The genetically diverse and promising genotypes were identified in the present study. The overall best performing

Table I: Clustering of 65 genotypes of fababean on the basis of D^2 statistics

Cluster	Number of genotypes	Name of genotypes
I.	20	HB-18,RFB-11,NDF-12,DFB13-1,DFB13-2,RMDFB-1,RMDFB-2,HB-39,RFB-7,EC-108 45,DFB-1,EC-354951,MLMK-7,RFB-12,NDF-14,EC-598938,EC-243770,EC-25085,EC-I, HB-19
II.	2	EC-243624,EC-628939
III.	20	HB-14,HB-176,HB-613,DFB10-1,DFB10-2,HB-604,NDF11,NDF12-1,NDF13-2,AFB 13-2,HB-28,HB-31,AFB13-1, NDF-9,NDF-4,RFB-8,DFB10-3,RFB-9,EC-10719,Vikrant
IV.	11	HB-33,EC-628962,NDF-1,PusaSumit,NDF-13,HB-48,HB-50,HB-62,HB-64,HB-3,HB-38
V.	1	NDF-8
VI.	2	ET-4101,ET-5108
VII.	2	EC-628955,EC-628942
VIII.	4	EC-628937,EC-628936,EC-591755,ET-3134
IX.	3	ET-2112,EC-628930,EC-591776

Table II: Average intra (diagonal) and inter (above diagonal) cluster D^2 values of different characters in faba bean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	2.062	3.633	2.676	3.355	6.223	5.928	6.063	5.746	7.705
II		2.122	4.487	5.256	7.401	7.792	7.039	6.225	7.672
III			1.995	3.324	6.337	5.761	6.47	6.396	8.167
IV				3.017	5.469	5.309	6.497	5.866	8.008
V					0	7.919	8.774	7.207	8.353
VI						1.981	4.849	6.03	7.648
VII							3.153	4.827	5.028
VIII								3.544	4.703
IX									3.585

Table III: Mean values of different clusters for 10 characters in faba bean

Cluster	DF	DM	PH	BP	CP	PP	PL	SP	100SW	SY
I	53.22	154.53	112.90	3.52	14.80	45.14	5.13	3.22	27.25	28.82
II	58.70	161.67	115.50	3.88	17.72	83.16	4.81	3.22	29.39	14.71
III	52.14	151.78	128.79	3.63	10.40	39.10	4.98	2.95	26.76	19.54
IV	59.58	157.67	106.42	4.08	6.78	32.76	5.11	3.23	28.72	24.17
V	61.67	164.67	88.33	10.33	7.99	25.00	4.10	3.00	24.18	19.00
VI	72.00	164.83	128.54	3.78	5.27	12.89	8.67	4.03	48.83	19.50
VII	72.83	159.33	130.00	4.05	15.50	36.17	8.03	4.11	94.17	151.00
VIII	86.42	185.92	110.03	4.71	15.23	40.23	5.67	3.75	77.22	116.50
IX	86.89	183.33	126.11	7.44	17.13	53.11	6.79	3.70	101.11	219.70
Mean	59.04	158.32	117.83	4.04	11.93	40.85	5.36	3.24	36.57	42.27
TreatMSS	1097.22	888.43	882.41	12.17	117.94	1006.01	7.06	0.87	4376.75	22969.10
ErrMSS	23.45	36.98	93.51	0.52	6.82	62.68	0.39	0.06	33.36	156.40

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, CP: Clusters per plant, PL: Pod length, SP: Seeds per pod, 100SW: 100 seed weight, SY: Seed yield

Table IV: Diverse and superior genotypes identified among different clusters

Genotype	Cluster	DF	DM	PH	BP	CP	PP	PL	SP	100SW	SY
EC-628955	VII	73.67	156.67	137.00	3.10	16.66	27.00	7.33	4.10	96.33	110.00
EC-628942	VII	72.00	162.00	123.00	5.00	14.33	45.33	8.72	4.11	92.00	192.00
EC-628937	VIII	87.00	172.33	101.67	4.96	16.42	39.33	5.05	4.00	70.67	116.33
EC-628936	VIII	90.00	187.67	122.33	4.00	20.89	45.33	6.20	4.00	73.00	115.00
EC-591755	VIII	85.67	189.67	113.79	5.08	9.00	36.71	7.33	4.00	79.67	123.33
ET-3134	VIII	83.00	194.00	102.33	4.79	14.62	39.55	4.10	3.00	85.53	111.33
ET-2112	IX	82.33	190.00	116.00	7.00	14.89	42.00	7.44	4.00	105.00	204.33
ET-628930	IX	92.33	193.67	131.67	7.00	18.33	60.00	6.44	4.10	92.67	245.43
EC-591776	IX	86.00	166.33	130.67	8.33	18.18	57.33	6.50	3.00	105.67	209.33

Table V: Superior genotypes (Character wise)

Number of days to maturity	Number of branches per plant	Number of cluster per plant	Number of pods per plant	Seed yield per plant
AFB 13-1 (142.33)	NDF-8(10.33)	EC-329612(21.00)	EC-628939(89.00)	EC-628930(245.33)
NDF-4 (148.00)	EC-591776(8.33)	EC-628936(20.89)	EC-243624(77.33)	EC-591776(209.33)
EC-329612 (148.00)	EC-628930(7.00)	EC-25085(18.78)	DFB 13-1(61.34)	ET-2112(204.33)
NDF 13-2 (148.67)	ET-2112(7.00)	EC-628930(18.33)	EC-628930(60.00)	EC-628942(192.00)
AFB 13-2 (149.00)	HB-3(5.57)	EC-591776(18.18)	DFB 13-2(58.66)	EC-628937(116.33)

genotypes belonging to different clusters were EC-628955, EC-628942, EC-628937, EC-628936, EC-591755, EC-3134, EC-2112, EC-628930 and EC-591776. The mean values for each character of these superior genotypes identified clusterwise are presented in Table 4.

The trait specific identification of the best genotype is important for estimating the worth of a genotype for inclusion in a breeding programme aimed at improving a single trait.In the present study different genotypes having different desired traits in desired values were identified (Table 5). AFB 13-1 (III)NDF-4(III) EC-329612 (I) NDF 13-2(III) and AFB 13-2 (III) were found to be the earliest maturing genotypes, NDF - 8(V), EC-591776 (IX), EC-628930(IX), ET-2112(IX), HB-3(IV), were the highest number of branches per plant type genotypes.The highest number of cluster per plant were present in EC-329612(I),EC-628936 (VIII), EC-25085 (I), EC-628930 (IX) and EC-591776 (IX) while highest number of pods per plant were recorded in EC-628939 (II), EC-243624 (II) EC-628930 (IX), DFB13-2(I) and DFB-13-1(I). The five top yielding genotypes were EC-628930 (IX), EC-591776 (IX), ET-2112(IX), EC-628942 (VIII) and EC-591755 (VIII). The corresponding cluster to which a genotype belonged is given in the parenthesis. The exotic collections seem to have a yield advantage, however, origin of genotypes among the best yielders was not found to have a correspondence with the yield. The findings of the present study are in agreement with Keneni *et al*. (2005), Keneni *et al*. (2007), Fikreselassie and Sekoba (2012), Al-Barri *et al*., 2013 and Shariffi and Aminpana (2014). In the present study the genetic variability was quantified in the Indian and exotic faba bean germ plasm and it was concluded that the Indian faba bean germ plasm has significantly high genetic variability and it differs significantly from the germ plasm of exotic origin. It was also concluded that themain factor behind the presence of high genetic diversity in the genotypes appears to be genetic drift and selection in differing environments rather than their geographic origin. The study resulted in the identification of promising faba bean genotypes for use in hybrid breeding and transgressive breeding for yield improvement. It is assumed that probability of obtaining superior transgressive segregants and maximum amount of heterosis will be manifested in cross combinations involving the genotypes

belonging to most divergent clusters identified in the present study.

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