Faba Bean (*Vicia faba* L.) Germplasm Evaluation and Genetic Divergence Analysis

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ABSTRACT

The present investigation was carried out involving sixty-seven germplasm lines evaluated of faba bean, normal soil under irrigated condition with three check varieties *viz.,* PRT7, PRT12 and Vikrant. Seed yield per plant showed highly significant and positive correlation with harvest index and biological yield per plant. Biological yield per plant exhibited highly significant and positive correlation with days to maturity. Days to maturity and number of pods per plant via biological yield per plant exerted substantial positive indirect effect on seed yield. The nine clusters in divergence analyses contained genotypes of heterogeneous origin, thereby indicating no parallelism between genetic and geographic diversity. Therefore, crosses between the members of clusters separated by high inter-cluster distance are likely to throw desirable segregants. Maximum inter cluster distance was recorded between cluster IV and cluster IX. However, maximum intra-cluster distance was observed in cluster I. The different clusters showed considerable differences in intra-cluster group means of eleven characters and genotypes having distinctly different mean performance for various characters were separated in to different clusters.

Keywords: Correlation, faba bean, genetic diversity, path and cluster analysis

INTRODUCTION

Faba bean (*Vicia faba* L.) is an important pulse crop of the world cultivated under both irrigated and rainfed conditions (Singh *et al.*, 2012b). Faba bean is an annual legume botanically known as *Vicia faba* L is one of the oldest crops grown by man and is used as a source of protein in human diet, as fodder and forage crop for animals, and for available nitrogen in the biosphere (Singh and Bhatt, 2012b). Wide cultivation and spread of faba bean (*Vicia faba* L.) in temperate and subtropical region has ranked it the fourth most important legume crop in the world next to dry beans, dry peas and chickpea (Singh and Bhatt, 2013). Faba bean is widely used in the Mediterranean region as source of protein in both human and animal nutrition (Larralde, 1982). It is grown as *Rabi* crop in diverse agro-ecological situations from hills to plain and even under poor management. In India it is grown in a sizeable acreage in Bihar, Madhya Pradesh and some part of Utter Pradesh (Singh *et al.*, 2012c). Its green pods are used as vegetable and dry seeds are use as split dal and the preparation of besan.

It is popularly called as "Bakla" in Hindi heartland. They were introduced to India by Arab traders. The name is derived from Arabic name "Baquila". In slang they are also called "Kala Mattar" In some Ayurvedic terms; it is also called "Anturi"(Singh *et al.*, 2013a). Seeds of faba bean greatly varied in size, shape, specific gravity, bulk density etc (Sundaram *et al.*, 2014). Its critical role in crop rotation, reducing energy cost, improving soil physical conditions and decreasing the amount of diseases and weed populations has long been recognized (Singh *et al.*, 2012a). In spite of its potential, the total area of faba bean cultivation has steadily decreased in many countries over the last century (Singh *et al.*, 2013b and Singh and Bhatt, 2012a).

Faba bean, like other beans, are a good source of calories, protein, carbohydrates, and fibre they are also rich in phosphorus, iron, potassium, and vitamin B complex (Singh *et al.*, 2014). To make faba bean into a perfect candidate for a sustainable agriculture, the crop should be beneficial both to farmers/producers and to users (human and/or animal nutrition). This goal could be achieved through the development of genotypes resistant to diseases and abiotic constrains such as

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over-wintering ability, frost resistance and drought avoidance, and free of anti-nutritional factors (Singh *and Bhatt,* 2012a). Lack of suitable varietal technology is one of the major bottlenecks to adopt this crop (Singh *and Bhatt,* 2012b). It has great production potential which has not been realized so for accordingly, the present study was carried out to evaluate the available germplasm to work out the character association and direct and indirect effects of different attributes with respect to yield. An attempt has been made to evaluate available faba bean germplasm for efficient utilization in breeding programme.

MATERIALS AND METHODS

The experimental material for the present investigation consisted of 67 germplasm lines of faba bean there grown in Augmented Design with three checks, repeated after every 8 lines of the test entries. The experiment was carried out at the Student's Instructional Farm of Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India. Each accession was grown in double row of 4m length with inter row spacing of 30cm. All the recommended cultural practices were adopted to raise a good crop.

The observation were recorded on plant height, number of branches/plant, number of pods/plant, number of seeds/plant (g), harvest index (%) and protein content (%) were recorded on five randomly selected plants while days to 50% flowering and days to maturity on plot basis. The mandate was subjected to analysis of variance following Federer (1956). Estimation of correlation coefficient was done following Path coefficient analysis was done as suggested by Dewey and Lu (1959). Genetic divergence analysis was done followed by Beale (1969) and Spark (1973).

RESULTS AND DISCUSSION

Analysis of variance (Table 1) due to treatment showed highly significant for days to 50% flowering , plant height, branches per plant, harvest index and protein content significant and other characters were found to be non significant.

Correlation Studies

Correlation analysis (Table 2) revealed that seed yield/plant was highly significantly and positively correlated with harvest index, biological yield per plant while significant and positive correlation with days to 50%

Table 1: Analysis of variance (Augmented design) for eleven characters in Faba bean germplasm

	d.f.	Days to 50% Flowering	Days to Maturity	Branch-es/Plant	Plant Height (cm)	Pods/Plant	Seeds/Pod	Bio-logical Yield/Plant (g)	Seed Yield/Plant (g)	Harvest Index (%)	100 Seed Weight (g)	Protein Content %
Block (ignoring Treatments)	7	122.91**	34.00**	0.49*	241.61**	111.77**	0.27*	237.08	29.84	32.10**	9.00*	0.33**
Treatment (eliminating Blocks)	66	12.42*	9.80	0.60**	82.72*	16.20	0.06	110.04	9.75	24.65**	4.91	0.91**
Checks	2	12.54	0.04	0.27	10.12	2.03	0.01	5.03	5.69	6.78	1.73	0.01
Checks+Var vs. Var.	64	12.42*	10.10	0.61**	84.99*	16.64	0.06	113.33	9.87	25.21**	5.00	0.94**
ERROR	14	3.97	7.47	0.16	30.85	10.53	0.07	88.44	10.95	3.76	2.47	0.04
Block (eliminating Check+Var.)	7	5.81	2.45	0.11	21.09	8.57	0.14	5.40	0.98	2.65	5.88	0.07
Entries (ignoring Blocks)	66	24.84**	13.14	0.64**	106.11**	27.14*	0.07	134.62	12.81	27.77**	5.24	0.94**
Checks	2	12.54	0.04	0.27	10.12	2.03	0.01	5.03	5.69	6.78	1.73	0.01
Varieties	63	24.51**	13.58	0.65**	109.57**	28.34*	0.07	139.46	12.97	28.88**	5.38	0.82**
Checks vs. Varieties	1	70.18**	11.82	0.62	80.53	1.76	0.05	88.40	16.98	0.18	3.05	10.01**
ERROR	14	3.97	7.47	0.16	30.85	10.53	0.07	88.44	10.95	3.76	2.47	0.04

*, ** Significant at P=0.05 and P=0.01 respectively

flowering and number of seed per pod. Seed per plant showed non-significant and positive correlation with 100-seed weight and protein content. However, seed yield per plant showed negative significant correlation with number of pods per plant and showed negative non significant correlation with number of branched/plant, plant height and days to maturity (Singh and Bhatt, 2012a). Biological yield/plant was highly significant and positive correlation with days to 50% flowering and highly significant negative correlation with days to maturity, harvest index with days to maturity showed positive and highly significant. However, negative and highly significant was observed with biological yield/plant, numbers of pods/plant was positive and highly significant correlations with number of branches/plant and plant height. However, days to 50% flowering was negative and highly significant association with found significant negative correlation with days to 50% flowering. Days to maturity were significant correlation with days to flowering (Singh *et al.*, 2013a).

Path Coefficient Analysis

The direct and indirect effects of different character on seed yield/ plant were estimated by path analysis using simple correlations given in Table 3. The highest positive direct effect on seed yield/plant was exhibited by harvest index (1.206) followed by biological yield/plant (1.067). The low and positive direct effect was recorded in case of number of pods/plant (0.022), 100-seed weight (0.020), number of pods/pant (0.019), protein content (0.017), plant height (0.016) and negative direct effect was recorded for number of branches per plant (-0.033), days to maturity (-0.028) and days to 50% flowering (-0.002). The days to maturity (0.495), protein content (0.175) and 100 seed weight (0.168) exerted substantial positive indirect effect on seed yield via harvest index while biological yield/plant (-0.766), plant height (-0.284), number of pods/plant (-0.170) exerted substantial negative indirect effect on seed yield via harvest index. Days to 50% flowering (0.481) and plant height (0.141) exerted substantial positive indirect effect on seed yield via biological yield/plant while harvest index (-0.582) days to maturity (-0.418) and number of pods/plant (-0.196) exerted substantial negative indirect effect (Ojha *et al.*, 2011).

Genetic Divergence

In the present study, 64 genotypes of faba bean were grouped into nine distinct non- overlapping clusters using non- hierarchical Euclidean cluster analysis (Table 4).Which is in agreement with earlier reports indicating substantial diversity in faba bean material (Bargale and

Table2: Estimates of simple correlation coefficients between different characters in 64 germplasm of faba bean

Characters	Days to 50 % flowering	Days to maturity	No. of branch-es/ plant	Plant height (cm)	Pods/ plant	Seeds/ pod	Biological yield/ plant (g)	Harvest index (%)	100 Seed weight (g)	Protein content (%)	Seed yield/ plant (g)
Days to 50% flowering	**1.0000**	-0.301*	-0.271*	-0.150	-0.322**	0.036	0.451**	-0.181	-0.011	0.010	0.271*
Days to maturity		**1.0000**	0.0678	-0.128	0.021	0.073	-0.446**	0.411**	0.031	0.109	-0.009
Number of branches / plant			**1.0000**	0.064	0.537**	0.089	-0.184	0.059	-0.129	0.069	-0.148
Plant height(cm)				**1.0000**	0.318**	-0.014	0.132	-0.236	0.072	-0.011	-0.118
Number of pods / plant					**1.0000**	-0.175	-0.149	-0.141	-0.197	-0.139	-0.334**
Number of Seeds / pod						**1.0000**	0.068	0.142	0.035	0.019	0.259*
Biological yield / plant (g)							**1.0000**	-0.634**	0.009	-0.062	0.320**
Harvest Index (%)								**1.0000**	0.139	0.146	0.519**
100 Seed Weight (g)									1.0000	-0.009	0.201
Protein Content (%)										**1.0000**	0.119
Seed yield plant^{-1} (g)											**1.0000**

*, ** Significant at P=0.05 and P=0.01 respectively

Table 3: Direct and indirect effect of different characters on seed yield per plant in faba bean germplasm

Characters	Days to 50% flowering	Days to maturity	Number of branches/ plant	Plant height (cm)	Pods/ plant	Seeds/ pod	Bio-logical yield/ plant (g)	Har-vest index (%)	100 Seed weight (g)	Protein content (%)	Cor-relation with seed yield
Days to 50% flowering	**1.0000**	-0.3014	-0.2712	-0.1504	-0.3217	0.0359	0.4512	-0.1805	-0.0105	0.0104	0.2712
Days to maturity	-0.3014	**1.0000**	0.0678	-01281	0.0205	0.0728	-0.4464	0.4105	0.0310	0.1091	-0.0089
Number of branches/ Plant	-0.2712	0.0678	**1.0000**	0.0641	0.5365	0.0890	-0.1837	0.0590	-0.1289	0.0690	-0.1478
Plant height (cm)	-0.1504	-0.1282	0.0641	**1.0000**	0.3181	-0.0135	0.1321	-0.2359	0.0724	-0.0108	-0.1184
Pods/ plant	-0.3217	0.0205	0.5365	0.3181	**1.0000**	-0.1747	-0.1499	-0.1410	-0.1970	-0.1389	-0.3339
Seeds/ pod	0.0359	0.0728	0.0890	-0.0135	-0.1747	**1.0000**	0.0680	0.1424	0.0348	0.0191	0.2590
Biological yield (g)	0.4512	-0.4464	-0.1837	0.1321	-0.1499	0.0680	**1.0000**	-0.6337	0.0098	-0.0623	0.3203
Harvest index (%)	-0.1805	0.4105	0.0590	-0.2359	-0.1410	0.1424	-0.6337	**1.0000**	0.1398	0.1456	0.5191
100- seed weight (g)	-0.0105	0.0310	-0.1289	0.0724	-0.1970	0.0348	0.0098	0.1398	**1.0000**	-0.0090	0.2008
Protein content (%)	0.0104	0.1091	0.0690	-0.0108	-0.1389	0.0191	-0.0623	0.1456	-0.0090	**1.0000**	0.1187

Residual factor = 0.1534, Bold figures indicate direct effects.

Billore, 1992). Cluster I had seven genotypes which were characterized by highest cluster mean for number of branches per plant and average cluster mean for remaining traits. The six genotypes present in cluster II result in lowest cluster means for protein content and average cluster mean for remaining traits. The cluster III had five genotypes resulting in highest cluster mean for days to maturity and plant height and lowest cluster mean for days to 50% flowering and number of seeds per pod and average cluster mean for all other characters. The cluster IV had four genotypes resulting in highest cluster mean for number of pods per plant and lowest cluster mean for days to maturity, harvest index, 100-seed weight and seed yield per plant and average cluster mean for all other characters. The cluster V had ten genotypes resulting in highest cluster mean for biological yield per plant and seed yield per plant and average cluster mean for all other characters. Cluster VI comprising nine genotypes had highest cluster mean performance for days to 50% flowering and number of seeds per pod and average cluster mean for all other characters. Cluster VII having for tine genotypes had average cluster mean for all characters. Cluster VIII had six genotypes with highest mean performance for 100-seed weight and lowest mean performance for number of branches per plant and average cluster mean for all

other characters. Cluster IX having six genotypes had highest mean performance for harvest index and protein content and lowest mean performance for plant height, number of pods per plant and biological yield per plant and average cluster mean for all other characters. The above observation confirm wide variation from one cluster to another in respect of cluster mean, which indicated that genotypes having distinct different mean performance for various characters were separated into different clusters (Dwevedi and Lal, 2009 and Sial *et al.*,2010).

The nine clusters in the aforesaid divergence analysis contained frequently the genotypes of heterogeneous origin, although the genotypes originated in same place or geographic region were also found to be grouped together in same cluster. The instances of grouping of genotypes of different origin or geographical region also in

same cluster were observed in case of all the ten clusters. This suggests lack of parallelism between genetic and geographic diversity. Therefore, the selection of parental material for hybridization programme simply based on geographic diversity may not be a successful exercise for the choice of suitable divergent parents. Selection on the basis of genetic divergence analysis would be

Table 4: Clustering pattern of 67 faba bean genotypes on the basis of non-hierarchical Euclidean cluster analysis

Cluster Number	No. of genotypes	Genotypes
I	7	HB 1, HB 16, HB 5, EC 10719, EC 117724, EC 117743, EC 117795
II	6	HB 57, EC 24312, EC 117705, EC 243761, HB 77, EC 25192
III	5	HB 15, HB 18, HB 20, HB 23, HB 31
IV	4	HB 37, EC 243756, HB 44, HB 50
V	10	HB 10, EC 117741, PRT 7(C), PRT 12(C), VIKRANT(C), EC 243781, EC 243782, EC 243762, EC 117748, EC 117749
VI	9	EC 7818, EC 10845, EC 117744, EC 32976, EC 243641, EC 10782, EC 117758, EC 243596, EC 243709
VII	14	HB 17, EC 243626, EC 108906, EC 243524, EC 243608, EC 117792, EC 243443, EC 117755, EC 117842, EC 243036, EC 117765, EC 243588, EC 243624, EC 243755
VIII	6	EC 1072, EC 5873, EC 25085, EC 243529, EC 117739, EC29058
IX	6	EC 117726, EC 243584, EC 5864, EC 3279, HB 76, EC 117727
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IX	6	EC 117726, EC 243584, EC 5864, EC 3279, HB 76, EC 117727

more rewarding than the choice made on the basis of geographic diversity. This finding is in agreement with the report advocating lack of definite relationship between genetic and geographic diversity in faba bean (Bargale and Billore, 1992).

An examination of the estimates of within and between cluster diversity presented by intra and inter cluster D^2 values revealed that the genotypes of the same cluster had little divergence from each other with respect to aggregate effect of 11 characters under study (Table 5). Therefore, the chances of obtaining good recombinants in segregating generation by crossing the members of the same cluster are very low. It is, therefore, suggested that crosses should be attempted between the genotypes belonging to clusters separated by large inter-cluster distance in this respect. The highest number of genotypes appeared in cluster VII which contained 14 genotypes followed by cluster V having 10 genotypes. Cluster VI, cluster I, cluster II, cluster VIII, cluster IX and cluster III having 9, 7, 6, 6, 6 and 5 genotypes, respectively. Cluster IV was represented by 4 entries and had minimum number of genotypes among all the clusters. The estimates of average intra and inter cluster distance for the nine cluster is presented. The highest intra-cluster distance was recorded for cluster I followed by cluster VI, while the lowest value was recorded in case of cluster II. The maximum inter cluster distance was recorded between cluster IV and cluster IX followed by cluster IV and cluster VIII and cluster I and cluster IV. The inter cluster distance between cluster III and cluster V, cluster III and cluster IX, cluster I and cluster VIII, cluster III and cluster VI, cluster IV and cluster V, cluster I and cluster VI, cluster I and cluster VII and cluster I and cluster IX were also in high orders. The

minimum inter cluster distance was observed between cluster V and cluster VIII followed by cluster V and cluster VII, cluster II and cluster V and cluster VIII and cluster IX. The crosses between genotypes belonging to the cluster separated by low inter cluster distances are unlikely to generate promising recombinants in segregating generations Dubey *et al.* (2007), Lokere *et al.* (2007), Dwevedi and Lal (2009), Sial *et al.* (2010) and Yadav *et al.* (2010).

The intra-cluster group mean for eleven characters revealed considerable differences between the clusters in respect of cluster means (Table 5). The crosses between the entries belonging to cluster pairs separated by large inter- cluster distances and having cluster means for one or other characters to be improved is likely to be more useful.

CONCLUSION

A wide range of variation for different characters and comparison of means of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the germplasm collection. The non-hierarchical Euclidean cluster analysis grouped all 67 genotype in to nine clusters. This indicated existence of high degree of genetic diversity in the germplasm evaluated in the present study. Therefore, crosses between the members of clusters separated by high inter-cluster distance are likely to throw desirable segregants; desirable selection may be made accordingly.

Table 5: Estimates of average intra and inter-cluster distances for the nine clusters in faba bean

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	16.934**	18.563	25.347	32.994	26.276	30.244	30.008	31.306	29.858
II		7.98*	22.029	25.057	16.584	18.831	21.127	16.936	17.398
III			15.975	24.814	32.106	30.882	26.505	28.178	32.097
IV				9.270	30.879	29.232	24.683	35.927	39.196**
V					10.521	17.786	16.141	15.884*	18.941
VI						16.125	18.084	19.009	25.904
VII							11.511	16.766	25.107
VIII								8.555	16.720
IX									12.379

Bold figures represent intra-cluster distances

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