

Study of Genetic Diversity for Selection of Promising Lines in Faba Bean (*Vicia faba* L.)

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ABSTRACT

This study was conducted to investigate the morphological and agronomical variations among eight faba bean (*Vicia faba* L.) populations and analyze their traits including: Days to flowering, days to pod picking, plant height, number of branches per plant, node of first flower, intermodal length, pod length, pod diameter, number of fruit clusters per plant, number of pods per plant, number of seeds per pod, harvesting span, pod yield per plant were studied. Wide range of variability was observed among genotypes for all the

traits. Positive skewness with leptokurtic distribution was exhibited mainly by days to first flowering and number of seeds per pod at edible stage, whereas positive skewness with platykurtic distribution was observed for the traits viz., pod length and pod diameter respectively. The eight faba bean populations were clustered into four groups based on thirteen morphological and agronomic traits. Bak-1 × Bak-11 and Bak-2 × Bak-5 is in cluster I, whereas Bak-1 × Bak-20 and Bak-16 × Bak-20 in cluster II, Bak-2 × Bak-20, and Bak-12 × Bak-5 reside in cluster III. The dissimilarity analysis reveals the highest inter-cluster distance between clusters II and IV (36.501), followed by cluster I and III (34.919) and lowest between clusters II and III (15.649). PC1, PC2, PC3 and PC4 contributed the maximum variability for the traits viz., days to first pod picking and days to first flowering.

Keywords Faba bean, Characterization, Principal component analysis, Dendrogram, Skewness and kurtosis.

INTRODUCTION

Faba bean (*Vicia faba* L.) holds significance as a crucial legume vegetable crop, particularly in India and the North-east region. It is an autogamous plant with a partial outcross ranging from 20 to 80%, characterized by being diploid with a limited number of large chromosomes ($2n = 2x = 12$) (Terzopoulos and Bebeli 2008 ; Al-Barri and Shtaya 2013 ; Bashier *et al.* 2013). Originating between the oriental Mediterranean countries and Afghanistan (Cubero

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1974), faba bean is commonly included in the diets of Middle Eastern, Mediterranean, Chinese, and Ethiopian inhabitants, presenting versatility as a vegetable, whether green or dried, fresh or canned (Bond *et al.* 1985). Rich in protein, carbohydrates, starch, total sugar, vitamins, and minerals, faba bean is also recognized for its L-dopa content, a natural source for treating Parkinson's disease (Duranti *et al.* 2008).

Despite its nutritional value, widespread consumption of faba bean is hindered by antinutritional components such as phytic acid, tannin, phenols, trypsin inhibitor, vicine and covicine, leading to hemolytic anemia known as favism. Although faba bean cultivation in India is limited, it ranks as the third most important pulse crop globally among legumes (Turk and Tawaha 2002).

Yield improvement stands as a primary breeding objective for selection of desirable lines in respect to qualitative and quantitative traits by estimating morphological diversity within and between germplasm (Maji and Shaibu 2012). In the context outlined above, this research aims to phenotypically characterize eight segregating populations of faba bean, with the goal of selecting elite lines from the existing variability in faba bean.

Table 1. Cross combination of F_3 population and Parentage.

Sl. No.	F_3 population of different crosses	Source
1.	Bak-1/Bak-5	State Non Plan Project, Deptt. of Plant Breeding and Genetics, BPSAC, Purnea
2.	Bak-1/Bak-11	-do-
3.	Bak-1/Bak-20	-do-
4.	Bak-2/Bak-5	-do-
5.	Bak-2/Bak-11	-do-
6.	Bak-2/Bak-20	-do-
7.	Bak-12/Bak-5	-do-
8.	Bak-16/Bak-20	-do-
9.	Vikrant (NC)	-do-
Parental genotypes		Source
1.	Bak 1	-do-
2.	Bak 2	-do-
3.	Bak 5	-do-
4.	Bak 11	-do-
5.	Bak 12	-do-
6.	Bak 16	-do-
7.	Bak 20	-do-

MATERIALS AND METHODS

The experiment was carried out at the Research Farm of Bhola Paswan Shastri Agricultural College, Purnea, India, during the *Rabi* season in the year 2022-23. The experimental materials comprised of eight lines of F_3 generation of faba beans, all these materials were sown with six rows without replication and row to row and plant to plant distance was maintained at 45 and 15 cm respectively and follows standard agronomical practices. These materials were obtained from the state non-plan project SNP/CI/*Rabi*/2018-6 and maintained at BPSAC, Purnea (Table 1). The Observations were recorded based on randomly selected plants from each population, focusing on yield and twelve component characters, including days to flowering, days to first pod picking, plant height (cm), number of branches, internodal length, node of the first flower, pod length (cm), pod diameter (cm), number of fruit clusters per plant, number of pods per plant, pod yield per plant (g), number of seeds per pod, and harvesting span. Skewness and kurtosis were calculated to assess the gene's effect on different traits, following the methods proposed by Snedecor and Cochran (1980) and Robson (1956). Skewness and kurtosis analysis were conducted using Excel software. Additionally, principal component analysis (PCoA) for quantitative traits was analyzed using Minitab software and dendrogram was constructed by using Ward's method.

RESULTS AND DISCUSSION

Mean performance of different traits

The performance of different segregating populations for yield and its contributing traits was evaluated, and the results indicated a wide range of genetic variability were observed in all studied traits. The statistical parameters including mean, maximum, minimum, skewness, and kurtosis for thirteen quantitative traits are presented in Table 2. The results revealed that the highest mean values for traits such as plant height, number of branches per plant, number of fruit clusters per plant, number of pods per plant, green pod length (cm), pod diameter (cm), harvesting span, number of seeds per pod at edible stage, and green pod yield per plant (g) in the cross combination Bak-16 $\times$ Bak-20.

Table 2. Mean performance, skewness and kurtosis in different crosses.

Crosses	PH	NB	IL	NFF	DFP	DPP	NFCP	NPP	PL	PD	HS	NSPPES	PY
Bak-1 × Bak-5	38.63	5.10	3.45	2.13	84.30	107.70	2.85	27.84	5.41	1.01	10.29	2.39	74.39
Bak-1 × Bak-11	42.46	4.50	3.46	2.34	70.70	105.40	1.73	21.90	5.12	0.95	5.69	2.31	48.26
Bak-1 × Bak-20	44.65	4.70	3.71	2.86	71.00	105.60	1.80	22.18	5.15	0.97	6.69	2.34	49.64
Bak-2 × Bak-5	56.65	5.06	3.60	3.66	66.90	106.10	2.79	27.50	5.38	0.98	10.46	2.40	57.78
Bak-2 × Bak-11	48.79	4.18	3.24	3.05	68.20	104.50	1.61	20.49	4.92	0.92	5.60	2.30	44.65
Bak-2 × Bak-20	50.83	4.28	2.88	2.83	67.70	107.10	1.63	21.05	5.10	0.94	4.31	2.31	45.75
Bak-12 × Bak-5	55.46	4.89	3.04	2.53	56.50	102.10	2.16	25.31	5.15	0.98	7.24	2.39	51.67
Bak-16 × Bak-20	60.41	5.29	3.40	3.53	62.90	109.30	3.03	30.33	5.63	1.06	11.55	2.63	78.21
Mean	49.74	4.75	3.35	2.87	68.51	105.97	2.20	24.58	5.23	0.98	7.73	2.38	56.29
SEm(±)	2.67	0.14	0.10	0.19	2.80	0.77	0.21	1.30	0.08	0.02	0.95	0.04	4.60
Skewness	-0.07	-0.21	-0.58	0.26	0.79	-0.31	0.44	0.40	0.61	0.87	0.33	2.07	1.10
Kurtosis	-1.2	-1.44	-0.47	-0.95	2.41	0.73	-2.04	-1.54	0.03	0.98	-1.66	4.85	-0.42

PH: Plant height (cm), NB: No. of branches per plant, IL: Internodal length (cm), NFF: Node of first flower, DFP: Days to first flowering, DPP: Days to first pod picking, NFCP: No. of fruit cluster per plant, NPP: No. of pods per plant, PL: Green pod length (cm), PD: Pod diameter (cm), HS: Harvesting span, NSPPES: No. of seeds per pod at edible stage, PY: Green pod yield per plant (g).

In contrast, the minimum mean value for internodal length was observed in cross Bak-2 × Bak-20, whereas the lowest values for node of first flower, days to first flowering, and days to first pod picking were observed in Bak-12 × Bak-5. Plant height among the genotypes ranged from 38.63 to 60.41 cm with an overall mean value of 49.74 cm. The maximum plant height (60.41 cm) was recorded in Bak-16 × Bak-20, while the minimum value (38.63 cm) was observed in Bak-1 × Bak-5. The number of branches per plant varied from 4.18 to 5.29 with a mean value of 4.75. The highest number of branches per plant (5.29) was recorded in Bak-16 × Bak-20, whereas the lowest value (4.18) was observed in Bak-2 × Bak-11. Internodal length ranged from 2.88 to 3.71 cm with a mean value of 3.35 cm among different populations. The minimum internodal length (2.20 cm) was observed in Bak-2 × Bak-20, while the maximum value (3.71 cm) was recorded in Bak-1 × Bak-20. The node of first flower ranged from 2.13 to 3.66 with a mean value of 2.87. The lowest node of first flower (2.13) was observed in the cross combination Bak-1 × Bak-5, whereas the highest value (3.66) was recorded in Bak-2 × Bak-5.

One of the F_3 progeny of the cross combination Bak-12 × Bak-5 was found earliness in respect to days to flowering (56 days) and first flowering (102 days) was recorded in Bak-16 × Bak-20.

The number of fruit clusters per plant ranged from 1.61 to 3.03 with a mean value of 2.20. The maximum number of fruit clusters per plant (3.03) was recorded in Bak-16 × Bak-20, while the minimum (1.61) was observed in Bak-2 × Bak-11. Similarly, the number of pods per plant varied from 21.05 to 30.33 with a mean value of 24.58. The highest number of pods per plant (30.33) was recorded in Bak-16 × Bak-20 followed by Bak-1 × Bak-5, whereas the lowest value (21.05) was observed in Bak-2 × Bak-20. Pod length exhibited variability ranging from 4.92 cm to 5.63 cm with a mean value of 5.23 cm. The maximum pod length (5.63 cm) was observed in the cross combination Bak-16 × Bak-20, whereas the minimum (4.92 cm) was recorded in Bak-2 × Bak-11. Pod diameter ranged from 0.92 cm to 1.06 cm with a mean value of 0.98 cm. The maximum pod diameter (1.06 cm) was observed in Bak-16 × Bak-20, while the minimum (0.92 cm) was recorded in Bak-2 × Bak-11.

Harvesting span ranged from 4.31 to 11.55 with a mean value of 7.73. The maximum harvesting span (11.55) was observed in Bak-16 × Bak-20, whereas the minimum value (4.31) was recorded in Bak-2 × Bak-20. The number of seeds per pod ranged from 2.30 to 2.63 with a mean value of 2.38. The maximum number of seeds per pod (2.63) was observed in Bak-16 × Bak-20, while the minimum value (2.30) was recorded in Bak-2 × Bak-11. Green pod yield

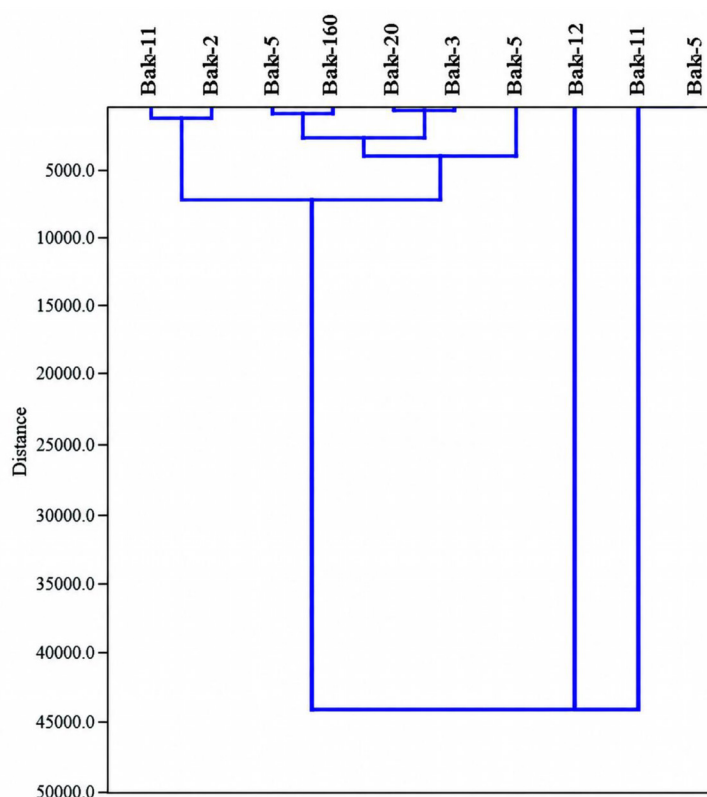


Fig. 1. Dendrogram of 8 faba bean crosses showing cluster analysis based on genetic similarity data.

per plant ranged from 44.65 to 78.21 g with a mean value of 56.29 g. The highest green pod yield per plant (78.21 g) was recorded in the cross combination Bak-16 $\times$ Bak-20, whereas the lowest yield (44.65 g) was observed in Bak-2 $\times$ Bak-11.

Improvement in any crop is directly proportional to the magnitude of genetic variability present in its genotypes (Mallor *et al.* 2011). Therefore, the present study indicates that these traits may be useful for further selection in breeding programmes. Similar results were also reported by Elshafei *et al.* (2019), Sharifi *et al.* (2020) and Dewangan *et al.* (2022).

Distribution pattern of skewness and kurtosis

The skewness of all the studied traits quantitative traits studied in the crosses ranged from -0.07 to 2.07 . Positive skewness was observed for traits such

as node of first flower, days to first flowering, number of fruit clusters per plant, number of pods per plant, green pod length (cm), pod diameter (cm), harvesting span, number of seeds per pod at edible stage, and green pod yield per plant (g). In contrast, negative skewness was recorded for plant height (cm), number of branches per plant, internodal length (cm), and days to first pod picking (Table 2).

Analysis of kurtosis indicated that most of the traits, including plant height (cm), number of branches per plant, internodal length (cm), node of first flower, days to first flowering, days to first pod picking, number of fruit clusters per plant, number of pods per plant, green pod length (cm), pod diameter (cm), harvesting span, number of seeds per pod at edible stage, and green pod yield per plant (g), exhibited platykurtic distribution. However, days to first flowering and number of seeds per pod at edible

Table 3. Proximity dissimilarity matrix (Euclidean distance) between faba bean genotypes.

Cluster	I	II	III	IV
I	0.000	33.214	34.919	30.974
II		0.000	15.649	36.501
III			0.000	24.950
IV				0.000

stage showed leptokurtic distribution.

The frequency distribution through skewness and kurtosis analysis provides valuable information regarding gene action and the number of genes controlling quantitative traits, as emphasized by Fisher *et al.* (1932) and Robson (1956). Positive skewness associated with platykurtic distribution suggests dominance-based complementary gene interaction and indicates the involvement of a large number of genes with decreasing effects. Conversely, negative skewness with platykurtic distribution implies the participation of many genes, predominantly showing duplicate gene interaction along with dominance effects that increase trait expression.

Traits governed by duplicate gene action under mild selection can lead to rapid genetic gain from the existing variability. In contrast, leptokurtic distribution coupled with positive skewness indicates traits controlled by dominance-based complementary gene action involving fewer genes with increasing effects. For such traits, achieving maximum genetic gain requires intense selection from the available variability. Similar observations have been reported by Prabhu *et al.* (2015), Kamdar *et al.* (2020) and Tripathi *et al.* (2022).

Cluster Analysis and Dissimilarity Matrix of faba bean populations

A genetic similarity matrix was used to construct a dendrogram employing the Unweighted Pair Group Method with Arithmetic Average (UPGMA). Based on the average linkage genetic similarity coefficient among the eight crosses, the dendrogram was generated to illustrate their genetic relationships (Fig. 1). The eight faba bean crosses evaluated in the present investigation were grouped into four distinct clusters

Table 4. Principal Components among faba bean genotypes.

Traits	Principal components			
	PC1	PC2	PC3	PC4
PH	38.63	46.68	56.06	60.41
NB	5.10	4.42	4.98	5.29
IL	3.45	3.32	3.32	3.40
NFF	2.13	2.77	3.09	3.53
DFF	84.30	69.40	61.70	62.90
DPP	107.70	105.65	104.10	109.30
NFCP	2.85	1.69	2.48	3.03
NPP	27.84	21.40	26.40	30.33
PL	5.41	5.07	5.27	5.63
PD	1.01	0.94	0.98	1.06
HS	10.29	5.57	8.85	11.55
NSPPES	2.39	2.32	2.40	2.63
PY	74.39	47.08	54.72	78.21
Eigen value	8.13	2.57	1.00	0.87
Percentage of variation	62.59	19.80	7.74	6.72
Cumulative (%)	62.59	82.39	90.13	96.86

PH: Plant height (cm), NB: No. of branches per plant, IL: Internodal length (cm), NFF: Node of first flower, DFF: Days to first flowering, DPP: Days to first pod picking, NFCP: No. of fruit cluster per plant, NPP: No. of pods per plant, PL: Green pod length (cm), PD: Pod diameter (cm), HS: Harvesting span, NSPPES: No. of seeds per pod at edible stage, PY: Green pod yield per plant (g).

using Ward's method, the dendrogram further illustrates the relationships among the eight faba bean populations based on thirteen morphological traits, as presented in Fig. 1. In the dendrogram, the horizontal axis represents dissimilarity among the populations, whereas the vertical axis denotes the objects and clusters. Each fusion of two clusters is indicated by a horizontal line, and the distance between clusters is represented by the short vertical bar connecting them. Cluster I comprised the crosses Bak-1 × Bak-11 and Bak-2 × Bak-5, while cluster II included Bak-1 × Bak-20 and Bak-16 × Bak-20. Cluster III consisted of Bak-2 × Bak-20 and Bak-12 × Bak-5, whereas the remaining crosses formed Cluster IV. The analysis of inter-cluster distance indicated that the highest genetic divergence was observed between cluster II and Cluster IV (36.501), followed by cluster I and cluster III (34.919). The lowest inter-cluster distance was recorded between Cluster II and Cluster III (15.649) (Table 3).

Assessment of genetic diversity among genotypes is valuable for the selection of promising parents in crop improvement programmes. The results

of the present study are in broad agreement with the findings of Sharifi and Aminpana (2014), Kumar *et al.* (2016), Rebaa *et al.* (2017), and Dewangan *et al.* (2022). These studies suggest that genotypes exhibiting maximum inter-cluster distance are more likely to contribute to higher yield potential. Therefore, hybridization between genotypes belonging to genetically diverse clusters can be advantageous for exploiting heterosis. Furthermore, genotypes selected from divergent clusters with higher cluster mean values may be utilized in breeding programmes to develop superior segregants and enhance heterotic responses in subsequent generations.

Principal Component Analysis in faba bean populations

Principal Component Analysis (PCoA) is an effective statistical tool used to assess genetic diversity in germplasm and to identify and rank genotypes based on economically important traits contributing to variability. In the present study, PCoA was performed for yield and its component traits in faba bean, considering only those principal components (PCs) with Eigen values greater than one for interpretation.

The analysis revealed that the first principal components accounted variation 62.50% with Eigen value 8.13 contributed by DPP, DFF and PY (Table 4). According to Singh *et al.* (2017), a cumulative variation exceeding 75% is considered adequate for the evaluation and characterization of cultivars. Similarly, the highest PC2 were also highly dominated by 82.39 for traits DPP, PY and PY; cumulative variation 90.13 and 96.86% respectively for trait DPP. In all the PC1, PC2, PC3 and PC4 maximum genetic variation were observed for trait DPP and exhibited highest loaded variation. These findings are in agreement with earlier reports by Tiwari and Singh (2019), Sharifi *et al.* (2020), Girgel (2021), Zayed *et al.* (2022) and Dewangan *et al.* (2022). Therefore; DPP in all PCoA might be useful in further breeding programme.

CONCLUSION

The findings from this study offer valuable guidance for selecting diverse genotypes, predicting potential benefits for genetic recombination, and formulating

an ideal plant type. The insights gained from the genetic diversity in faba bean germplasm aid in selecting parents for hybridization programs and are instrumental in effective germplasm conservation. Wide range of genetic variability were observed for quantitative and qualitative traits based on mean performance cross Bak-16 × Bak-20 and Bak-1 × Bak-5 may be selected as parent in breeding programme.

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