

EVALUATION OF VARIATIONS IN FABA BEAN (*VICIA FABA*) YIELD AND ITS ATTRIBUTING TRAITS UNDER SEMI-ARID CONDITIONS BY PRINCIPAL COMPONENT ANALYSIS

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SUMMARY

To estimate the extent of genetic diversity of 53 faba bean genotypes for 17 morpho-biochemical characters, an experiment was carried out based at Research Farm of MAP Crop Section, Department of Genetics & Plant Breeding, CCS HAU, Hisar in *rabi* 2019-20. The principal component analysis developed 17 principal components. Out of seventeen, only six PCs (PC1, PC2, PC3, PC4, PC5, and PC6) exhibited eigen value greater than one viz. 4.31, 2.11, 1.86, 1.61, 1.21 and 1.09, respectively. A total of 71.7% variation was explained by first six PCs. Maximum variation was explained by PC1 (25.36%) followed by PC2 (12.42%), PC3 (10.95%), PC4 (9.48%), PC5 (7.12%) and PC6 (6.42%). PC1 was the most informative PC as it explained 25.36% of total variation and positive correlation with seed yield, pod yield per plant, number of pods per plant, biological yield and number of clusters per plant. PC2 added 12.42% of total variation and was mostly correlated to pod length and number of seed per pod. PC3 was dominated by phenological traits viz. days to 50% flowering and days to maturity whereas PC4 was explained positively by seed protein content and 100 seeds weight. Trait biplot ordination of 17 traits in faba bean genotypes on principal component axes indicated positive association of seed yield with harvest index, number of branches per plant, 100 seeds weight, weight per pod, number of seeds per pod, pod yield per plant and biological yield, because the vectors of these attributes intersected at an acute angle. These findings can be used in breeding strategies for future hybridization programs for yield improvement and are appropriate for classification of diversity among faba bean germplasm.

Key words : Eigen value, Faba bean, Principal Component and Variation

The faba bean (*Vicia faba* L.) is a hardy winter plant that can withstand freezing temperatures. In terms of area and output, China dominates the faba bean market. The acreage and output of faba bean in India are limited, which is why it is still classified as a minor crop (Arya 2018; Arya *et al.*, 2020). The seeds of the faba bean are high in L-DOPA, a precursor to dopamine that is used to treat Parkinson's disease. Fresh pods and immature seeds of the faba bean contain anti-nutritional elements such as polyphenols, which add a beany taste and are known to produce astringency (Kumar *et al.*, 2019).

Genotypes are a valuable source of genes for breeding programmes, building new agricultural methods, diversifying production and producing new high-quality goods due to their genetic variety (Dewangan *et al.*, 2019). Genetic diversity information aids in the selection of parental genotypes from random

populations. Accurate prediction of genetic diversity levels and patterns is important for estimating the possibility of heterotic combinations before trying crosses, saving time and money (Nguyen *et al.*, 2019). Such data may be used to introduce desired genes from wild germplasm into a high-yielding germplasm pool, to analyse genetic diversity in germplasm and to identify alternative combinations for developing segregating progenies with the most genetic variability (Raiger *et al.*, 2021).

PCA approaches may be used to identify groups of genotypes with desirable attributes for breeding and to find the patterns of variation in genotype accession, as well as to determine correlations between genotypes. The variability between the original data is summarised using principal components analysis (Choudhary *et al.*, 2015). The present study was carried out to estimate the extent

of genetic diversity in 53 faba bean genotypes for 17 morpho-biochemical characters by principal component analysis, which will help to select prospective parents to develop transgressive segregates.

MATERIALS AND METHODS

The current study was conducted on 53 genotypes of faba bean that were evaluated from various sources and raised in *rabi* 2019-20 at the Research Farm of the MAP Crop Section, Department of Genetics & Plant Breeding, CCS HAU, Hisar, in a randomised block design with three replications. To grow a healthy crop, all of the prescribed cultural practises were followed. Each genotype's seeds were sown in a 4-metre-long paired row with a 45 cm row to row spacing and a 10 cm plant to plant spacing. While allotting in each replication, each treatment was randomly assigned. Plant height (cm), number of pod clusters per plant, number of branches per plant, number of pods per plant, number of pods per cluster, weight per pod (g), pod length (cm), pod breadth (cm), number of seeds per pod, 100 seeds weight (g), protein content (per cent), pod yield per plant (g), biological yield (q/ha), harvest index percent and seed yield (q/ha) were all observed on five competitive plants per paired row in each replication. The seed protein content was calculated using Jackson's Micro-kjeldahl technique (1973). Principal component was executed on 53 genotypes of faba bean by SPSS 26. The graphs were drawn also via SPSS 26 and Excel.

RESULTS AND DISCUSSION

Principal component analysis (PCA) is a multivariate technique for analyzing a data table in which observations are characterized by number of correlated quantitative dependent variables. Its purpose is to extract the key data from the table, represent it as a set of new orthogonal variables known as principal components, and display the pattern of similarity between the observations and variables as points on maps (Abdi and Williams, 2010). In the present study, PCA was conducted to describe and better understand the origins of variation among fababean genotypes. The number of characteristics responsible for the highest proportion of total variance in the experimental data is also reduced using principal component analysis. Seventeen principal components (PCs) axes are shown in Table 1 and Fig. 1. Only those principal components were selected for interpretation whose

TABLE 1
Principal component analysis of fababean genotypes

Principal components	Eigenvalue	% of Variance	Cumulative %
1	4.312	25.365	25.365
2	2.111	12.420	37.785
3	1.862	10.951	48.737
4	1.613	9.487	58.223
5	1.211	7.124	65.347
6	1.092	6.424	71.771
7	0.838	4.931	76.702
8	0.771	4.536	81.238
9	0.648	3.815	85.053
10	0.599	3.526	88.579
11	0.508	2.991	91.569
12	0.435	2.558	94.127
13	0.391	2.300	96.427
14	0.308	1.810	98.237
15	0.217	1.276	99.513
16	0.075	0.439	99.951
17	0.008	0.049	100.000

eigen value was greater than one (Kaiser, 1958 and Jeffers, 1967). Out of seventeen, only six PCs (PC1, PC2, PC3, PC4, PC5, and PC6) exhibited eigen value greater than one viz. 4.31, 2.11, 1.86, 1.61, 1.21 and 1.09, respectively. A total of 71.7% variation was explained by first six PCs. Maximum variation was explained by PC1 (25.36%) followed by PC2 (12.42%), PC3 (10.95%), PC4 (9.48%), PC5 (7.12%) and PC6 (6.42%). Previous studies also supported the present findings in which researchers analyzed fababean genotypes using PCA (Oujiet *al.*, 2011 and Terzopouloset *al.*, 2003) and found that the first few PCs were the most informative in representing genotypic variation patterns and that traits highly associated with these should be employed as selection indices for fababean breeding programmes.

Furthermore, using the rotation method (Kaiser, 1958), principal factor analysis was employed to get a clear picture of interaction among yield and

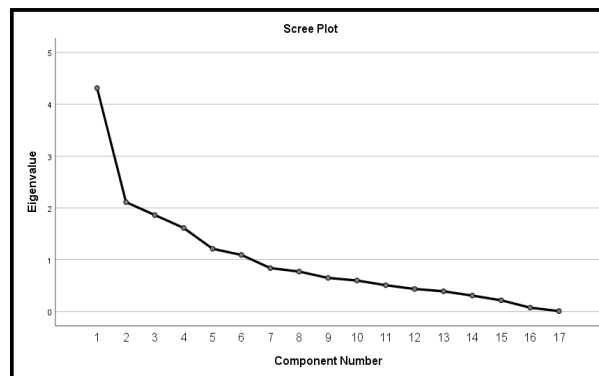


Fig. 1. Graph showing eigenvalues in response to number of components of fababean genotypes.

its component traits in terms of common factor accounts for residual variance (including error) with regard to principal factors (correlation values > 0.5).

PC1 was the most informative PC as it explained 25.36% of total variation and positive correlation with seed yield, pod yield per plant, number of pods per plant, biological yield and number of clusters per plant. PC2 added 12.42% of total variation and was mostly correlated to pod length and number of seed per pod. PC3 was dominated by phenological traits viz. days to 50% flowering and days to maturity whereas PC4 was explained positively by seed protein content and 100 seeds weight. The main variables of PC5 were number of pods per cluster and number of branches per plant. Lastly, PC6 was dominated by pod breadth and harvest index. Thus, PC1 had shown maximum variation for seed yield and its contributing traits whereas PC3 did same for phenological traits. The pattern of the variation explained by different PCs for various traits was fairly consistent with the previous works in different pulse crops (Janghel *et al.*, 2020; Sharma *et al.*, 2020; Parihar *et al.*, 2014).

A vector is generated from the origin of biplot to each symbol of the characteristics in the vector view of biplot to make visualization of the correlations between the traits easier (Yan and Rajcan, 2002). The correlation coefficient between any two characteristics can be estimated by the cosine of the angle between the vectors if the biplot explains a sufficient amount of the overall variance (Yan and Kang, 2003). If the angle between the vectors is less than 90, they are positively correlated; if the angle is greater than 90, they are negatively correlated; and if the angle is greater than 90, they are independent (Yan and Rajcan, 2002).

Trait biplot ordination of 17 traits in fababean genotypes on principal component axes indicated positive association of seed yield with harvest index, number of branches per plant, 100 seeds weight, weight per pod, number of seeds per pod, pod yield per plant and biological yield, because the vectors of these attributes intersected at an acute angle. However, days to 50% flowering, days to maturity and plant height was found negatively correlated with seed yield as portrayed by obtuse angle between them. These results were supported by the finding of Malek *et al.* (2021), who observed the significant positive correlation between seed yield and pods per plant, biological yield and branches per plant.

Lastly, traits showing positive association with most informative principal component (PC1) especially seed yield, pod yield per plant, number of pods per plant, biological yield and number of clusters per plant could be considered as the best selection criteria in

TABLE 2
Factor loading of traits with respect to different principal component (Varimax rotation)

Trait	Principal component					
	1	2	3	4	5	6
SY	0.855	0.224	-0.255	0.200	0.063	-0.155
PY/P	0.826	0.252	-0.302	0.133	0.218	0.029
PD/P	0.823	0.059	0.068	-0.126	-0.152	-0.117
BY	0.699	0.005	-0.390	-0.014	0.022	0.495
PC/P	0.632	0.017	0.288	0.021	-0.175	-0.164
P.L	0.009	0.827	0.009	0.094	0.014	-0.057
SD/PD	0.281	0.748	-0.199	-0.041	0.088	-0.021
Wt/PD	0.402	0.456	0.025	0.356	-0.072	0.304
D.M	-0.103	0.080	0.859	0.095	-0.053	-0.068
50% FI.	-0.007	-0.250	0.771	-0.057	0.151	0.044
PH	0.049	-0.251	0.092	-0.795	0.195	0.120
PC%	-0.039	-0.266	0.117	0.601	0.482	-0.095
100 S Wt	0.413	-0.009	0.106	0.559	0.173	0.225
PD/PC	0.163	0.038	0.024	0.025	0.804	-0.014
B/P	0.370	-0.100	-0.015	0.033	-0.681	-0.133
HI	0.196	0.276	0.144	0.278	0.066	-0.795
P.B	-0.104	0.269	0.155	0.319	0.203	0.597
Eigen value	4.312	2.111	1.862	1.613	1.211	1.092
Variance %	25.365	12.420	10.951	9.487	7.124	6.424
Cumulative	25.365	37.785	48.737	58.223	65.347	71.771

PH: Plant height (cm), 50% FI: Days to 50% flowering, D.M: Days to maturity, PC/P: Number of clusters per plant, B/P: Number of branches per plant, PD/P: Number of pods per plant, PD/PC: Number of pods per cluster, W/P: Weight per pod (g), PL: Pod length (cm), PB: Pod breadth (cm), SD/PD: Number of seeds per pod, 100 SW: 100 seeds weight (g), PC%: Seed protein content (%), PY/P: Pod yield per plant (g), BY: Biological yield (q/ha), HI: Harvest index, SY: Seed yield (q/ha).

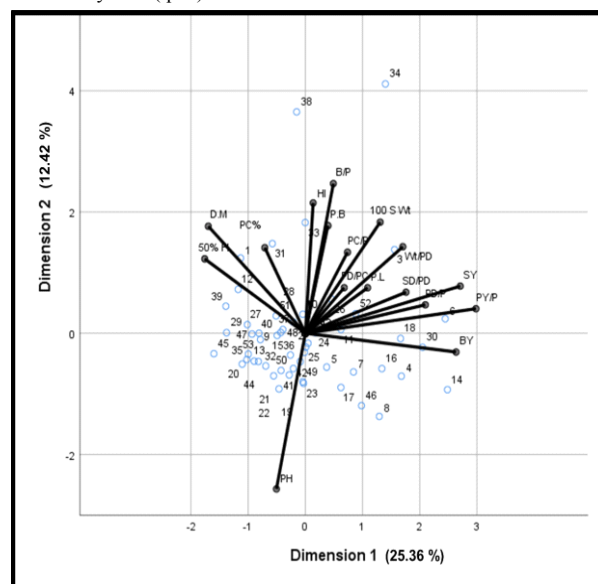


Fig. 2. Trait biplot ordination of 17 traits in fababean genotypes on principal component axes.

fababean breeding programmes for the development of high yielding varieties. PC3 was mainly dominated by phenological traits viz. days to 50% flowering and days to maturity, and these traits were negatively associated

with seed yield. Therefore, genotypes superior for traits significantly influencing PC1 should be hybridized with genotypes with lower values for traits dominating PC3 (early flowering and maturing genotypes) to early and high yielding transgressive segregants.

CONCLUSION

The principal component analysis resulted in the development of 17 major components. Only six PCs (PC1, PC2, PC3, PC4, PC5, and PC6) had an eigen value bigger than one, namely 4.31, 2.11, 1.86, 1.61, 1.21, and 1.09, respectively, out of seventeen. The top six PCs explained 71.7 percent of the variance. PC1 (25.36 per cent) explained the most variance, followed by PC2 (12.42 per cent), PC3 (10.95 per cent), PC4 (9.48 per cent), PC5 (7.12 percent), and PC6 (7.12 percent) (6.42 per cent). PC1 was the most informative PC, explaining 25.36 percent of total variance and having a positive correlation with seed yield, pod yield per plant, pod number per plant, biological yield and cluster number per plant. PC2 contributed 12.42 percent of overall variance and was mostly related to pod length and seed per pod quantity. PC3 was dominated by phenological parameters such as days to 50% flowering and days to maturity, but PC4 was strongly influenced by seed protein content and seed weight. Trait biplot ordination of 17 traits in faba bean genotypes on principal component axes indicated positive association of seed yield with harvest index, number of branches per plant, 100 seeds weight, weight per pod, number of seeds per pod, pod yield per plant and biological yield, because the vectors of these attributes intersected at an acute angle. These findings can be used in breeding strategies for future hybridization programs for yield improvement and are appropriate for classification of diversity among faba bean germplasm.

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