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RESEARCH TOPIC- PHENOTYPIC EVALUATION OF FABA BEAN (*VICIA FABA* L.) FOR SELECTING SUPERIOR GENOTYPES

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ABSTRACT

The present study was conducted to assess genetic variability, heritability, correlation, and genetic divergence among 23 faba bean (*Vicia faba* L.) genotypes for yield and its component traits. The results suggested that analysis of variance revealed significant differences among genotypes for most traits, indicating ample genetic variability. Heritability estimates ranged from 0.22 (days to 50% flowering) to 0.86 (seed yield), with high values recorded for seed yield, 100-seed weight, plant height, and days to maturity, suggesting the effectiveness of direct selection for these traits. Correlation analysis showed that seed yield was strongly and positively associated with number of pods per plant and 100-seed weight, identifying them as reliable selection criteria. Cluster analysis grouped the genotypes into four distinct clusters, with maximum divergence observed between clusters II and IV, indicating the potential of these groups as diverse parents for hybridization. The results highlight that exploiting genetic diversity and focusing on yield-contributing traits can accelerate breeding progress for higher productivity in faba bean.

Key words: Faba bean, genetic variability, heritability, correlation, cluster analysis.

Introduction

Legumes are considered the second most valuable plant source for health and nutrition. The faba bean (*Vicia faba* L., $2n = 2x = 12$), also known as broad bean, horse bean, pigeon bean, bakla, or kala matar, is a significant legume used for both food and feed. Its seeds have high nutritional content, offering a good source of protein and carbohydrates (Singh *et al.*, 2013). The faba bean is a strong plant that can endure very cold temperatures. It is either an annual or biennial erect herb. The area cultivated for faba beans is 2.72 million hectares, with a global production of 5.96 million tonnes (FAO, 2021). This legume has a high biomass and protein content, providing food

for both animals and humans (Musallam *et al.*, 2004). The protein content of mature faba bean seeds varies from 22.7 to 34.7% (Martineau-Côté *et al.*, 2022).

However, anti-nutritional factors like lectins, saponins, trypsin inhibitors, phytic acid, and condensed tannins, along with other secondary metabolites present in faba beans, can lower their overall biological value (Revilla, 2015). One important method for assessing the degree and pattern of diversity in this crop is through characterization and preliminary assessment (Singh and Bhatt, 2012). In this study analysis of variance (ANOVA) was used to confirm the existence of significant genotypic variation among the tested material, while heritability

Table 1: Heritability (H^2) for all the traits.

Trait	HB	CG
Days to 50% flowering (D50F)	0.224	Low
Days to maturity (DM)	0.810	High
Plant height (PH)	0.604	High
Number of pods per plant (NPP)	0.570	Moderate
Pod length (PL)	0.265	Low
Seeds per pod (SPP)	0.294	Low
100-seed weight (HSW)	0.708	High
Seed yield per plant (SY)	0.861	High
Days to germination (DG)	0.307	Low
Days to first flowering (DFFL)	0.505	Moderate
Number of branches per plant (NBP)	0.292	Low
Leaf length (LL)	0.338	Low
Leaf width (LW)	0.588	Moderate
HB: Heritability (H^2); CG: Category		

estimates were calculated to assess the proportion of genetic control over the observed variability and to predict the effectiveness of selection. Correlation analysis was employed to understand the interrelationships among yield and its associated parameters, thereby identifying traits that could serve as reliable indirect selection criteria. In addition, cluster analysis and dendrogram construction were carried out to measure genetic divergence and classify genotypes into distinct groups, facilitating the identification of diverse parents for use in hybridization.

Material & Methods

Plant Materials and Field Conditions

A set of 20 diverse Faba bean accessions, along with two checks (HFB 1, Vikrant), were collected from the ICAR – National Bureau of Plant Genetic Resources, New Delhi, and used in the study to characterize key plant morphological traits. The accessions were sown in the Randomized block design in the Horticultural Research Farm at the Department of Horticulture, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, during rabi 2023-24. Two checks were replicated in each block, whereas each genotypes were grown in plots with six rows of faba bean. In each replication, a 1.5×2.0 m² area was used, and five plants were tagged and data was recorded.

Data collection

In the present study, a set of 13 phenotypic traits was evaluated for faba bean to understand their breeding importance. The traits evaluated in the present study included days to 50% flowering (D50F), days to maturity (DM), plant height (PH, cm), number of pods per plant (NPP), pod length (PL, cm), seeds per pod (SPP), 100-seed weight (HSW, g), seed yield (SY, kg/ha), days to

Table 2: List of genotypes under D2 clusters.

Cluster	Genotypes
1	RFBGP-90, RFBGP-92, RFBGP-93, RFBGP-94, RFBGP-95, RFBGP-96, RFBGP-97, RFBGP-98, RFBGP-99, RFBGP-100, RFBGP-101, RFBGP-102, RFBGP-103
2	RFBGP-91, RFBGP-104, RFBGP-107, RFBGP-108, RFBGP-109
3	RFBGP-105, RFBGP-106, RFBGP-110
4	HFB -1, Vikrant

germination (DG), days to first flowering (DFFL), number of branches per plant (NBP), number of nodes on the main branch (NNB), number of flowers per plant (NFP), leaflet length (LL), and leaflet width (LW).

Result and Discussion

ANOVA and Heritability

ANOVA revealed significant genotypic differences for most traits, confirming the presence of genetic variability among the tested faba bean genotypes. Highly significant variation ($p < 0.001$) was observed for days to maturity, seed yield per plant, and 100-seed weight, while traits such as pod length and seeds per pod showed non-significant variation, indicating greater environmental influence.

Heritability estimates varied from 0.224 (days to 50% flowering) to 0.861 (seed yield per plant) (Table 1). High heritability was recorded for days to maturity, plant height, 100-seed weight, and seed yield, suggesting the effectiveness of direct selection. Moderate values were observed for number of pods per plant, leaf width, and days to first flowering, whereas low heritability for pod length, seeds per pod, branches per plant, and leaf length indicated stronger environmental influence. These results are consistent with earlier reports in faba bean (Abo-Hegazy, 2022; Merhij *et al.*, 2024;).

D2 Clustering and cluster trait variation

Cluster analysis grouped the evaluated faba bean genotypes into four distinct clusters. Cluster I was the largest, comprising the majority of the genotypes, indicating a broad genetic base within this group. Cluster II also contained several genotypes with moderate diversity, while Cluster III included only three genotypes. Cluster IV was the smallest, consisting of the two check varieties (HFB-1 and Vikrant). The distribution of genotypes into different clusters reflects the existence of genetic diversity among the studied material, which can be effectively exploited for selecting diverse parents in hybridization programmes to maximize heterosis and genetic gain.

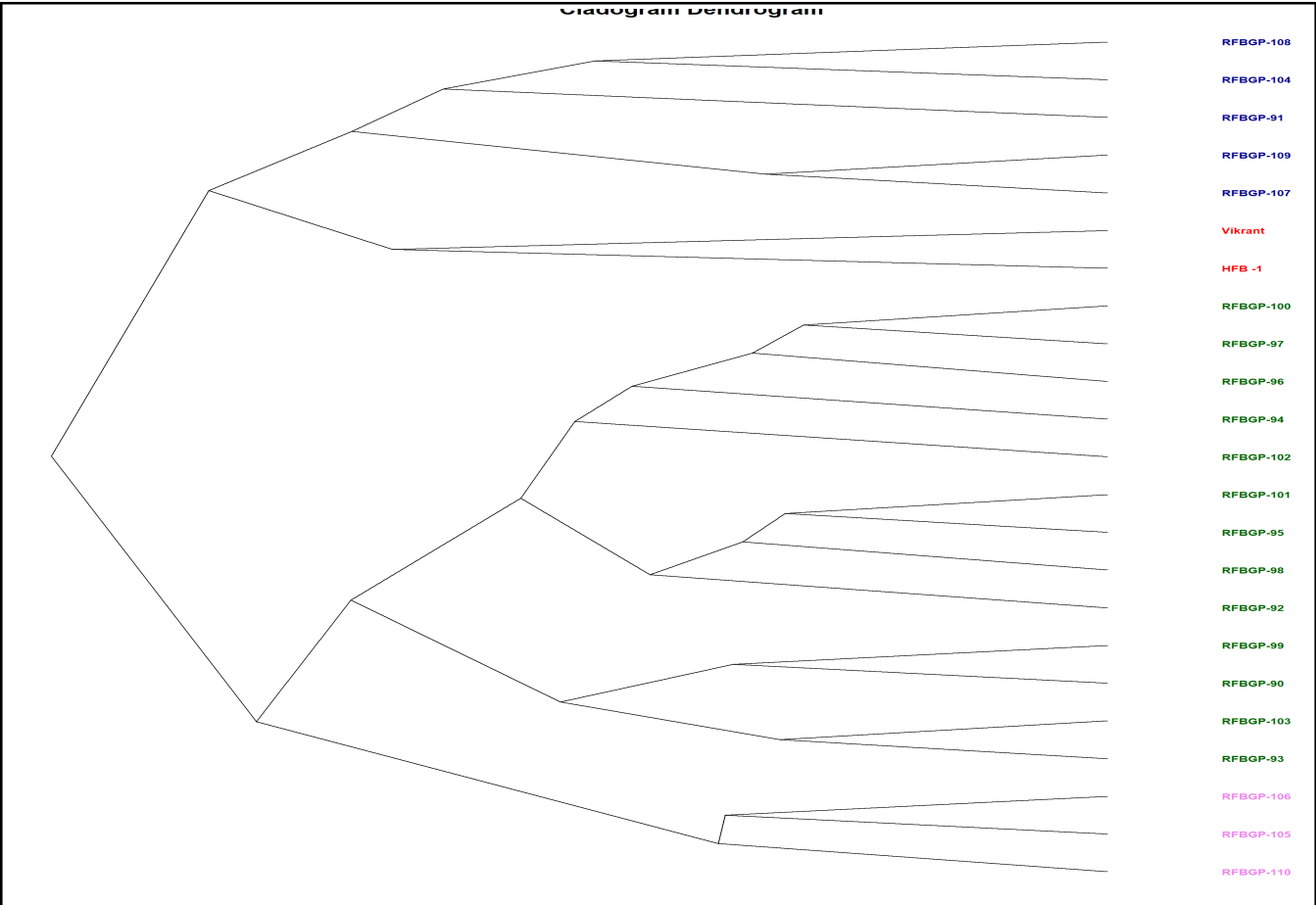


Fig. 1: D2 Clustering of the faba bean accessions based on phenotypic traits.

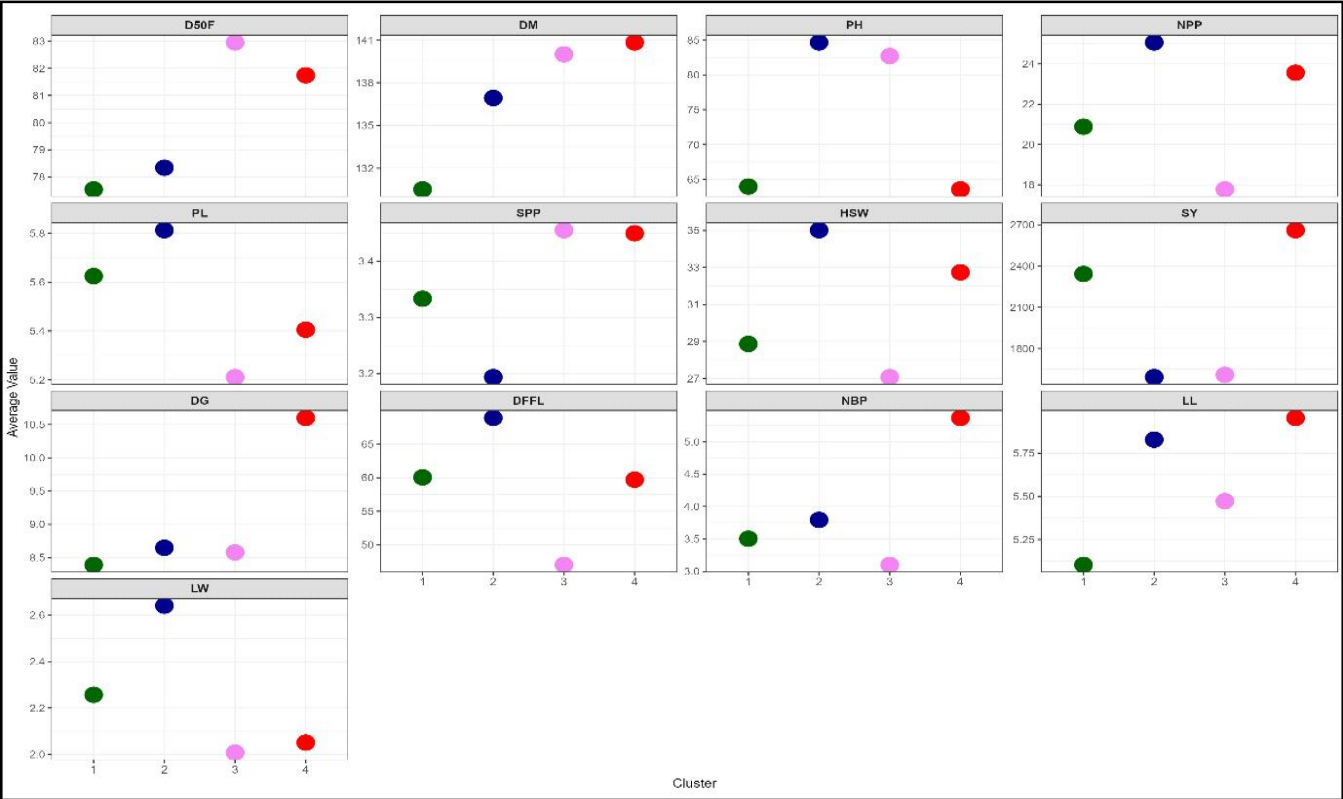


Fig. 2: Cluster wise variation of the traits in each cluster.

Cluster mean analysis showed clear differences among the groups (Fig. 1). Cluster IV recorded the highest seed yield (2660.46 g) along with more branches and leaf length, while Cluster II was superior for plant height, number of pods per plant, and 100-seed weight. Cluster III was earliest to flower and mature, whereas Cluster I showed moderate but stable performance for most traits. The wide variability across clusters highlights the scope for selecting diverse parents. Genotypes from Cluster IV (high yield) and Cluster III (earliness) or Cluster II (pods and seed weight) could be crossed to exploit heterosis and recover transgressive segregants.

Similar observations were reported by, Alghamdi *et al.*, (2009) in Saudi Arabian collections.

Correlation across the morphological traits

The correlation matrix revealed that seed yield (SY) was strongly and positively associated with number of pods per plant (NPP; $r = 0.73$) and 100-seed weight (HSW; $r = 0.59$), identifying these as key yield determinants. Similar findings have been reported in faba bean by Li and Yang (2014). NPP also showed a negative association with days to 50% flowering ($r = -0.36$), suggesting that early flowering genotypes tend to produce

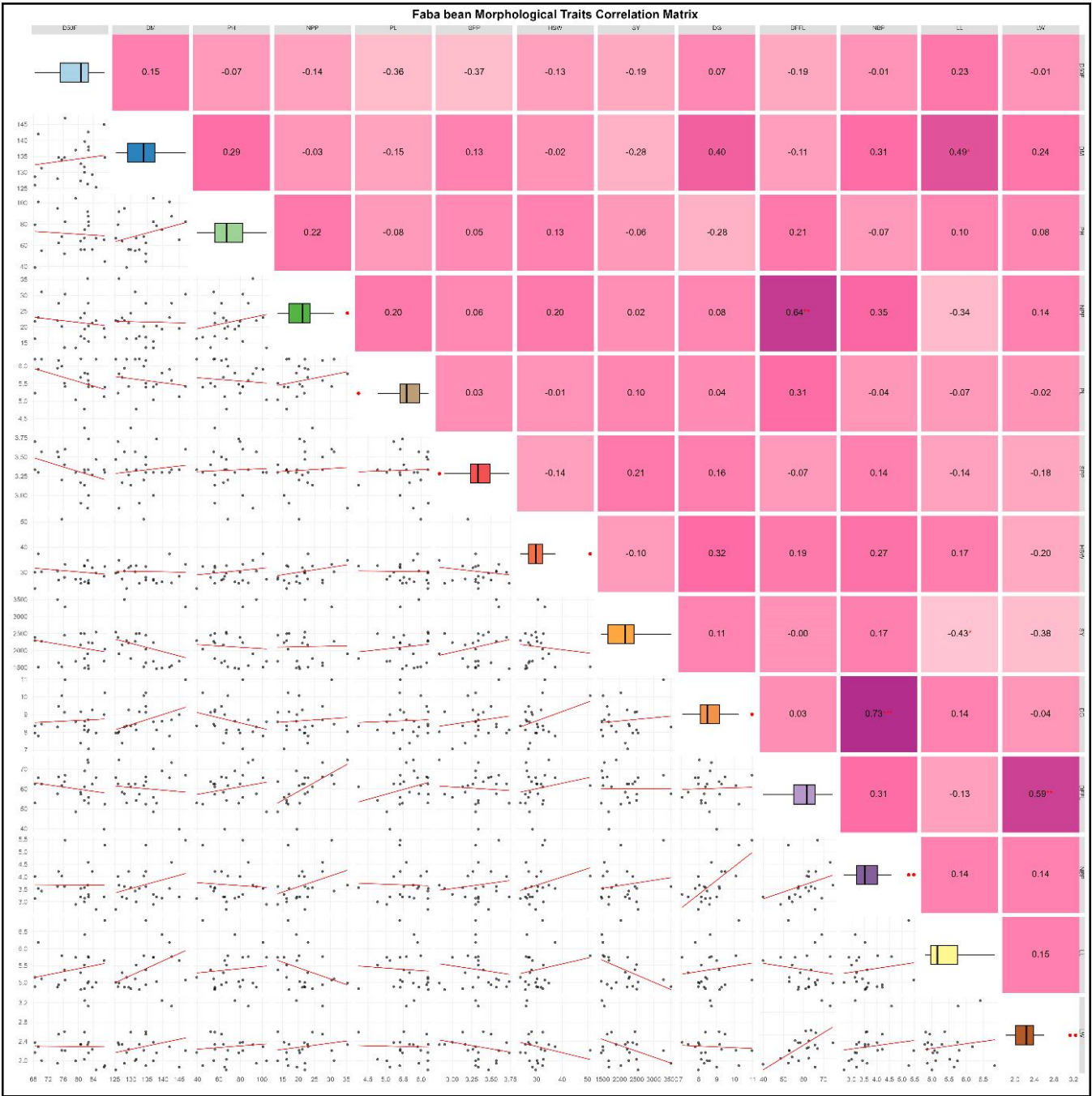


Fig. 3: Correlation Scatterplot for the faba bean morphological traits.

more pods, which agrees with observations in Ethiopian germplasm (Hiywotu, 2023). These associations highlight pods per plant and seed weight as effective indirect selection criteria for yield improvement in faba bean.

Conclusion

The study found significant genetic differences among faba bean genotypes for most of the traits measured. High heritability for seed yield, 100-seed weight, plant height, and days to maturity shows that these traits are mostly controlled by genetic factors. They can be effectively improved through direct selection. Cluster analysis divided the 23 genotypes into four distinct groups, showing considerable diversity. Genotypes from different clusters, like Cluster IV (high yield) and Cluster III (earliness) or Cluster II (pods and seed weight), could be promising parents for hybridization programs. Correlation analysis also confirmed that pods per plant and 100-seed weight are the most reliable yield components. Overall, the findings suggest that using genetic diversity and focusing on key yield-related traits will improve the efficiency of faba bean breeding for higher productivity.

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