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Studies on Genetic Divergence in Faba bean (*Vicia faba* L.)

Devendra Upadhyay[1], Krishna Kumar Pandey[2]

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ABSTRACT

Background: The genetic divergence in faba bean genotypes is critical for breeding programs aiming to improve yield and other agronomic traits. Understanding the extent of genetic variability among different genotypes can guide the selection of superior varieties and enhance crop improvement efforts. This study was conducted to evaluate the genetic diversity among 47 faba bean genotypes grown under the specific agro-climatic conditions of Chhattisgarh.

Methods: The experiment was conducted during the *Rabi* season of 2022-23 at the Hi-Tech-Nursery, Dau Kalyan Singh College of Agriculture and Research Station, Bhatapara, under Indira Gandhi Krishi Vishwavidyalaya, Chhattisgarh. A total of 47 faba bean genotypes were evaluated for genetic divergence using Mahalanobis D^2 statistics and Tocher's method. Ten quantitative characters, including marketable pod yield per plant and marketable pod weight appearance, were measured and analyzed. The genotypes were grouped into clusters based on their genetic distances.

Result: The clustering pattern indicated that genetic diversity was independent of geographical diversity. Cluster II contained the highest number of genotypes (19), followed by Cluster I (13), while Cluster IV had the least (1). Among the ten quantitative characters studied, marketable pod yield per plant contributed most to genetic divergence, followed by marketable pod weight appearance. The maximum intra-cluster D^2 value was observed in Cluster IV (477.35), followed by Cluster III (250.07). The highest inter-cluster D^2 value was between Cluster I and Cluster IV (7917.34), followed by Cluster IV and Cluster V (6156.43).

Key words: Cluster, D^2 statistics, Faba bean, Genetic divergence.

INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the most important leguminous vegetables among the potential crop grown in winter season. It is commonly known as the bakala, kala matar, broad bean, fava bean or horse bean. The name horse bean and field bean refer to cultivars used for animal feed while broad bean is grown for human food and it is used as a vegetable, green or dried, fresh or canned (Bond *et al*., 1985) and faba bean is belongs to thefamily Fabaceae and its chromosome number is 2n =2x = 12, 14. The Near East Asia is considered a center of origin for faba bean (Cubero, 1974). The genus *Vicia* encompasses about 150 to 210 species distributed mainly in Europe, Asia, North America, the temperate regions of South America and tropical Africa (Jalilian *et al*., 2014). It can fix nearly 300 kg N per ha of free atmospheric nitrogen (Singh *et al*., 2010). Due to its biological ability to fix nitrogen, as well as improved weed and disease management in succeeding crops, it is a very valuable crop (Preissel *et al*., 2015). It is considerably more resistant to acidic conditions than the majority of other legumes (Singh *et al*., 2010). It is a self-pollinating annual herb and effective source of levodopa (L-dopa), a precursor to dopamine and a source of lysine-rich protein, both of which have the potential to be used as Parkinson disease treatments (Oplinger, 1982; Vered *et al*., 1997). Wide variation of protein content (20-41%) has been reported in broad bean (Chavan *et al*., 1989). Faba bean was rated as the eighth-most important grain legume by the Consultative Group for International Agricultural Research (CGIAR) (Sharifi, 2015) (Yadav *at al*., 2017).

[1]Department of Vegetable Science, Indira Gandhi Krishi Vishwavidyalaya, Raipur-492 012, Chhattisgarh, India.
[2]Department of Agricultural Statistics, Indira Gandhi Krishi Vishwavidyalaya, Raipur-492 012, Chhattisgarh, India.

Corresponding Author: Devendra Upadhyay, Department of Vegetable Science, Indira Gandhi Krishi Vishwavidyalaya, Raipur-492 012 Chhattisgarh, India. Email: devendra.upadhyay@igkv.ac.in

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Given the importance and high demand for faba beans, there is an urgent need to enhance their cultivation to improve output and productivity. Effective selection of superior genotypes requires a comprehensive understanding of genetic variability and the exploitation of genetic diversity, particularly in Chhattisgarh. Consequently, it is imperative to develop and improve faba beans as a new potential crop for Chhattisgarh, leveraging their genetic diversity to meet regional legumes vegetable needs and boost productivity.

MATERIALS AND METHODS

The present research investigation was conducted during the 2022-23 period at the Hi-Tech Nursery of Dau Kalyan Singh College of Agriculture and Research Station, Bhatapara, under Indira Gandhi Krishi Vishwavidyalaya. This study is notable as it marks the first time such an experiment has been undertaken in the Chhattisgarh plains.

The experimental design utilized was the Augmented Design, as proposed by Federer in 1956. The study involved 47 genotypes, which included 43 germplasm lines and 4 check varieties: VIKRANT, GIZA-4, HFB-1 and HFB-2. Observations were recorded on five randomly selected plants from each genotype were evaluated for plant height (cm), the number of branches per plant, days to first flowering, days to 50% flowering, marketable pod weight, 100 seed weight (gm), pod length (cm), the number of seeds per pod, the number of pods per plant and marketable pod yield per plant (gm). These observations provided a comprehensive dataset for evaluating genetic performance.

To analyse the genetic divergence among the genotypes, the collected data were subjected to multivariate analysis using Mahalanobis D^2 statistic. This statistical method, developed by Murty and Arunachalam (1966), is particularly useful for assessing the genetic variation within a population. It allows to quantify the extent of genetic differences among the genotypes, facilitating the identification of distinct genetic groups. To assess the degree of genetic divergence in various crops, Rao (1952) proposed a method known as multivariate analysis. During clustering, genetically divergent populations are divided into distinct groups or clusters, allowing for the selection of superior parents. The grouping of the 47 genotypes was conducted using Tocher's method, which is a well-regarded technique for classifying genetic material based on multivariate analysis. This method aids in the effective clustering of genotypes into distinct groups, each representing a unique combination of genetic traits. This study is expected to provide valuable insights into the genetic makeup of the faba bean genotypes in the Chhattisgarh plains.

RESULTS AND DISCUSSION

Grouping of genotypes into different clusters

Considering the method detailed by Rao in 1952, genotypes were grouped into various clusters Table 1. Tocher's technique was used to divide the 47 genotypes into five clusters. Cluster II was the largest, comprising of 19 genotypes followed by cluster I (13), cluster III (9), cluster IV (5) and cluster IV (1).

The analysis of genetic divergence among the 47 genotypes of faba bean revealed substantial variability, as indicated by the D^2 values for both intra-cluster and inter-cluster distances. The clustering pattern, as detailed in Table 2 and illustrated in Fig 1, provides important insights into the genetic structure and relationships among the genotypes.

Intra-cluster distance

The maximum intra-cluster D^2 value was observed in Cluster IV (477.35), suggesting that the genotypes within this cluster possess the highest genetic variability compared to other clusters. This high intra-cluster divergence could be attributed to the presence of diverse genotypes within Cluster IV, which may possess a wide range of genetic traits. Cluster III followed with an intra-cluster D^2 value of 250.07, indicating a moderate level of genetic diversity. Cluster II and Cluster I showed relatively lower intra-cluster D^2 values of 216.58 and 214.67,

Table 1: Grouping of genotypes into different clusters using Tocher's method.

Cluster group	No. of genotypes	List of genotypes
Cluster I	13	ET-226481, ET-226528, ET-226468, ET-226425, ET-226464, ET-226472, ET-226568, ET-226411, ET-226434, ET-2264, ET-252885, ET-226474 and ET-226480
Cluster II	19	HB-14-36, HB-70-52, HB-16-15, HB-15-55, HB-15-34, RFB-45, RFB-40, RFB-44, RFB-43, HB-15-21, HB-2, HB-53, HB-16-16, HB-15-22, RFB-15, RFB-35, HB-15-04, RFB-39 and RFB-37
Cluster III	9	Giza-4, HFB-2, VIKRANT, HFB-1, RFB-38, ET-226423, ET-226532, ET-226487 and ET-2265
Cluster IV	5	HB-16-03, AFB-22-1, FB-04, HB-16-07 and AFB-22-2
Cluster V	1	ET-252887

Table 2: Intra (diagonal) and inter-cluster (above diagonal) average D^2 values.

	Cluster distances				
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	214.67	3125.11	1080.38	7917.34	340.55
Cluster II		216.58	870.46	1449.23	2075.92
Cluster III			250.07	3678.09	560.09
Cluster IV				477.35	6156.43
Cluster V					0.00

respectively, suggesting more genetic homogeneity among the genotypes within these clusters.

Inter-cluster distance

The inter-cluster D^2 values showed substantial genetic distance between clusters, with the highest inter-cluster D^2 value recorded between Cluster I and Cluster IV (7917.34). This significant distance indicates that the genotypes in these clusters are highly distinct from each other, offering a valuable opportunity for selecting genetically diverse parents for breeding programs. The next highest inter-cluster D^2 value was between Cluster IV and Cluster V (6156.43), followed by Cluster III and Cluster IV (3678.09). These values further underscore the genetic distinctiveness of Cluster IV from other clusters, reinforcing its importance as a potential source of unique genetic traits. Additionally, considerable inter-cluster distance was observed between Cluster I and Cluster II (3125.11), Cluster II and Cluster V (2075.92) and Cluster II and Cluster IV (1449.23). These results indicate that substantial genetic differences exist among these clusters, which could be exploited for hybridization to develop new genotypes with improved traits.

The high genetic distance between clusters suggests that crossing genotypes from highly divergent clusters (such as Cluster I and Cluster IV) could produce progenies with broad genetic bases and potentially superior agronomic traits. The observed genetic variability within clusters also indicates the presence of diverse alleles, which can be harnessed to enhance specific traits such as yield, disease resistance and stress tolerance. The significant genetic distance observed between Cluster IV and other clusters suggests that genotypes from Cluster IV may carry unique genetic traits that are not present in genotypes from other clusters. This can be particularly useful in breeding programs aiming to introduce novel traits into the existing gene pool. The method of selecting parents for hybridization from the clusters exhibiting the greatest inter-cluster distance was additionally placed out by Chaubey *et al*. (2012); Fikreselassie and Seboka (2012); Sharifi and Aminpana (2014); Kumar *et al*. (2017); Tiwari and Singh (2019); Dewangan *et al.* (2022).

Cluster means and contribution of individual characters towards genetic divergence

The analysis of cluster means and the contribution of individual characters towards genetic divergence provides valuable insights into the genetic structure of the 47 faba bean genotypes. The cluster means for the ten yield and component characters, as presented in Table 3, highlight the distinctive traits of each cluster and their potential utility in breeding programs. Cluster IV exhibited the highest mean values for several key agronomic traits. This cluster had the maximum values for plant height (49.28 cm), number of primary branches per plant (6.76), marketable pod weight (5.47 g), 100 seed weight (29.86 g), pod length (6.17 cm), number of pods per plant (28.28) and marketable pod yield per plant (119.91 g). These yield and yield contributing traits are crucial for overall plant Vigor and productivity, indicating that genotypes within Cluster IV possess superior growth characteristics and yield potential. The high marketable pod yield per plant in Cluster IV suggests that genotypes in this cluster are particularly valuable for breeding programs focused on improving yield. Cluster V displayed the highest mean values for days to first flowering (52.8) and days to 50% flowering (78.4).

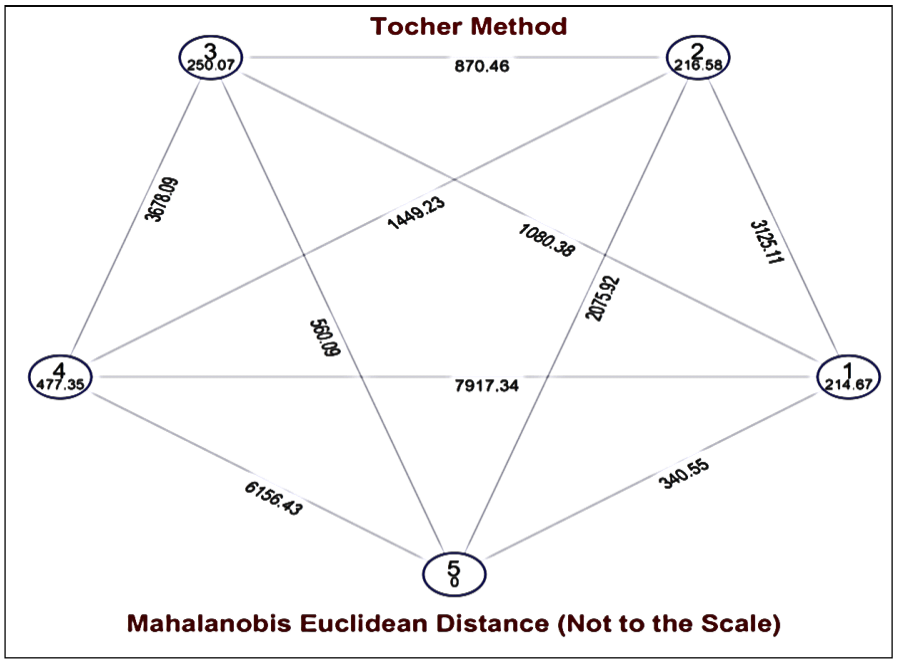


Fig 1: Diagram showing the intra and inter-cluster D^2 values.

Table 3: Mean value of different clusters for yield and component characters.

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Plant height (cm)	40.43	49.05	43.81	49.28	43.22
Number of primary branches per plant	3.97	6.17	4.86	6.76	5.00
Days to first flowering	47.20	42.61	48.00	43.00	52.80
Days to 50% flowering	70.48	67.33	67.74	62.44	78.40
Marketable pod weight	3.10	3.78	4.50	5.47	3.20
100 Seed weight (g)	26.88	26.69	27.58	29.86	28.10
Pod length (cm)	5.04	5.71	5.67	6.17	5.30
Number of seeds per pod	2.43	3.23	3.38	3.12	2.20
Number of pods per plant	12.09	24.79	15.49	28.28	15.00
Marketable pod yield per plant (g)	35.17	86.65	64.06	119.91	46.50

Table 4: Cluster means: Tocher Method.

Source	Contribution %
Plant height (cm)	5.63
Number of primary branches per plant	6.33
Days to first flowering	7.98
Days to 50% flowering	5.74
Marketable pod weight	13.54
100 Seed weight (g)	6.52
Pod length (cm)	11.32
Number of seeds per pod	10.22
Number of pods per plant	12.55
Marketable pod yield per plant (g)	20.17

This indicates that the genotypes in Cluster V tend to flower later than those in other clusters. The late flowering characteristic can be advantageous in breeding programs aimed at extending the growing season or adapting crops to specific climatic conditions where a delayed flowering time is beneficial. Cluster III had the highest mean value for the number of seeds per pod (3.38). This trait is significant as it directly impacts the overall seed yield. Genotypes within Cluster III could be valuable for breeding programs that aim to increase the number of seeds per pod, thereby enhancing the total seed production. The above observation, which indicated that genotypes with entirely different mean performances for various features were divided into different clusters, indicates that there is a significant variation between clusters in terms of the cluster mean. Chaubey *et al*. (2012); Girish *et al*. (2012) and Thamaraiselvi *et al*. (2024) reported observing similar results.

The distinct characteristics of each cluster provide a rich genetic resource for developing new faba bean varieties with enhanced traits. Genotypes from Cluster IV could be selected for improving plant height, branch number, pod weight, seed weight, pod length and overall pod yield. Similarly, the late flowering genotypes in Cluster V can be utilized in breeding programs targeting extended growing seasons or regions where late flowering is advantageous. The genotypes in Cluster III, with their higher number of seeds per pod, offer a genetic basis for increasing seed production efficiency.

The contribution of individual characters to genetic divergence underscores the importance of specific traits in differentiating the genotypes. Traits such as marketable pod yield, pod weight, plant height and number of branches per plant significantly contributed to the observed genetic divergence. These traits should be prioritized in breeding programs aiming to enhance overall plant productivity and adaptability.

The analysis of the contribution of individual characters towards genetic divergence among the 47 faba bean genotypes reveals the relative importance of various traits in differentiating the genotypes. The percentage contributions of each trait to genetic divergence, as presented in Table 4, highlight the key attributes that drive genetic variability within this population.

The highest contribution to genetic divergence was recorded for marketable pod yield per plant, accounting for 20.17% of the total variation. This significant contribution underscores the critical role of pod yield in the overall genetic differentiation of the genotypes. Marketable pod yield is a direct measure of productivity, making it a principal trait for selection in breeding programs aimed at enhancing yield. Marketable pod weight contributed 13.54% to the genetic divergence. This trait is closely related to yield and is an essential factor in determining the economic value of the crop. The number of pods per plant contributed 12.55% to the genetic divergence, indicating its significant role in differentiating the genotypes. This trait directly influences the total yield, as more pods per plant typically result in higher productivity. Pod length and the number of seeds per pod contributed 11.32% and 10.22%, respectively, to the genetic divergence. These traits are important yield components, as longer pods and more seeds per pod can enhance the overall seed production. Days to first flowering and days to 50% flowering contributed 7.98% and 5.74%, respectively, to the genetic divergence. Flowering time is a crucial trait for adapting crops to different growing environments and optimizing the growing season. The contribution of 100 seed weight (6.52%) and the number of

primary branches per plant (6.33%) to genetic divergence highlights their roles in determining plant productivity and structure. Seed weight is directly related to the economic value of the crop, while the number of primary branches influences the plant's architecture and potentially its yield. Plant height contributed 5.63% to the genetic divergence, making it the trait with the lowest contribution among those studied. Although plant height is less influential in genetic differentiation compared to other traits.

CONCLUSION

In the present investigation based on D^2 value demonstrates substantial genetic divergence among the 47 faba bean genotypes, are grouped into five clusters through cluster analysis. Cluster II consisted 19 genotypes, making the largest cluster. The maximum intra cluster distance was observed for cluster IV, followed by cluster III, whereas, minimum intra cluster distance was observed for cluster V and the maximum inter-cluster distance was observed between cluster I and cluster IV, whereas, minimum inter cluster distance was recorded between cluster I and cluster V. Genotypes from cluster IV indicated highest mean value for marketable pod yield per plant, therefore, genotypes in this cluster can be selected for hybridization to develop high marketable pod yielding variety in faba bean.

Conflict of interest

The authors declare no conflicts of interest.

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