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Research paper

Evaluation of genetic diversity in faba bean (*Vicia faba* L.)

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ABSTRACT

The present investigation was carried out to study inherent genetic diversity among 35 genotypes of faba bean (*Vicia faba* L.) using Mahalonobis D^2 statistics. D^2 analysis grouped studied genetypes into 16 clusters in Environment 1 (Early sowing) and 12 clusters in Environment 2 (Late sowing). The intra-cluster distance was greater in Cluster I of Environment 1 (8.48) and Cluster V of Environment 2 (7.99). While greater inter-cluster distance was observed between cluster X and XIV in Environment 1 and between cluster X and XII in Environment 2. Seed yield per plant contributed the highest towards total divergence in the present study under both environments (49.25% in Environment 1 and 28.41% in Environment 2). The genotypes RFB-14, ET226414, ET226415, HFB-1, ET226430, ET226426 and ET226417 belonging to different clusters in both environments had higher genetic distance and can be used as a parent for further hybridization program for generating the useful variability.

Key words : D^2 statistics, Faba bean (*Vicia faba* L.), Genetic diversity

INTRODUCTION

Faba bean is one of the important pulse crops in India. It is mainly a rabi pulse in the plains of India, although it is successfully grown during kharif (rainy season) in hilly and mountainous regions (Singh and Bhatt, 2012). It has multiple uses as a vegetable, green or dried, fresh or canned (Haw *et al.,* 1985; Yadav *et al*., 2022), and as excellent green manure that can fix nitrogen up to 66-220 kg/ha, (Singh *et al.,* 2013). It is also an excellent fodder crop for animals. As in other legume crops, faba bean is a source of excellent vegetable protein content ranging from 20 to 28% (Crepon *et al.,* 2010). Most of these proteins include globulins (79%), albumins (7%), and gluten in (6%) (Hussein and Amortize, 2006). It is also a good resource of starch, cellulose, and minerals.

Faba bean was probably introduced during the period 1206-1555 AD in India. Initially, it was grown by Europeans as a garden crop in India. This crop is identified as an argonomically viable alternative to cereals and other pulses. It has been still categorized as a minor/unutilized/underutilized/less utilized potential crop due to very little area for cultivation of this crop in India and still not fully exploited crop. Therefore statistics on the area and production of this crop are not available in India (Pradhan and Sinha, 2012). However, the maximum area under this crop is found in Bihar state because it is a traditional legume crop of this state in India. Other major faba bean-growing states are Haryana, Jharkhand, Madhya Pradesh, Chhattisgarh, and Eastern Uttar Pradesh (Singh *et al.,* 2012). As in other minor pulses, the yield potential is almost stagnant in this crop.

The existence of genetic diversity in this species is represented in the form of wild species, related species, breeding stocks, mutant lines etc. which may serve as the source of desirable alleles and may assist plant breeders in developing climate-resilient varieties (Nurmansyah *et al.,* 2020; Yilmaz, 2020; Avola *et al*., 2009; Attia *et al.,* 2019; Sozen and Karadavut, 2016; Aboukarima *et al.,* 2020). The breeding of climate-resilient varieties requires novel traits like tolerance towards potential new insect pests, diseases, extreme heat, extreme cold, and various air/soil- pollutants. For ever-changing breeding goals, different genes need to be reserved in cultivated and cultivable crop species in the form of germ plasma resources (Zhang *et al.,* 2023). The presence of genetic diversity within and between crop plant species helps the breeders to select superior genotypes either to be directly used as new varieties or to be used as parents in the hybridization programs. Genetic variability between two parents is essential for obtaining good recombinants including transgressive segregants having tolerance to biotic and abiotic stresses besides high yield. It also facilitates the development of new lines. Diversity is also important for the adaptability of crop plants to varied environments with special reference to changing climatic conditions (Zhang *et al.,* 2023). High temperatures at the pod development stage, significantly affect the grain yield, floral development, and anthesis leading to yield losses in faba bean (Bishop *et al*., 2016). Therefore the present study aimed to identify the stable parents based on genetic distance for hybridization programme under various environmental conditions.

MATERIALS AND METHODS

The experiment material consisted of 35 diverse genotypes of faba bean, which were evaluated under two different environments by growing them at two different dates. One set of genotypes was evaluated under early sown conditions, while another set of genotypes was evaluated under late sown conditions in randomized block design (RBD) with three replications. The early sowing of the genotypes was done on November 10, 2021, and late sowing- was done on December 8, 2021 during *Rabi* season, 2021-2022 at Pulse Research Farm of Birsa Agricultural University, Akanke, Ranchi. The plot size was 3 m long having 3 rows and row-to-row and plant-to-plant distances were maintained at 30 cm and 10 cm, respectively. Five randomly selected plants were used to record the data for twelve (12) quantitative characters including ays to 50% flowering, days to pod initiation, plant height (cm), primary branches/plant, pods/plant, clusters/plant, pods/cluster, day to maturity, seeds/pod, seed yield/plant (g), 100-seed weight (g) and protein content (%). Mahalanobis (1936) D^2 statistics were used to quantify the degree of divergence. Tocher's method was used to group genotypes in clusters following (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance showed a significant difference among the studied genotype for studied 12 characters indicating the existence of genetic variability. The test of significance based on Walks criteria for the pooled effect of characters also showed significant differences among the genotypes. These has been discussed character-wise below.

Table 1. Cluster Distances between different clusters of faba bean in Environment 1 (Early) and Environment 2 (Late sowing)

Cluster	Env.* Groups	Group I	Group II	Group III	Group IV	Group V	Group VI	Group VII	Group VIII	Group IX	Group X	Group XI	Group XII	Group XIII	Group XIV	Group XV	Group XVI
Group I	E1 E2	8.48 7.04	9.79 8.24	10.45 10.29	10.16 8.75	10.64 11.49	9.73 8.02	10.38 7.97	9.74 9.24	10.11 9.00	13.12 13.43	9.94 10.84	12.98 9.69	14.47	13.46	14.71	14.92
GroupII	E1 E2		0 0	9.39 11.93	15.31 5.29	14.87 11.70	13.91 8.14	12.77 11.34	13.58 10.60	14.28 11.60	14.25 13.99	12.35 11.51	14.36 10.79	16.96	18.31	18.58	18.97
Group III	E1 E2			8.42 7.46	12.92 13.51	12.97 11.59	12.61 9.39	10.64 10.54	14.29 14.47	14.26 9.49	12.63 9.38	11.48 9.63	12.08 13.18	14.09	16.99	15.92	16.05
Group IV	E1 E2				0 0	5.55 13.25	6.31 9.15	8.87 12.27	8.77 11.67	6.75 12.86	13.02 15.24	9.95 12.44	13.04 11.50	9.97	11.73	10.8	10.34
Group V	E1 E2					0 7.99	6.36 10.58	8.27 12.12	9.75 13.47	9.07 10.86	11.03 16.09	12.21 15.09	12.19 10.26	8.7	15.23	9.24	10.89
Group VI	E1 E2						0 0	11.24 9.51	7.52 11.52	7.68 8.90	14.9 11.15	7.61 10.27	14.98 10.72	10.55	11.9	13.59	9.41
Group VII	E1 E2							0 0	13.92 8.14	12.26 7.85	6.87 14.96	13.29 12.11	10.43 7.90	10.01	17.67	10.05	14.92
Group VIII	E1 E2								0 0	6.76 12.10	16.6 17.78	10.51 13.66	15.06 9.31	15.06	10.61	14.51	12.79
Group IX	E1 E2									0 0	16.05 14.36	9.22 11.91	15.32 11.56	13.98	9.77	13.3	10.5
Group X	E1 E2										0 0	17.58 8.24	8.13 18.02	12.84	21.06	9.54	18.69
Group XI	E1 E2											0 0	17.13 15.57	14.68	10.03	18	11.58
GroupXII	E1 E2												0 0	15.42	19.43	10.29	17.3
Group XIII	E1													0	19.69	11.47	12.44
Group XIV	E1														0	18.74	14.29
Group XV	E1															0	13.91
GroupXVI	E1																0

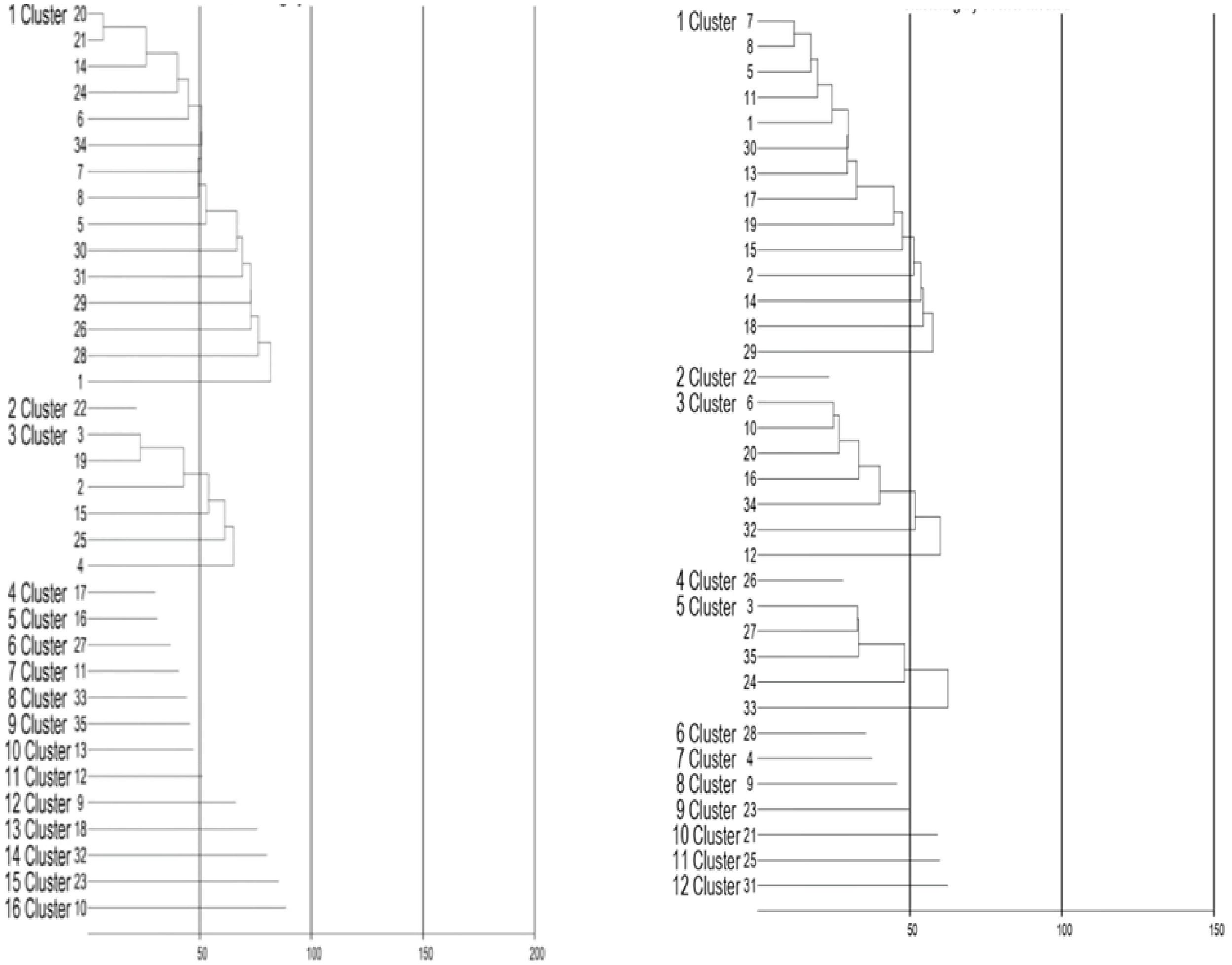
* E1 = Environment 1 (Early sowing) E2 = Environment 2 (Late sowing)

Cluster pattern

Based on the relative magnitude of the D^2 value in environment 1 (Early sowing), all 35 genotypes grouped into 16 clusters (Mahalanobis, 1936; Rao, 1952). Maximum number of genotypes (i.e. 15 genotypes) grouped in cluster I followed by cluster III (i.e. 6 genotypes), while remaining clusters contained one genotype each. In Environment 2 (Late sowing), all the 35 genotypes were grouped into 12 clusters. Cluster I comprised of 14 genotypes followed by Cluster III (7 genotypes) and Cluster V (5 genotypes). The remaining clusters had one genotype each (Fig. 1). This indicated the pattern of divergence differs with environments.

Intra- and Inter-cluster distance

The calculated inter and intra-average distances is presented in Table 1**.** In Environment 1, Cluster I had the greater intra-cluster distance (8.48) followed by Cluster III (8.42), while Cluster V had the greatest intra-cluster distance (7.99), followed by Cluster III (7.46) in Environment 2. These results indicated that the genetic constitution of genotypes belonging to these clusters have close proximity to each other. Similar findings were observed by Dwivedi and Lal (2009), Dubey and Srivastava (2007), Lokere *et al.* (2007). The inter-cluster distance for Environment 1, was found highest between clusters X and XIV (21.06) followed by clusters XIII and XIV (19.69)



Environment – I (early sowing) Environment – II (late sowing)

Fig. 1. Clustering pattern by Troche's method in faba beans over environments**.**

Genotyps: 1-ET226411, 2-ET226420, 3-ET226423, 4-ET226416, 5-ET226410, 6-ET226425, 7-ET226418, 8-ET226413, 9-ET226417, 10-RFB-14, 11-ET226431, 12-HFB-1, 13-ET226415, 14-ET226414, 15-ET226408, 16-Rebaya-40, 17- Hudalbu, 18-Hanma-1, 19-Basabeer, 20-ET226428, 21-ET226430, 22-ET226422, 23-RFB-6, 24-PRT-12, 25-ET226421, 26-ET226429, 27-Hanma-2, 28-ET226424, 29-ET226427, 30-ET226432, 31-ET226426, 32-Sambad-75, 33-Habidulla, 34-ET226419, 35-Vikrant whereas in Environment 2 maximum inter-cluster distance was observed between clusters X and XII (18.02) followed by clusters VIII and X (17.78) and clusters V and X (16.09). The genotypes under these four clusters should be preferred for hybridization programs as they possess maximum genetic diversity. By considering these genotypes for hybridization programs erotic hybrids and transgressive sergeants can be obtained from the respective crosses under late sown conditions for developing terminal heat tolerant lines. The selection of parents from the clusters having maximum cluster distance for hybridization was also supported by other workers (Chubby *et al.*, 2012; Sharif and Aminpana, 2014). Mishra *et al.* (2003) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter-cluster distances to realize much variability and high erotic effect.

In the present investigation, seed yield per plant showed the highest contribution in the manifestation of genetic divergence under both environments i.e. 49.3% in Environment 1 and 28.4% in Environment 2 followed by clusters per plant (26.7% in Environment 1) and days to 50% flowering (20.8% in Environment 2). Hence, these characters should be given importance during hybridization and subsequent selection in the segregating population (Table 2).

It is well known that crosses between divergent parents usually produce greater erotic effects than between closely related ones (Dubey *et al.*, 2007). Considering the importance of genetic distance and the relative contribution of characters towards total divergence, it may be concluded from the present study that the hybridization between parental lines 'RFB-14' with 'ET226414', 'ET226415' with 'ET226414' and 'HFB-1' with 'ET226414' in early sown conditions may produce a wide range variablity for selection. Further, 'ET226430' with 'ET226426' and 'ET226417' with 'ET226430' in environment 2 may be useful in the future to produce better transgressive segregates. The presence of stress resistance genes in the above genotypes helps to develop varieties for the future that will have good resistance towards terminal heat.

Table 2. Percentage of the contribution of each character of faba bean towards total divergence over environments

Characters	Environment 1	Environment 2
Days to 50% flowering	0.51	20.84
Days to pod initiation	0.17	0.50
Plant height (cm)	0.50	0.17
Primary branches/plant	0.67	0.34
Pods/plant	6.55	14.79
Clusters/plant	26.72	12.27
Pods/cluster	0.001	1.68
Day to maturity	5.38	5.71
Seeds/pod	3.88	0.67
Seed yield/plant (g)	49.25	28.41
100-seed weight (g)	5.21	11.43
Total protein content (%)	0.17	3.19

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