RESEARCH ARTICLE

STUDY ON GENETIC DIVERGENCE FOR SEED YIELD AND ITS CONTRIBUTING CHARACTERS IN FABA BEAN (*VICIA FABA* L.) GENOTYPES UNDER SEMI-ARID CONDITION

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Abstract: The experimental material was consisted of 53 genotypes of faba bean, raised in RBD design with three replications during *rabi* 2019-20 at Research Farm of MAP Crop Section, Department of Genetics & Plant Breeding, CCS HAU, Hisar. The results of analysis of variance indicated that the substantial genetic variability was present for seed yield and its contributing characters. The 53 genotypes were grouped into 6 clusters using Tocher's method. The maximum intra-cluster D^2 value was recorded for cluster IV, which suggested that the cluster IV had maximum genetic heterogeneity among the genotypes presented in this cluster, whereas, the maximum inter- cluster D^2 value was recorded between cluster V (HB-24) and VI(HB-01), which indicated that the genotypes present in these clusters had highest genetic diversity. Therefore, these genotypes could be utilized in breeding program for the development of high yielding and nutritionally superior genotypes.

Keywords: Faba bean, Genetic diversity, Genetic variability, Tocher's method

INTRODUCTION

Faba bean (*Vicia faba* L.; 2n = 2x = 12, 14; Family: *Fabaceae*) is known by many names like broad bean, horse bean, winter bean, Windsor bean, pigeon bean and popularly known as bakla and kalamatar in India (Singh *et al*., 2013). It is a hardy plant, which can tolerate extreme low as well as high temperature. It is widely believed to have originated in the North Africa and South Caspian Sea (Tanno and Willcox, 2006) and introduced in India by Arab traders. In 2018-19, faba bean ranked 6th with respect to production worldwide, after the common bean, pea, chickpea, cowpea and lentil with total production of 4.5 M tons, while the area harvested was 2.5 M ha (Khazaei and Vandenberg, 2020). China is a leading growing country of faba bean with respect to area and production. In India, the area and production of faba bean is low and that is why it is still categorized as minor crop. It is a traditional legume crop of Bihar that is why in India, faba bean have maximum area in Bihar. In India, it is also cultivated in Madhya Pradesh, Odisha and Uttar Pradesh (mainly eastern part) (Singh *et al*., 2012). Faba bean have limited area in Haryana state as compared to other legume crops because of lack of suitable high yielding varieties as well as improper pest management.

Faba bean have great role in world agriculture due to its high performance with respect to yield, compared to alternative grain legumes. It can also be used as break crop in area where cereal-based mono-cropping system is dominated. It is a highly profitable crop because of its biologically nitrogen fixation capacity and enhanced weed and disease controls in subsequent crops are considered (Preissel *et al*., 2015). Faba bean is an annual herb. The faba bean haslarge and white flowers that originate on short pedicles in clusters. The fruit of faba bean is known as pod which is leathery, green maturing to blackish-brown (Lindemann and Glover, 2003). Faba bean is a dual-purpose crop, green pod is used as vegetable, whereas, dry seed are used as grain legume (Arya, 2018; Dewangan *et al*., 2019). Among the most commonly cultivated crops, faba bean has not only the highest crude protein content but also has the highest yield of protein per hectare. In 100g of edible portion, it contains 7.2g carbohydrate, 4.5g protein, 0.1g fat, 0.08mg thiamine, 12.0mg ascorbic acid, 50mg calcium and 1.4mg iron. Faba bean is recognized as a potential grain legume crop by ICAR and included it in AICRP program. The Consultative Group of International Agricultural Research (CGIAR) ranked the faba bean as 8th major grain legumes on priority basis.

Faba bean have many medicinal values as it is used as ingredients and applications to soften stiff limbs. Its seeds are good source of L-DOPA, a precursor dopamine, which is used as a medicine for the treatments of Parkinson's disease (Kumar *et al*., 2019). Faba bean is an excellent dietary source of natural antioxidant for prevention of chronic disease and health promotion (Oomah *et al*., 2006). It also contains certain anti-nutritional factors in fresh pods as well as in immature seeds such as polyphenols which impart beany flavour (Bjerg *et al*., 1988) which known to cause astringency. The seed of faba bean contain vicine and co-vicine that causes

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hemolytic anemia due to oxidation of erythrocytes. However, the activity of anti-nutritional factors may reduce by heat treatment in boiling water as well as presoaking (Batra *et al*., 1990).

Faba bean is a self-pollinated crop, having partial allogamous nature (5-20 *per cent*). Due to the partial allogamous nature, high degree of genetic variability prevails in this crop (Hanelt and Mettin, 1989). The presence of the adequate variability in the basic genetic material of any crop is prerequisite for initiating a systemic breeding programme for the improvement of a crop (Raiger *et al*., 2021). The genetic variability study has paramount role in breeding for wide adaptation. It helps in selection of desirable parents for an efficient hybridization program. Due to hybridization divergent groups are develop, which is the main aim of plant breeding programme. Mahalanobis's D^2 techniques (based on multivariate analysis), is a powerful tool for accessing genetic divergence and serves to be a good index of genetic diversity (Ngoc *et al*., 2017; Panchta *et al*., 2021). In faba bean genotypes great extent of diversity is present for various quantitative characters suggested decent scope for improvement. Keeping in view all above points about faba bean the present investigation was carried out to study the genetic divergence among faba bean different genotypes.

MATERIALS AND METHODS

The present investigation was carried out on 53 faba bean genotypes during *rabi* season 2019-20 at Research Area, Medicinal, Aromatic and Potential Crop Section, Department of Genetics and Plant Breeding, CCSHAU, Hisar, Haryana. The location of experiment in Hisar was situated at 29.09° N latitude and 75.43° E longitude and at elevation of 216 m above mean sea level. Hisar city of Haryana lies on the outer margins of the south-west (SW) monsoon region. It has tropical monsoonal climate and is characterized as arid type of climate. The main characteristics of climate in Hisar district are its dryness, extremes temperature and scanty rainfall. The average annual rainfall is around 452 mm. The soil exhibits mixed pattern of Aeolian and Alluvial deposits. The mean weekly weather condition during *rabi* 2019-20 is depicted in fig.1.

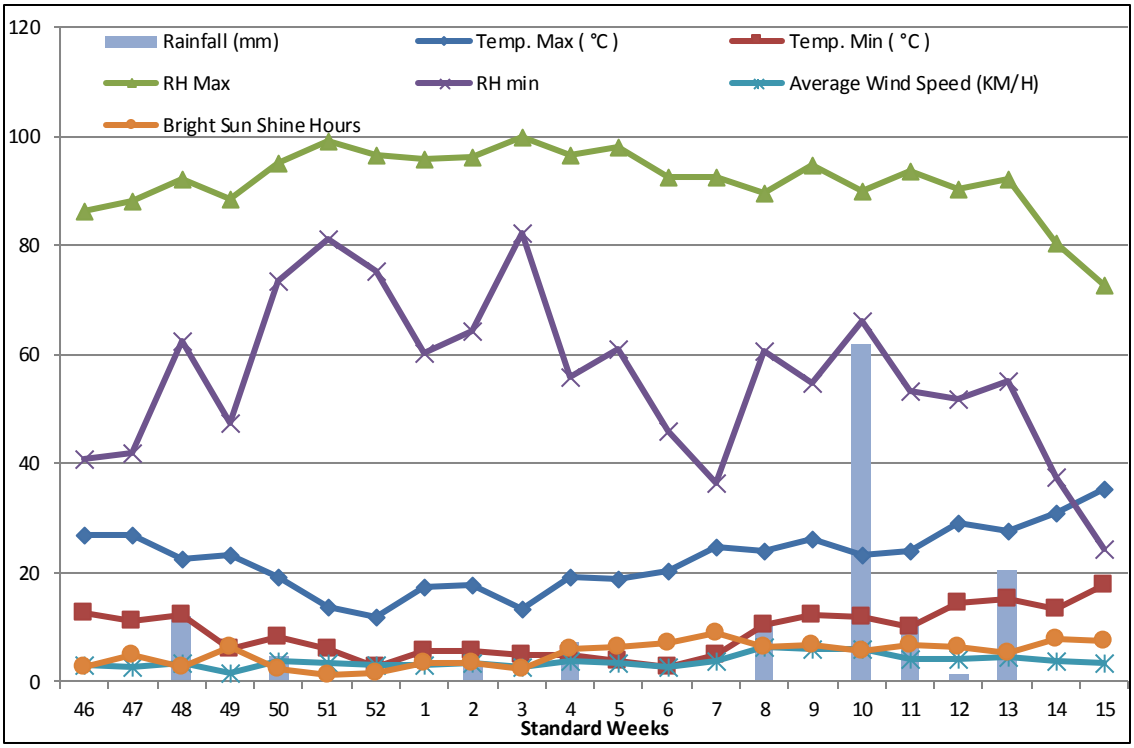

Fig. 1. Mean weekly weather condition during cropping period, *rabi* 2019-20

Source: Department of Agricultural Meteorology, CCSHAU, Hisar

The observations for all the characters were recorded on randomly selected five competitive plants per paired row in each replication except for days to 50% flowering and days to maturity, where, observations were recorded on whole paired row basis. The observations for yield and yield contributing characters namely, plant height(cm), days to 50% flowering, days to maturity, no. of pods cluster per plant, no. of branches per plant, no. of pods per plant, no. of pods per cluster, weight per pod(g), pod length (cm), pod breadth (cm), no. of seeds per pod, 100 seeds weight (g), protein content (%), pod yield per plant (g), biological yield (q/ha), harvest index % and seed yield (q/ha) were recorded on all the 53 genotypes. Analysis of variance for the recorded observations on different characters was carried out.

Analysis of variance in a Randomizedblock design for each quantitative character was statistically analysed as described by Panse andSukhatme (1967). The genetic diversity D2 analysis was done using the method suggested by Mahalanobis (1936) and elaborated by Murty and Arunachalam (1966).

RESULTS AND DISCUSSION

The results of analysis of variance revealed that there were sufficient variability present in 53 genotypes for the 17 characters under investigation, but it did not explain the extent of variability. To find extent of variability among the genotypes, Mahalanobis D^2 statistics (1936) as described by Rao (1952) were used.

Group constellation

Grouping of genotypes into different clusters was done by the method suggested by the Tocher and described by the Rao, 1952. The 53 genotypes were grouped into 6 clusters using Tocher's method, as shown in table 1. The maximum number of genotypes was found in the cluster II (24) followed by cluster I (23), cluster IV (3). cluster III, V and VI were monophyletic and each having one genotype only. The pattern of clustering of genotypes revealed that there was substantial diversity presented among the genotypes for the characters under investigation. The knowledge of sufficient amount of diversity will helpful in the selection of diverse and better parents for any hybridization program for isolating the better segregates. Similar results were also reported in the literature by Chaubey *et al*. (2012) and Sharifi and Aminpana (2014).

Table 1. Grouping of genotypes into different clustersusing Tocher's method

Cluster	No. of Genotypes	Name of Genotypes
Cluster 1	23	HB-78, EC-243596, HB-63, EC-361485, HB-21, HB-05, HB-65, EC-363781, HFB-01, EC-628942, EC-331564, EC-628940, EC-32976, HB-79, HB-73, HB-82, EC-351587, EC-287710, HB-02, HB-71, EC-591784, EC-343691, HB-37
Cluster 2	24	HB-38, EC-366272, ET-3279, EC-329681, HB-30, EC-628925, PRT-12, NDFB-12, NDFB-08, HB-28, EC-243793, HB-15, HB-33, NDFB-14, EC-25192, EC-117744, HB-90, EC-25085, EC-32905, HB-68, EC-32923, VIKRANT, HB-66, EC293820
Cluster 3	1	HB-61
Cluster 4	3	HB-03, HB-19, EC-243036
Cluster 5	1	HB-24
Cluster 6	1	HB-01

The results of group constellation also indicated that the genotypes from the different sources were also present together in same cluster and hence; geographical diversity, though important, but is not a necessary parameter of group constellation. Therefore, selections of parents merely on the basis of geographical diversity are not a rewarding performance for any hybridization program. Therefore, while selection of parents for any hybridization program; it is desirable to select the diverse parents on the basis of genetic diversity rather than the geographical diversity (Ngoc *et al*., 2017). This finding of lack of parallelism between genetic and geographical diversity were in consonance with the finding of Chaubey *et al*. (2012), Fikreselassie and Seboka (2012). The reason of lack of parallelism between genetic and geographical diversity may be due to the genetic drift.

Intra- and inter-cluster average D^2 value

The average D^2 value for intra- cluster and inter-cluster for six clusters were shown in table 2. The maximum intra- cluster D^2 value was recorded for cluster IV (11.51) followed by cluster II (9.68) and cluster I (9.07). The maximum inter- cluster D^2 value was recorded for cluster V and VI (22.51) followed by cluster III and VI (21.76), cluster I and IV (17.41), cluster VI and V (16.84), cluster II and V (16.58), cluster II and III (16.41), cluster IV and VI (16.04), cluster II and IV (14.40), cluster III and IV (14.10), cluster I and II (14.05), cluster II and VI (13.23) and cluster I and IV (13.12).

In the present investigation, the maximum inter-cluster D^2 value was recorded among cluster V and VI (22.51) which indicated that the genotypes present in these two clusters had highest genetic diversity. The selection of parents from theses clusters for hybridization programme will be fruitful, as the genotypes are genetically diverse. Selection of parents from the clusters having maximum inter-cluster distance for hybridization had also been

proposed by Chaubey *et al*. (2012), Fikreselassie and Seboka (2012), Sharifi and Aminpana (2014). The minimum inter- cluster D^2 value was recorded among cluster V and III (8.76), which suggested the close relationship among the genotypes of these clusters.

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

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	**9.07**	14.05	10.98	13.12	12.28	17.41
Cluster 2		**9.68**	16.41	14.40	16.58	13.23
Cluster 3			**0.00**	14.10	8.76	21.76
Cluster 4				**11.51**	16.84	16.04
Cluster 5					**0.00**	22.51
Cluster 6						**0.00**

Cluster means

The cluster means value of 6 clusters for 17 characters under studied were presented in the table 3. Plant height had maximum value in cluster III (134.56 cm), whereas, minimum value in cluster VI (77.87 cm). Days to 50% flowering had maximum value in cluster II (64.59), whereas, minimum value in cluster VI (61.60). Days to maturity had maximum value in cluster VI (154.79), whereas, minimum value in cluster V (145.79). Number of pod clusters per plant had maximum value in cluster IV (14.33), whereas, minimum value in cluster V (6.63). Number of branches per plant had maximum value in cluster IV (4.03), whereas, minimum value in cluster VI (3.17). Number of pods per plant had maximum value in cluster III (50.67), whereas, minimum value in cluster VI (24.80). Number of pods per cluster had maximum value in cluster III (2.21), whereas, minimum value in cluster IV (2.09). Weight per pod had maximum value in cluster IV (1.43 g), whereas, minimum value in cluster III (1.11 g). Pod length had maximum value in cluster IV (4.79 cm), whereas, minimum value in cluster V (4.37 cm). Pod breadth had maximum value in cluster VI (0.80 cm), whereas, minimum value in cluster II &III (0.74 cm). Number of seeds per pod had maximum value in cluster IV (3.48), whereas, minimum value in cluster VI (2.60). 100 seeds weight had maximum value in cluster IV (38.51 g), whereas, minimum value in cluster I (30.85g). Seed protein content had maximum value in cluster VI (30.15 %), whereas, minimum value in cluster III (25.78 %). Pod yield per plant had maximum value in cluster III (51.39 g), whereas, minimum value in cluster VI (22.69 g). Harvest index had maximum value in cluster VI (29.82%), whereas, minimum value in cluster V (21.27%). Seed yield had maximum value in cluster IV (9.49 q/ha), whereas, minimum value in cluster VI (4.86 q/ha).

Table 3. Mean value of different clusters for 17 characters

Sr. No.	Character	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
1	Plant Height (cm)	112.19	105.65	134.56	87.52	100.82	77.87
2	Days to 50% Flowering	64.17	64.59	63.20	64.53	63.73	61.60
3	Days to Maturity	148.48	149.01	145.93	148.82	145.79	154.79
4	No. of Pods Cluster per Plant	10.11	10.17	11.88	14.33	6.63	12.49
5	No. of Branches per Plant	3.52	3.43	3.43	4.03	3.47	3.17
6	No. of Pods per Plant	31.96	32.81	50.67	45.11	42.67	24.80
7	No. of Pods per Cluster	2.11	2.19	2.21	2.09	2.12	2.26
8	Weight per Pod (g)	1.15	1.14	1.11	1.43	1.14	1.14
9	Pod Length (cm)	4.72	4.73	4.73	4.79	4.37	4.69
10	Pod Breadth (cm)	0.75	0.74	0.74	0.76	0.75	0.80
11	No. of Seeds per Pod	3.09	3.10	3.37	3.48	2.87	2.60

12	100 Seeds Weight (g)	30.85	32.98	34.73	38.51	33.59	31.27
13	Seed Protein Content (%)	26.38	30.03	25.78	27.68	26.22	30.15
14	Pod Yield per Plant (g)	27.48	31.39	51.39	43.53	43.49	22.69
15	Biological Yield (q/ha)	25.27	26.41	35.56	32.08	32.65	17.79
16	Harvest Index (%)	24.20	25.54	28.46	29.82	21.27	21.44
17	Seed Yield (q/ha)	5.89	6.52	9.62	9.49	6.96	4.86

The results of cluster mean were presented in table 3. From the above discussion, it was observed that the cluster IV had maximum cluster value of number of pods cluster per plant (14.33), number of branches per plant (4.03), weight per pod (1.43 g), pod length (4.79 cm), no. of seeds per pod (3.48), 100 seeds weight (38.51 g), harvest index (29.82%) and seed yield (9.49 q/ha). Cluster III had maximum cluster means of plant height (134.56 cm), number of pods per plant (50.67), number of pods per cluster (2.21), pod yield per plant (51.39 g) and biological yield (35.56 q/ha). Cluster VI had maximum cluster means of days to maturity (154.79), pod breadth (0.80 cm) and protein content (30.15 %), while cluster II had maximum cluster means of days to 50% flowering, 64.59. The above finding was in consonance with the finding of Chaubey *et al*. (2012) and Girish *et al*. (2012). Table 4 depicted the superior genotypes selected from the different cluster on the basis of their performances for various characters.

Table 4. Superior genotypes among clusters

Clusters	Genotypes	Superior Characters
Cluster 1	EC-591784	Days to 50% Flowering, Days to Maturity, Pod Length, Seeds Per Pod, Seed Yield
Cluster 2	EC-32905	Days to 50% Flowering, Days to Maturity, Weight Per Pod, Seeds Protein Content, Pod Yield Per Plant, Seed Yield
Cluster 3	HB-61	Plant Height, No. of Pods Per Plant, Pod Yield Per Plant, Biological Yield
Cluster 4	EC-243036	No. of Pod Cluster Per Plant, No. of Branches Per Plant, No. of Pods Per Plant, Pod Breadth, Seeds Per Pod, 100 Seeds Weight, Biological Yield, Harvest Index, Seed Yield
Cluster 5	HB-24	No. of Pod Cluster Per Plant, No. of Pods Per Plant, 100 Seeds Weight, Pod Yield Per Plant

Contribution of individual characters towards genetic divergence

The results of contribution of individual characters towards genetic divergence were depicted in the table 5. The *per cent* contribution of seed yield and its attributing characters in genetic divergence were reported maximum for seed protein content (58.27%) followed by no. of pods cluster per plant (7.55%), no. of pods per cluster (4.57%), no. of pods per plant (4.28%), pod breadth (4.28%), pod length (4.14%), weight per pod (3.63%), no. of seeds per pod (3.19%), no. of branches per plant (2.47%), pod yield per plant (2.39%), seed yield (1.38%) and 100 seeds weight (1.31%). The rest of the characters had minute (below than zero) *per cent* contribution in genetic divergence.

Table 5. Contribution of individual Character towards genetic divergence

Sr. No.	Characters	*Per cent* Contribution
1	Plant Height (cm)	0.51%
2	Days to 50% Flowering	0.94%
3	Days to Maturity	0.07%
4	No. of Pods Cluster per Plant	7.55%
5	No. of Branches per Plant	2.47%
6	No. of Pods per Plant	4.28%
7	No. of Pods per Cluster	4.57%
8	Weight per Pod (g)	3.63%
9	Pod Length (cm)	4.14%
10	Pod Breadth (cm)	4.28%

11	No. of Seeds per Pod	3.19%
12	100 Seeds Weight (g)	1.31%
13	Seed Protein Content (%)	58.27%
14	Pod Yield per Plant (g)	2.39%
15	Biological Yield (q/ha)	0.07%
16	Harvest Index (%)	0.94%
17	Seed Yield (q/ha)	1.38%

CONCLUSIONS

The genotypes namely EC-32905, EC-243036, EC-591784, HB-03, HB-19, HB-61 and Vikrant are selected on the basis of their mean performance for different characters. These genotypes are important for including in crossing programme to further exploit genetic variability among populations, to affect selection of elite superior lines for hybridization programme and/or elite populations for composite varieties.

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