



ISSN (E): 2277- 7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2021; 10(7): 1238-1240  
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Received: 06-04-2021

Accepted: 27-06-2021

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## Studies on genetic variability, heritability and genetic advance for quantitative traits in faba bean (*Vicia faba* L.)

**Upendra Kumar Mishra, RM Tripathi, OP Verma, Aman Singh, Brijesh Maurya and Amarjeet Patel**

### Abstract

Thirty-nine genotypes of faba bean (*Vicia faba* L.) were evaluated in a field study to assess genetic variability, heritability and genetic advance. The analysis of variance revealed that there were highly significant differences for all the characters except pods per plant, pod fertility percent, seeds per pod and yield per plant. Higher genotypic coefficient and phenotypic coefficient of variation were observed for number of branches per plant and harvest index. Heritability and Genetic advance were high for all the characters except seeds per pod and pods per plant which had low genetic advance along with moderate heritability indicating the involvement of additive type of gene action in controlling these characters.

**Keywords:** Heritability, genetic advance, coefficient of variation, genotypic coefficient of variation

### Introduction

Pulses are a wonderful gift from nature and has been recognized as the 2nd most valuable plant source for health and nutrition. More than a dozen types of legumes are cultivated in various parts of the world. Traditionally, these crops were used to meet protein requirements. Faba bean (*Vicia faba* L.), a protein-rich leguminous plant from the Fabaceae family. Usually it is called Broad bean, Bakela, Ful masri, Horse bean, Windsor bean, Tick bean, etc. The large-seeded cultivars are known as broad beans in the UK, Australia and New Zealand, while small-seeded varieties are field beans (more like wild species), mainly used as fodder for livestock. In India, it is known by various names, such as Bakala, Anhuri, Kala matar in Hindi; Raj-rawan in Urdu and Kadu huralikayee in Kanada (Akbar *et al.* 1990) [2]. It is considered the third most consumed legume as grain in the world and one of the oldest food crops in the world. In about 58 countries, faba beans are grown on a large scale (FAO, 2009) [4]. *Vicia narbonensis* L. and *V. galilaea* Plitmann & Zohary, wild species are taxonomically similar to cultivated species, but they have  $2n = 14$  chromosomes, while cultivated field beans have  $2n = 12$  chromosomes. At most of the occasions crossing between them is generally unsuccessful (Bond *et al.*, 1985) [3]. In Uttar Pradesh state, Faba bean is grown in Ayodhya, Varanasi, Badohi, Mirazpur, Sultanpur district etc. The productivity of Faba bean in Uttar Pradesh state is quite lower as compared to other legume crops because of improper nutrient and pest management practices and also due to lack of suitable high yielding varieties for plains of this state. In Uttar Pradesh, Faba bean are grown during November to April. Seeds of faba bean are consumed as green to dry as vegetable and pulse. It is most widely grown due to its short duration, excellent nutritional status and dual use as vegetable and pulse crop. It contains very high nutritive value ranging 24 – 30% protein and 35 – 39% Carbohydrates. Faba Bean having a very good source of Ca, P and Vitamins. Green pod of faba bean is mainly used as vegetables, dry cotyledons are one of the excellent and cheap sources of lysine rich protein for poor's (Bond, 1976; Hawtin and Hebblethipiat, 1983; Abdel, 2008) [1]. Genetic variability is the key to crop improvement programme. It provides opportunity for enhancing the yield and stability of the crop at specific region of India.

### Materials and Method

The experimental materials for the present investigation consist of 39 accessions of faba bean including 4 checks *viz.* Vikrant, HFB-1, Rebya -40 and Giza -4. The experiment were laid out in Augmented Block Design carried out at the Genetics and Plant Breeding Research Farm of

Acharya Narendra Dev University of Agriculture and Technology Kumarganj Ayodhya. The experimental field were divided into five blocks of equal size. Eleven entries including four checks will be accommodated in each block. Each treatment were planted in 3 rows of 3m length with inter and intra row spacing of 45 cm and 15 cm, respectively. To avoid the border effect experimental plots were surrounded on all side by non-experimental rows. Five plants from each treatment were selected randomly for data recording.

The observation were recorded for Days to 50% flowering, Days to maturity, Plant height (cm), Number of branches per plant, Number of pods per plant, Pod fertility percent, Number of seeds per pod, 100- seed weight (g), Biological yield per plant (g), Harvest index (%), Seed yield per plant (g).

## Result and Discussion

### Analysis of variance

Existence of sufficient variability in a crop is an inevitable requirement for an effective crop improvement. In the present study, the analysis of variance for different yield and its contributing traits indicated that sufficient variation present among the genotypes as revealed from significant estimates of

mean squares for different characters. In some characters blocking was effective in reducing the experimental error to some extent as revealed by significant estimates of replication mean square. The analysis of variance was carried out for all the characters and result are presented in Table 1. The difference among the entries were significant for days to 50% flowering, days to maturity, plant height (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), biological yield per plant and harvest index and remaining were found non- significant. The differences among the checks were significant for seven characters viz., days to 50% flowering, days to maturity, plant height (cm), number of pods per plant, seeds per pod, 100 seed weight, biological yield per plant and seed yield per plant (g) and, branches per plant, pod fertility percent and harvest index were found non-significant. In the present study, the analysis of variance for different yield and its contributing traits indicated that sufficient variation is present among the genotypes as revealed from significant estimates of mean squares for different characters. In some characters blocking was effective in reducing the experimental error upto some extent as revealed by significant estimates of replication mean square.

**Table 1:** Analysis of variance for eleven characters in Faba bean germplasm

S.V	DF	Day to 50% flowering	Plant height (cm)	Day to maturity	Branches per plant	Pods per plant	Pod fertility percent	Seeds per pod	100- seed weight (g)	Biological yield (g)	Harvest index (%)	Yield per plant (g)
Block	04	9.21**	34.09**	12.38**	0.20	6.81*	5.84	0.28**	3.19**	40.11**	10.75**	1.01
Treatment	03	10.62**	36.07**	9.69**	1.93**	8.76**	37.70**	0.29**	2.77**	72.16**	12.11**	5.84**
Check	3	37.91**	55.38**	42.95**	0.60	6.71*	3.57	0.72**	2.07**	8.27**	3.095	4.32*
Error	12	-0.001	0.766	0.935	0.18	1.64	2.28	0.05	0.14	1.188	1.265	0.787

\*,\*\* Significant at 5% & 1% probability levels of significance, respectively

### Mean performance

The mean performances for different traits of 39 faba bean accessions are given in table number-2. Data revealed that there is a wider range of variability observed for the traits biological yield per plant (60.78-93.82) followed by pod fertility percent (70.51-90.90), harvest index (19.85-34.46), plant height (68.90-90.25) and seed yield per plant (16.90-24.98). These result reflect that the selection prospects for these traits to improve the performance through breeding programmes like selection and hybridization.

### Coefficient of variation

The phenotypic and genotypic coefficient of variation for all the 11 characters has been given in Table 2. In general, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters. The highest estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation were observed in case of branches per plant (PCV= 16.681% & GCV=14.964%) followed by harvest index (PCV=11.318% & GCV=10.540%), Seed per pod (PCV=10.826% & GCV=8.927%), pods per plant (PCV= 9.666 & GCV= 7.947) respectively and lowest for days to maturity i.e. (PCV=1.758&GCV=1.592).

The assessment of PCV and GCV in the germplasm collection was done and similar results were also get reported by Mesfin

*et al.* (2019) [6] computed genotypic (GCV) and phenotypic coefficient of variation (PCV) values were ranged from 1.08-23.05 and 1.20-23.26%, respectively.

### 4.4 Heritability and genetic advance in percent of mean

The estimate of broad sense heritability ( $h^2_b$ ) and genetic advance in per cent of mean (Ga) for different character are given in Table 2.

The highest estimate of heritability in broad sense was recorded in days to 50% flowering (99.0%) followed by biological yield per plant (97.88%), plant height (96.63%), 100 seed weight (92.08) and pod fertility percent (91.33%).

The moderate estimate of heritability (50-75) were found for pod per plant (68.06%) and seeds per pod (67.99%).

Neda *et al.* (2021) [7] report broad-sense heritability also revealed medium to high values for most of the traits Mesfin *et al.* (2019) [6] also evaluates and supported the results.

The high estimates of genetic advance in per cent of mean (>20%) were estimated for branches per plant (27.65) and harvest index (20.22). The moderate estimates of genetic advance (10-20%) resulted in case of biological yield per plant (19.06), seeds per pod (15.16), seed yield / plant (14.93), pods per plant (13.55) plant height (11.99), pod fertility percent (11.77) and 100 seed weight (10.12). The low value of genetic advance in percent of mean were showed by days to 50% flowering (7.14) and days to maturity (2.96).

**Table 2:** Range, mean and least significant differences for eleven characters in Faba bean genotypes

Characters	Range		Grand Mean	Coefficient of variation		Heritability in broad sense	Genetic advance	Genetic advance in % of mean at 5%
	Minimum	Maximum		PCV (%)	GCV (%)			
Days to 50% flowering	63	73	67.92	3.470	3.470	99.98	4.8558	7.1469
Days to maturity	125	134	129.56	1.758	1.592	81.99	3.8478	2.9696
Plant height (cm)	68.90	90.25	79.67	6.026	5.923	96.63	9.4882	11.9944
Branches per plant	4.30	8.00	5.83	16.681	14.964	80.47	1.6218	27.6522
Pods per plant	19.20	29.10	23.66	9.666	7.974	68.06	3.1805	13.552
Pod fertility percent	70.51	90.90	82.48	6.260	5.982	91.33	9.6541	11.7775
seeds per Pod	2.90	4.40	3.72	10.826	8.927	67.99	0.5597	15.1624
100-seed weight(g)	23.00	28.70	25.57	5.340	5.124	92.08	2.5707	10.1299
Biological yield per plant (g)	60.78	93.82	79.49	9.454	9.353	97.88	15.0772	19.0621
Harvest index (%)	19.85	34.46	27.29	11.318	10.540	86.73	5.5157	20.2207
Seed yield/plant (g)	16.90	24.98	21.53	9.138	8.140	79.36	3.1915	14.9375

### Conclusion

Existence of sufficient variability in a crop is an inevitable requirement for an effective crop improvement. However, in recent days, varietal improvement is centered on utilization of limited germplasm in breeding programme. On the basis of variability, heritability and genetic advance studies, it was concluded that the selection of genotype to improve seed yield per plant should be imposed preliminary for number of pods per plant, number of seeds per pod, pod fertility percent, number of branches per plant, plant height, while other characters should be considered as second most important characters.

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