

## Selection of promising genotypes of faba bean (*Vicia faba*) by deciphering genetic variability and trait association

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### ABSTRACT

Twenty-five genotypes of faba beans were evaluated for selection of promising genotypes by deciphering genetic variability and trait association. The experiment was conducted in a Randomized Block Design with three replications at Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj during *rabi* season of 2023. The plant-to-plant distance was 20 cm and row-to-row distance of 30 cm. The data were recorded from randomly selected five plants for each genotypes for each replications for nineteen characters *viz.* days to first flowering; days to 50% flowering; plant height (cm); number of branches/plant; number of nodes on main branch; number of flowers/plant; leaflet length (cm); leaflet width (cm); days to pod initiation; number of pods/plant; pod length (cm); pod width (cm); days to maturity; number of seeds/pod; seed index (gm); harvest index (%); biological yield (gm); seed yield; seed yield/hectare (tonnes/ha). Analysis of variance showed significant variation among different genotypes for all characters studied. Moderate GCV and PCV was recorded for number of branches/plant, number of pods/plant, pod width, number of seeds/pod, seed index, biological yield and seed yield per hectare. High estimate of heritability coupled with high genetic advance as percent of mean and moderate GCV was recorded for number of branches/plant, number of pods/plant, pod width, number of seed/pod, seed index, biological yield and seed yield. This indicates closeness of respective  $\sigma_p^2$  and  $\sigma_g^2$  value thereby low environmental effect on expression of these characters. Positive and significant correlation were observed for number of branches/plant, number of nodes in main branch, number of flowers/plant, number of pods/plant, pod length, days to maturity, plant height, leaflet length, number of seeds/pod, biological yield, days to first flowering, seed index and seed yield with seed yield (per plant) at genotypic level. While rest of the characters showed non-significant association with seed yield. Significant positive association of these above attributes indicated that these attributes were mainly influencing the seed yield in faba bean.

**Key words:** GCV, PCV, Variability, Heritability, Correlation coefficient, Genetic parameters

Faba beans, *Vicia faba* (L.), belongs to the Leguminosae family, sub-family Fabioideae. It is a diploid, self-pollinated species with *Vicia narbonensis* (L.) and *V. galilaea* Plitmann & Zohary, wild species are taxonomically similar to cultivated species, but they have  $2n=2x=14$  chromosomes, while cultivated field beans (*V. faba* L.) have a chromosome number of  $2n=2x=12$  chromosomes. At most of the occasions crossing between them is generally unsuccessful (Bond *et al.*, 1985). Faba bean is assigned to the Central Asian, Mediterranean, and South American centres of Diversity and believe to be a native to North Africa and southwest Asia, and extensively cultivated elsewhere (Harlan, 1969; Zohary and Hopf, 2000). Omima *et al.* (2018) suggested that having information on the magnitude of genetic variability is number one criterion for successful breeding. Genetic variability is a key for the success of a plant breeding program since it provides an opportunity to breeders to make the selection for desirable superior individuals from a genetically diverse base population (Partap *et al.* 2019). Understanding the level of genetic variability might support plant breeders' decision on the selection of parental genotypes with a broad genetic

base for further genetic improvement and amenities in development of breeding strategy (Omima *et al.* 2018). The lack of adequate variability has been considered as one of the major bottlenecks in crop improvement and the success of its improvement needs use of wide genetic variability in respect of important economic characters present in the population (Bhanu *et al.*, 2016). The estimation of heritability along with genetic advance is more applicable than the heritability value alone (Johnson *et al.* 1955). Therefore, study was designed to evaluate genetic variability and correlation coefficients in faba beans genotypes for eastern zone of Uttar Pradesh.

### MATERIALS AND METHODS

The present study was carried out at the Experimental Research Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj, during *rabi* season of 2023. The data were recorded from randomly selected five plants for each genotypes for each replications for nineteen characters *viz.* days to first flowering; days to 50% flowering; plant height (cm); number of branches/plant; number of nodes on main branch; number of flowers/plant; leaflet length (cm);

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leaflet width (cm); days to pod initiation; number of pods/plant; pod length (cm); pod width (cm); days to maturity; number of seeds/pod; seed index (gm); harvest index (%); biological yield (gm); seed yield (g/plant); seed yield (tons/ha). The experiment was set up using a randomized block design. The Fisher and Yates, 1963 method was used to statistically analyse the data. Johnson *et al.*, (1955); formulae was used to calculate GCV and PCV. Heritability (in broad sense) was eliminated by the formula Burton and Devane (1953). Correlation was calculated using methods suggested by Al-Jibouri *et al.* (1958).

## RESULTS AND DISCUSSION

### Analysis of variance

The analysis of variance showed highly significant differences ( $\alpha=0.05$ ) among 25 genotypes for all characters studied indicating the presence of considerable amount of genetic variability among germplasms (Table 1). Based on data on character values and analysis of variance, significant genotype differences were found for all 19 characters, indicating that the material has enough genetic variability to support a breeding programme aimed at increasing the yield of faba beans seeds. The results are in line with those of Dubey *et al.* (2022) and Ertiro *et al.* (2023).

### Genetic parameters

In general, estimates of phenotypic coefficient of variation (PCV) was found higher than their corresponding genotypic coefficient of variation (GCV) indicating the influence of environment on expression of these characters (table 2). Phenotypic coefficient of variation (PCV) ranged from 0.58% for days to maturity to 18.37% for pod width. Genotypic coefficient of variation (GCV) ranged from 0.48% for days to maturity to 17.43% for pod width. Both moderate GCV and PCV were recorded for number of branches/plant, number of pods/plant, pod width, number of seeds/pod, seed index, biological yield and seed yield in comparison to other characters indicating the presence of high amount of genetic variability for these characters. This also suggests that improvement in these characters might be gained to a reasonable extent therefore, selection for these characters would be effective because the response to selection is directly proportional to variability present. While both low GCV and PCV were recorded for days to first flowering, days to 50% flowering, number of nodes on main branch, leaflet length and leaflet width, days to pod initiation, pod length, days to maturity and harvest index. Rest characters observed to have comparably significant and more difference between GCV

**Table 1.** Analysis of Variance (ANOVA) for 17 characters in faba bean

ANOVA Summary			
Mean Sum of Squares (MSS)			
Degree of freedom	Replication (df=2)	Genotype (df=24)	Error (df=48)
Days of first flowering	3.04	3.36**	1.53
Days of 50% flowering	1.35	5.37**	1.07
Plant height	2.84	243.11*	18.37
Number of branches/plant	0.01	0.92**	0.03
No. of nodes on main branch	0.16	4.04**	0.74
Number of flowers/plant	0.36	12.58*	1.41
Leaflet length	0.01	0.32**	0.08
Leaflet width	0.01	0.04**	0.01
Days to pod initiation	6.01	8.91**	4.02
Number of pods/plant	0.17	13.16*	1.11
Pod length	0.04	0.26**	0.09
Pod width	00.01	0.09**	0.01
Days to maturity	0.40	0.97**	0.13
Number of seeds/pod	0.01	0.61**	0.05
Seed index	0.02	48.52*	4.63
Harvest Index	7.87	46.06**	16.55
Biological yield	0.39	47.24**	7.69
Seed yield (per plant)	0.08	10.06**	2.30
Seed yield	0.01	0.10**	0.01

\*\* and \* at 1% and 5% level of significance

**Table 2.** Genetic Parameters for 17 characters of 25 Faba beans genotype.

Genetic Parameter	GCV (%)	PCV (%)	Heritability (%) [broad sense]	Genetic advance	Genetic advance as per cent of Mean
Days of first flowering	1.30	2.44	28.59	0.86	1.44
Days of 50% flowering	1.85	2.44	57.19	1.86	2.88
Plant height	9.90	11.05	80.31	15.98	18.27
Number of branches/plant	16.66	17.55	90.18	1.07	32.59
No. of nodes on main branch	6.37	8.23	59.90	1.67	10.15
Number of flowers/plant	9.92	11.65	72.52	3.38	17.40
Leaflet length	5.38	7.50	51.50	0.42	7.95
Leaflet width	4.34	6.52	44.22	0.13	5.94
Days to pod initiation	1.73	3.22	28.91	1.42	1.92
Number of pods/plant	14.40	16.27	78.37	3.66	26.26
Pod length	4.89	7.91	38.21	0.30	6.23
Pod width	17.43	18.37	90.01	0.34	34.06
Days to maturity	0.48	0.58	67.95	0.90	0.81
Number of seeds/pod	13.91	15.78	77.78	0.78	25.28
Seed index	13.33	15.30	75.94	6.87	23.94
Harvest Index	5.56	9.11	37.27	3.94	7.00
Biological yield	12.38	15.58	63.15	5.94	20.27
Seed yield (per plant)	9.77	13.43	52.89	2.41	14.64
Seed yield	11.04	11.30	95.53	0.37	22.23

**Table 3.** Correlation coefficient between yield and its attributing traits in 25 faba beans genotypes at phenotypic level

Phenotypic correlation matrix																		
Characters	DF50	PH	NPB	NNMB	NFPP	LL	LW	DPI	NPPP	PL	PW	DM	NSPP	SI	HI	BY	SYPH	SYPP
DFF	0.268*	-0.0097	0.158	0.0439	0.224	0.228*	0.084	-0.2233	0.251*	0.0627	-0.490**	0.0212	-0.0566	0.426**	-0.1405	0.1062	0.1408	0.1465
DF50	1.000	0.244*	-0.340*	0.1372	0.0768	0.0646	-0.1964	-0.1532	0.0854	0.1886	-0.1609	0.0438	0.0767	0.277*	0.0216	0.0327	0.0011	0.0205
PH		1.000	-0.496**	0.391**	0.1246	0.1748	-0.1457	0.256*	0.1491	0.372*	0.1605	0.252*	-0.1203	0.1043	0.1385	0.351*	0.403**	0.341*
NPB			1.000	0.0529	0.396**	-0.0864	0.274*	-0.095	0.429**	-0.0815	-0.2211	0.1378	0.0494	0.1505	-0.373**	0.297*	0.270*	0.2127
NNMB				1.000	0.366*	-0.2037	-0.0271	0.1808	0.327*	0.1865	-0.0139	-0.0147	-0.2019	-0.0554	-0.0287	0.341*	0.265*	0.1789
NFPP					1.000	0.1585	0.228*	0.0426	0.809**	-0.0053	-0.1868	0.349*	-0.0056	0.451**	-0.1926	0.498**	0.620**	0.442**
LL						1.000	0.289*	-0.005	0.1952	0.1172	-0.0549	0.376**	0.1541	0.466**	-0.0192	0.08	0.271*	0.253*
LW							1.000	-0.119	0.234*	-0.2025	-0.1324	0.356*	0.0879	0.217	-0.0258	-0.0072	0.0849	0.0888
DPI								1.000	-0.0874	0.128	0.2248	-0.0445	-0.2	-0.354*	0.0677	-0.0306	0.058	0.0157
NPPP									1.000	0.0132	-0.2254	0.325*	0.091	0.462**	-0.2017	0.590**	0.723**	0.629**
PL										1.000	-0.0052	0.0673	0.1099	0.0075	0.230*	0.300*	0.356*	0.344*
PW											1.000	0.0696	-0.1222	-0.357*	0.0345	-0.0761	-0.0571	-0.0648
DM												1.000	0.1396	0.367*	-0.1109	0.334*	0.395**	0.285*
NSPP													1.000	0.0974	0.1241	0.1191	0.259*	0.2092
SI														1.000	-0.1505	0.229*	0.376**	0.341*
HI															1.000	-0.236*	0.011	0.021
BY																1.000	0.744**	0.635**
SYPH																	1.000	0.907**

and PCV value depicting greater influence of environment on expression of character. Hiywotu *et al.* (2022), Kebede *et al.* (2022) and Kumar *et al.* (2023) gave similar conclusions. The characters that showed lesser effect of environment on expression should be selected for breeding programme.

In the study, heritability (broad sense) ranged from 28.91% for days to pod initiation to 95.53% for seed yield (95.53%) [table 2]. High heritability (broad sense) estimates (60% and above) had been observed for plant height, number branches/plant, number of flowers/plant, number of pods/plant, pod width, days to maturity, number of seeds/pod, seed index, biological yield, and seed yield. Therefore, these characters are predominantly governed by additive gene action and could be improved through individual plant selection owing to their high heritability values. Such characters, according to Panse and Sukhatme (1957), are primarily controlled by additive gene action and, because of their high heritability values, could be enhanced by individual plant selection. Similar results for high heritability for plant height, number branches/plant, number of pods/plant, pod width, days to maturity, biological yield was reported earlier by Kumar *et al.* (2020) and Mishra *et al.* (2022). High heritability was found earlier by Singh *et al.* (2013), Chaurasia *et al.* (2022), for the number of seeds/pod, seed index, biological yield. Shift in gene frequencies towards superior side under some selection pressure is termed as genetic advance and is generally expressed as percentage of mean (genetic gain) to compare the advance of different characters having different units of measurements.

High estimate of heritability coupled with high genetic advance as percent of mean and moderate GCV was recorded for number of branches/plant, number of pods/plant, pod width, number of seeds/pod, seed index, biological yield and seed yield. This indicates closeness of respective  $\sigma^2_p$  and  $\sigma^2_g$  value thereby low environmental effect on expression of these characters. Such values may be attributed to the additive gene effects and direct selection for these traits would be fruitful. Thus, phenotypic selection may be effective for these characters with high to moderate GCV along with high heritability coupled with high genetic advance as percent of mean. This also pointed out the fact that these characters have appreciable genetic potential and are comparably less influenced by environment, hence desirable for simple selection in breeding programmes. Al-Barri and Shtaya (2013), Mishra *et al.* (2022), and Ertiro *et al.* (2023) all reported similar results for the harvest index.

### Correlation coefficient analysis

Our results revealed that there was a comparative higher degree of genotypic correlation coefficients than

**Table 4.** Correlation coefficient between yield and its attributing traits in 25 faba beans genotypes at genotypic level

Characters	Genotypic correlation matrix														
	DF50	PH	NPB	NNMB	NPPP	LL	LW	DPI	NPPP	PL	PW	DM	NSPP	SI	HI
DF50	0.575**	-0.073	0.389**	0.206	0.372*	0.1751	0.278*	-0.369*	0.308*	0.326*	-0.758**	0.0225	0.0721	0.728**	0.0308
PH	1.000	0.282*	-0.446**	0.228*	0.0953	0.1966	-0.341*	-0.282*	0.0587	0.2238	-0.244*	-0.0093	0.1714	0.356*	0.0925
NPB	1.000	1.000	-0.561**	0.544**	0.1696	0.262*	-0.240*	0.569**	0.1189	0.711**	0.2258	0.361*	-0.1124	0.0576	0.330*
NNMB	1.000	1.000	1.000	0.1134	0.492**	-0.1609	0.540**	-0.308*	0.506**	-0.105	-0.273*	0.1479	0.0454	0.1967	-0.587**
NPPP	1.000	1.000	1.000	1.000	0.428**	-0.246*	-0.2265	0.514**	0.379**	0.585**	-0.011	0.0114	-0.274*	-0.0418	-0.1274
LL	1.000	1.000	1.000	1.000	1.000	0.271*	0.323*	-0.1168	0.1233	0.1281	-0.286*	0.490**	0.0894	0.589**	-0.381**
LW	1.000	1.000	1.000	1.000	1.000	1.000	0.631**	-0.322*	0.2203	0.315*	-0.0676	0.695**	0.324*	0.746**	0.389**
DPI	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.1675	0.320*	-0.1675	-0.2072	0.493**	-0.0159	0.366*	0.0946
NPPP	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.0508	0.514**	0.416**	-0.280*	-0.312*	-0.620**	0.485**
PL	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.279*	0.475**	0.1305	0.590**	-0.279*
PW	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.268*	0.327*	0.1068	0.058
DM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.238*	0.1043
NSPP	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.0203
SI	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.145
HI	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.1325
BY	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
SYPH	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
SYPP	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

**NPB:** No. of primary branches; **NN:** No. of nodes on main branch; **NPPP:** No. of flowers per plant; **PL:** Pod length; **PW:** Pod width; **HI:** Harvest index; **DM:** Days to maturity; **PH:** Plant height; **LL:** Leaflet length; **LW:** Leaflet width; **DPI:** Days to first flowering; **DF50:** Days to 50% flowering; **SI:** Seed index; **SYPH:** Seed yield per hectare; **SYPP:** Seed yield per plant

their phenotypic counterparts in most of the characters (Table 3 and 4). This indicated that there was a higher degree of association between two characters of genotypic association, their phenotypic association was lessened due to the influence of environment. Positive and significant correlation was observed for number of flowers/plant (0.442\*\*), number of pods/plant (0.629\*\*), pod length (0.344\*), days to maturity (0.285\*), plant height (0.341\*), leaflet length (0.253\*), biological yield (0.635\*\*), seed index (0.341\*) and seed yield (0.907\*\*) with seed yield per plant at phenotypic level. While rest of the characters showed non-significant association with seed yield.

Positive and significant correlation was observed for number of branches/plant (0.350\*), number of nodes in main branch (0.478\*\*), number of flowers/plant (0.972\*\*), number of pods/plant (0.913\*\*), pod length (0.585\*\*), days to maturity (0.628\*\*), plant height (0.501\*\*), leaflet length (0.390\*\*), number of seeds/pod (0.353\*), biological yield (0.843\*\*), days to first flowering (0.241\*), seed index (0.462\*\*) and seed yield (0.543\*\*) with seed yield/plant at genotypic level. While rest of the characters showed non-significant association with seed yield. Significant positive association of these above attributes indicated that these attributes were mainly influencing the seed yield in faba bean. Thus, selection practiced for improvement in one character will automatically result in the improvement of the other character even if direct selection for improvement has not been made for the yield character.

For phenotypic correlation coefficient, Kumar *et al.* (2020) and Kebede *et al.* (2022) reported significant and positive correlation with seed yield/plant for number of flowers /plant, number of pods/plant, pod length, days to maturity, plant height. Khamassi *et al.* (2021) and Ertiro *et al.* (2023) concluded seed yield to be significantly and positively correlated with number of flowers/plant, number of pods/plant, pod length, days to maturity, plant height, number of seeds/pod, biological yield, days to first flowering, seed index at genotypic level.

## CONCLUSION

It is concluded that analysis of variance showed significant variation among different genotypes for all characters studied. Both moderate GCV and PCV was recorded for number of branches/plant, number of pods/plant, pod width, number of seeds/pod, seed index, biological yield and seed yield.

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