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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS STUDIES IN BUSH TYPE FRENCH BEAN (*PHASEOLUS VULGARIS* L.)

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ABSTRACT

A study evaluating eighteen bush type French bean genotypes for genetic variability and correlation revealed low environmental influence on pod yield and its contributing traits. Seed yield per plant showed the highest genetic coefficient of variation (29.98 %) and phenotypic coefficient of variation (31.45%). The highest heritability estimate was observed for the number of pod yield per plant (92.99%). Pod yield per plant was significantly positively correlated with several traits, including number of pods per plant, test weight, plant spread, plant height, seed yield per plant, chlorophyll content, single pod weight, number of branches per plant and number of seeds per pod. Path analysis identified seven key characters with a high direct positive impact on pod yield per plant: number of pods per plant (0.8011), single pod weight (0.29448), plant spread (0.21165), test weight (0.19641), days taken for first flower initiation (0.19197), number of seeds per pod (0.11829) and pod length (0.08898). These findings suggest that selecting for plant spread, number of pods per plant, single pod weight, number of seeds per pod and test weight can improve pod yield.

Key words : Variability, Genetic advance, Heritability, Correlation, Path analysis.

Introduction

French bean (*Phaseolus vulgaris* L., 2n= 2x= 22) is an important legume vegetable belonging to family Fabaceae. It has many synonyms like snap bean, kidney bean, haricot bean and also as called rajmah in hindi. Beans are essentially used for their tender green pods. The dried pods are used as pulse and provide valuable protein to the human diet. The nutritive value of the french bean per 100 g of green pod is 1.7 g protein, 0.1 g fat, 4.5 g carbohydrate, 1.8 g fiber and is also rich in minerals and vitamins. Beans are also called as “meat of the poor”, contribute essential protein to the undernourished people and it can be grown under different cropping patterns of hills and plains of India. Being a short duration crop, french bean can be grown under different cropping patterns of hills and plains of India. In India, it is mainly grown in Himachal Pradesh, Punjab, Haryana, Uttar Pradesh, Bihar, Gujarat, Madhya Pradesh, Maharashtra, Karnataka, Andhra Pradesh and Tamil Nadu. In India, french bean is grown over an area of 3.08 lakh hectare with annual production of 28.31 lakh tons (Anon., 2022-23). For a crop breeding program to be effective, it’s essential to consider both genetic variability and heritability when selecting for desirable traits. The transmission of variability from parents to progeny is critical. In French bean, several traits showed high heritability and significant genetic gain, including pod yield per plant, seed yield per plant, test weight, number of pods per plant. (Lyngdoh *et al*., 2018). The results of character association studies provide valuable insights for selection programs, as selecting for specific traits can have a ripple effect on other related traits. By conducting path analysis, breeders can determine the direct and indirect impacts of each component on yield, ultimately identifying the most influential characters that contribute to yield. The current research focused on assessing genetic diversity, heritability

and potential genetic improvement in immature pod characteristics. Furthermore, statistical techniques, including correlation and path analysis, were employed to explore the interrelationships among these traits, aiming to uncover valuable insights for enhancing yield.

Materials and Methods

The study was conducted during the late *kharif* seasons of 2023 and 2024 at the Herbal Garden, College of Agriculture, Raichur. Eighteen bush-type French bean genotypes, including Arka Arjun, Arka Komal, Arka Suvidha, EC559573, Malgudi beans, EC13097, FB-117, Anup beans, Willvine contender, Arka Sharath, FBGC-1, FBGC-2, FBGC-3, FBGC-4, Palguni, FBGC-5, FBGC-6 and EC-13099 were evaluated in a randomized block design with three replications. Each plot measured 5 x 1 m^2, with rows spaced 45 cm apart and plants spaced 15 cm apart within rows, accommodating 66 plants per plot.

Observations were recorded on ten randomly selected plants from each replication for yield and its associated traits *viz.*, plant height (cm), plant spread (cm^2), number of branches per plant, chlorophyll content (mg/g), days taken for first flower initiation, days taken for 50 per cent flowering, number of pods per plant, pod length (cm), single pod weight (g), number of seeds per pod, seed yield per plant (g), test weight (g) and pod yield per plant (g). Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967). Estimation of parameters of variability, genotypic and phenotypic coefficient of variation was done following Burton and De Vane (1953). The expected genetic advance as percent of mean (GAM) was calculated as per Johnson *et al*. (1955). The phenotypic, genotypic and environmental coefficients of correlation were computed following Al-Jibouri *et al.* (1958). The path coefficients were calculated by employing the method suggested by Dewey and Lu (1957).

Results and Discussion

Both phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) corresponded closely for most of the characters under study indicating less influence of the environment and selection will be effective on the basis of genotype alone with equal chance of success (Table 1). Highest genotypic and phenotypic coefficient of variation was recorded for seed yield per plant, pod yield per plant, number of pods per plant and test weight. However, GCV and PCV estimates were also found to be moderate for plant spread, chlorophyll content, pod length and single pod weight which suggested comparatively high genetic variation among the genotypes for these characters. Similarly, high value of PCV and GCV were recorded by Basavaraja *et al*. (2021) for seed yield per plant, number of pods per plant and test weight.

Heritability is a measure of the value of selection for the particular character and as an index of transmissibility of characters from parent to offspring. Close correspondence between PCV and GCV estimates was reflected on the broad sense heritability estimates that were high (more than 60%) for all the characters whereas

Table 1 : Variability estimates for growth and yield in French bean (*Phaseolus vulgaris* L.) genotypes.

S. no.	Characters	Range		Mean	GCV(%)	PCV(%)	h^2 bs(%)	GA	GAM(%)
		Min	Max						
Growth parameters									
1.	Plant height (cm)	36.95	52.33	44.93	9.16	11.20	66.94	6.99	15.44
2.	Plant spread ($cm^{2)}$	865.23	1761.87	1157.32	17.40	19.46	79.89	370.73	32.03
3.	Number of branches per plant	20.93	22.37	18.35	7.19	11.47	39.34	1.71	9.29
4.	Chlorophyll content (mg/g)	1.43	2.37	1.97	12.80	14.59	76.88	0.46	23.11
Reproductive parameters									
5.	Days taken for first flower initiation	27.33	38.33	34.33	8.62	10.14	72.40	5.19	15.12
6.	Days taken for 50 per cent flowering	31.33	44.33	38.65	8.03	9.73	68.14	5.28	13.65
Yield parameters									
7.	Number of pods per plant	19.33	41.33	27.31	22.70	24.10	88.70	12.03	44.04
8.	Pod length (cm)	8.97	13.75	11.91	10.00	11.47	76.08	2.14	17.97
9.	Single pod weight (g)	3.29	5.76	4.67	13.73	15.17	81.94	1.19	25.60
10.	Number of seeds per pod	4.80	6.07	5.39	5.69	8.36	46.33	0.43	7.98
11.	Seed yield per plant (g)	19.06	49.13	32.86	29.98	31.45	90.84	19.34	58.86
12.	Test weight (g)	18.30	33.70	22.32	21.80	22.94	90.33	9.53	42.68
13.	Pod yield per plant (g)	85.34	184.13	122.41	23.83	24.71	92.99	57.94	47.33

Table 2 : Phenotypic correlation coefficient for various traits in French bean (*Phaseolus vulgaris* L.) genotypes.

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1	1 **												
2	0.5019 **	1 **											
3	0.5939 **	0.3763 **	1 **										
4	0.5037 **	0.3342 *	0.3837 **	1 **									
5	-0.0569	-0.453 **	0.0741	-0.0588	1 **								
6	0.0051	-0.4078 **	0.1316	0.0035	0.9105 **	1 **							
7	0.7247 **	0.5272 **	0.6948**	0.5138**	0.0263	0.1023	1 **						
8	-0.0872	0.1989	-0.3497**	0.1928	-0.3296 *	-0.4072**	-0.2701*	1 **					
9	0.1142	0.3484 **	-0.0745	0.432 **	-0.4978**	-0.5167 **	0.0243	0.6351 **	1 **				
10	0.4064 **	0.237	0.2923	0.2291	0.0664	0.1812	0.2916*	-0.0771	0.0868	1 **			
11	0.6425 **	0.6042 **	0.5402 **	0.2234	-0.1648	-0.1396	0.7553 **	-0.2037	-0.0483	0.317 *	1 **		
12	0.5814 **	0.7377 **	0.461**	0.4159 **	-0.4379 **	-0.4534**	0.5645 **	0.1578	0.4138 **	0.2221	0.6473 **	1 **	
13	**0.5678 ****	**0.6759 ****	**0.439 ****	**0.5288 ****	**-0.2112**	**-0.1895**	**0.7329 ****	**0.1691**	**0.4728 ****	**0.3181 ***	**0.5481 ****	**0.6953 ****	**1 ****

*Significant @ 5%, ** Significant @ 1%

Where,

1- Plant height, 2-Plant spread, 3- Number of branches per plant, 4-Chlorophyll content
5-Days taken for first flower initiation, 6-Days taken for 50 per cent flowering, 7-Number of pods per plant, 8-Pod length
9-Single pod weight, 10-Number of seeds per pod, 11-Seed yield per plant, 12-Test weight
13-Pod yield per plant

number of branches (39.34%) and number of seeds per pod (46.33%) recorded moderate heritability. The overall scenario of broad sense heritability estimates for different characters *viz*., pod yield per plant (92.99%), seed yield per plant (90.84 %), test weight (90.33%), number of pods per plant (88.70%), single pod weight (81.94%), plant spread (79.89%), chlorophyll content (76.88%), pod length (76.08%), days taken for first flower initiation (72.40%), days taken for 50 per cent flowering (68.14%) and plant height (66.94%) indicates the reliability with which a genotype can be recognized by its phenotypic expression. However, this broad sense heritability values are likely to be over-estimated as in this calculation it was not possible to exclude variation due to different genetic component and their interrelation.

Hence, heritability in combination with genetic advance would be more reliable for predicting the effect of selection because, genetic advance depends on the amount of genetic variability, the magnitude of masking effect of genetic expression (environmental influence) and the intensity of selection (Johnson *et al*., 1955). In the present investigation, mean genetic advance was high (>20%) for seed yield per plant (58.86), pod yield per plant (47.33%), number of pods per plant (44.04%), test weight (42.68%), plant spread (32.03%), single pod weight (25.60%) and chlorophyll content (23.11%).

In this context, high GCV coupled with high broad sense heritability and high genetic advance was registered in four characters *viz*., number of pods per plant, seed yield per plant, test weight, pod yield per plant, which indicated the role of additive gene action for the inheritance of these traits and are likely to respond better to selection. The results were in accordance with findings of Lyngdoh *et al*. (2018) for number of pods per plant and pod yield per plant.

Correlation studies help us to know the suitability of multiple characters for indirect selection, because selection for one or more traits results in correlated response in several other traits (Searle, 1965). The intensity and direction of association among the characters is measured by phenotypic correlation

Table 3 : Phenotypic path analysis for French bean (*Phaseolus vulgaris* L.) genotypes.

	1	2	3	4	5	6	7	8	9	10	11	12	13
1	**-0.09224**	0.10623	-0.05259	-0.03756	-0.01092	0.00061	0.58056	-0.00776	0.03366	0.04807	-0.11444	0.11419	**0.5678 ****
2	-0.0463	**0.21165**	-0.03332	-0.02493	-0.08696	0.04782	0.42234	0.0177	0.1026	0.02803	-0.10762	0.14489	**0.6759 ****
3	-0.05478	0.07964	**-0.08856**	-0.02863	0.01424	-0.01543	0.55668	-0.03111	-0.02188	0.03449	-0.09622	0.09057	**0.439 ****
4	-0.04642	0.07071	-0.03398	**-0.07498**	-0.01142	-0.00047	0.4116	0.017	0.12739	0.02739	-0.03981	0.08169	**0.5288 ****
5	0.00525	-0.09588	-0.00657	0.00444	**0.19197**	-0.10678	0.02107	-0.02933	-0.14659	0.00787	0.02935	-0.08601	**-0.2112**
6	0.00048	-0.08631	-0.01165	-0.0003	0.17479	**-0.11727**	0.08195	-0.03623	-0.15222	0.02145	0.02487	-0.08905	**-0.1895**
7	-0.06685	0.11158	-0.06154	-0.03834	0.00505	-0.012	**0.8011**	-0.02404	0.00713	0.03446	-0.13453	0.11087	**0.7329 ****
8	0.00804	0.0421	0.03096	-0.01425	-0.06327	0.04774	-0.21638	**0.08898**	0.18694	-0.00903	0.03628	0.03099	**0.1691**
9	-0.01054	0.07374	0.00658	-0.03228	-0.09556	0.06062	0.01939	0.05649	**0.29448**	0.01001	0.00859	0.08129	**0.4728 ****
10	-0.0375	0.05018	-0.02583	-0.01729	0.01279	-0.02127	0.23352	-0.0068	0.02494	**0.11829**	-0.0565	0.04368	**0.3181 ***
11	-0.05926	0.12788	-0.04784	-0.01668	-0.03164	0.01637	0.60507	-0.01813	-0.01419	0.0375	**-0.17812**	0.12714	**0.5481 ****
12	-0.05363	0.15613	-0.04083	-0.03104	-0.08406	0.05317	0.45222	0.01404	0.12189	0.02629	-0.1153	**0.19641**	**0.6953 ****

Residual (0.188)

Where,

1- Plant height; 2-Plant spread; 3- Number of branches per plant; 4-Chlorophyll content
5-Days taken for first flower initiation; 6-Days taken for 50 per cent flowering; 7-Number of pods per plant; 8-Pod length
9-Single pod weight; 10-Number of seeds per pod; 11-Seed yield per plant; 12-Test weight
13-Pod yield per plant

coefficient. The correlation coefficient between pod yield per plant and other quantitative traits attributing to yield showed that pod yield was significantly and positively correlated with number of pods per plant (r_p = 0.7329), test weight (r_p = 0.6953), plant spread (r_p = 0.6759), plant height (r_p = 0.5678), seed yield per plant (r_p = 0.5481), chlorophyll content (0.5288), single pod weight (r_p = 0.4728), number of branches per plant (r_p = 0.439) and number of seeds per pod (r_p = 0.3181) (Table 2). The results are in conformity with the findings of Lyngdoh *et al*. (2018), Luitel *et al*. (2021) and Haralayya *et al*. (2015).

Path coefficient technique is more useful in establishing the direct and indirect relationship among any character which is a more realistic interpretation regarding influence of a character on a particular trait. The path coefficient analysis using phenotypic correlation coefficient among pair of characters depicting direct and indirect effect on pod yield, which shows that seven characters *viz*., number of pods per plant (0.8011), single pod weight (0.29448), plant spread (0.21165), test weight (0.19641), days taken for first flower initiation (0.19197), number of seeds per pod (0.11829) and pod length (0.08898) had high and positive direct effect suggesting the importance of these traits in selection programme for improving yield (Table 3). Seed yield per plant showed the highest negative direct effect on green pod yield per plant which contributed for its negative correlation with green pod yield. The next maximum negative direct effect was exerted by days taken for 50 per cent flowering followed by plant height, number of branches per plant and chlorophyll content. The maximum negative indirect effect on pod yield per plant was exhibited by pod length through number of pod per plant. That means, this trait affected green pod yield per plant *via* their negative indirect effects on number of pod per plant. The low magnitude of residual effect (0.188) indicated that the traits included in the present investigation accounted for most of the variation present in the dependent variable. These results are also in consonance with Haralayya *et al.* (2017), Alemu *et al.* (2017).

Conclusion

It can be concluded from the study that a wide range of variability is present for all the characters and selection based on plant spread**,** days taken for first flower initiation, number of pods per plant, pod

length, single pod weight**,** number of seeds per pod and test weight**,** will help the crop breeder in making effective selection for improving the pod yield which leads to the development of varieties with higher yield potential in French bean.

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