



International Journal of Research in Agronomy

E-ISSN: 2618-0618

P-ISSN: 2618-060X

© Agronomy

www.agronomyjournals.com

2024; SP-7(7): 642-645

Received: 27-05-2024

Accepted: 30-06-2024

Aashima Dhiman

M.Sc. Scholar, Department of
Genetics and Plant Breeding,
School of Agriculture University,
Mandi, Himachal Pradesh, India

Alok Kumar

Assistant Professor, Department of
Genetics and Plant Breeding,
School of Agriculture, Abhilashi
University, Mandi, Himachal
Pradesh, India

Ravi Sharma

Assistant Professor, Department of
Genetics and Plant Breeding,
School of Agriculture, Abhilashi
University, Mandi, Himachal
Pradesh, India

Gunjan

M.Sc. Scholar, Department of
Genetics and Plant Breeding,
School of Agriculture University,
Mandi, Himachal Pradesh, India

Karan Rana

M.Sc. Scholar, Department of
Genetics and Plant Breeding,
School of Agriculture University,
Mandi, Himachal Pradesh, India

Corresponding Author:

Alok Kumar

Assistant Professor, Department of
Genetics and Plant Breeding,
School of Agriculture, Abhilashi
University, Mandi, Himachal
Pradesh, India

Genetic variability, heritability and genetic advance in French bean (*Phaseolus vulgaris* L.) genotypes

Aashima Dhiman, Alok Kumar, Ravi Sharma, Gunjan and Karan Rana

DOI: <https://doi.org/10.33545/2618060X.2024.v7.i7Si.1159>

Abstract

Twenty five genotypes were evaluated to study the genetic variability, correlation coefficient and path coefficient. The experiment was set up in a randomized block design. The coefficients of variation for both the genotypic coefficient variation (GCV) and the phenotypic coefficient variation (PCV) were high for plant height, number of pods per plant, pod length. High heritability coupled with genetic advance was found for days to 50% flowering, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), seed width (mm), 100 seed weight (g), seed yield per plant. A positive and significant correlation of seed yield per plant with days to 50% flowering and days to maturity was observed.

Keywords: Variability, heritability, genetic advance, correlation

Introduction

Rajmash (*Phaseolus vulgaris* L.) also known as Kidney beans which belong to the family *Fabaceae*. It is also known as red kidney beans, French bean, haricot bean, snap bean, dry bean, pole bean etc. The species shows wide variation in the growth, habitat, pigmentation, pod morphology and seed morphology. Available local land races consist of a combination of beans with varying seed coat colours, form sizes, plant morphology, and yield potential. French beans are relatively tolerant of temperature fluctuations but are sensitive to frost and extreme cold conditions. Therefore, in areas prone to frost or colder temperatures, cultivation practices such as providing protective measures like mulching or selecting appropriate planting times are essential to prevent damage to the crop. It is widely cultivated in tropics, subtropics and temperate regions across the globe receiving 60 cm-150 cm of rainfall annually. The primary growing regions for French beans include Shimla, Chamba, Sirmour, Kullu, Kinnaur, and certain parts of Mandi and Solan district. French beans have therapeutic qualities that can help with diabetes and certain cardiac issues. French beans are versatile and can be consumed fresh, dried, or canned. Rajmash is high in fiber, protein, and vitamins and serves as a primary food legume. Rajmash has several health benefits, including avoiding cancer and improving brain function. The genetic estimates in the form of variance, coefficients of variation, heritability, genotypic, phenotypic and environmental correlations help the scientific community to know the magnitude of population's genetic variability, deducing interrelationships between traits, thus assisting in the plant selection process. Correlation coefficient, in general, shows association among characters (Toker and Cagirgan, 2004) [11]. However, correlation studies do not provide the exact picture of relative importance of direct and indirect effects of each of the component characters. Both genotypic and phenotypic coefficients of variation can be used to determine the amount of variety in a population, heritability shows how transmissible a trait is and how well selection has worked. In addition, heritability estimates must be paired with genetic advancement to determine the anticipated genetic gain in the following generation. Studies on heritability, genetic advance, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), correlation, and path analysis help breeders understand the genetic potential and relationships between different traits, guiding effective breeding programs to improve French bean varieties. Correlation and path coefficient analysis could be used together to understand the

cause and effects relationship between seed yield and its components to identify the traits which may be considered as indirect selection criteria.

There are several methods to study genetic diversity using morphological, cytological and biochemical markers and more recently through DNA based technologies, but knowledge of the phenotype given by morphological and agronomical descriptors is still important (Sudre *et al.* 2010) [10] for the assessment of genetic diversity and considered as a good source of information for the breeders with the target traits (Yadeta *et al.* 2011) [12].

Therefore, the present investigation was undertaken to study the components of variation, broad sense heritability (h^2_{bs}), genetic advance among different genotypes.

Materials and methods

The present investigation was carried out at the Research Farm, School of Agriculture, Abhilashi University, Mandi (H.P). The experimental materials consisted of 25 genotypes of French bean including five checks were evaluated in Randomized Block design with 3 replications with a spacing of 30 cm x 10 cm during *kharif* season. The genotypes were received from NBPGR regional station, Shimla. The characters such as days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, plant height (cm), pod length (cm), seed length (mm), seed width (mm), number of seeds per pod, 100 seed weight (g), harvest index (%) and seed yield per plant. Coefficients of variation of three different kinds were estimated *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV). According to Burton and De Vane (1953) [1], the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated. The methods of Johnson *et al.* (1955) [5] and Robinson *et al.* (1949) [7] were used to calculate heritability (broad sense) and genetic progress (percentage of mean). Searle (1961) [8] and Dewey and Lu (1959) [3] were used for correlation and path coefficient analysis, respectively.

Results and discussion

Plant breeders use the character variation of any crop species as a starting point, and their capacity to develop agricultural plants is largely dependent on the degree of diversity in the population regarding different features. Greater variability increases the likelihood of yielding the desired crop variety. For every variable under investigation, there were highly significant differences between the genotypes. (Table 1). For each characteristic under investigation, the estimates of the phenotypic coefficient of variation exceeded the corresponding genotypic coefficient, suggesting that environmental influences also contribute to the apparent variance in addition to genotypic variations (Table 3). According to Burton and Vane's recommendations, the PCV and GCV represented as percentages

were calculated (1953). Meanwhile, three groups were established for PCV and GCV: less than 10% (Low), 10-20% (Moderate), and more than 20% (High). The estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient variation (GCV) for all the characters. Highest range of variation was observed to be high in phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed in days to 50% flowering, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), moderate for days to 50% flowering, number of branches per plant, number of seeds per plant, seed width (mm), 100 seed weight (g), seed yield per plant and low for days to maturity, seed length (mm), harvest index (%) (Table 2).

Genetic advance refers to the possible improvement over the base population as a result of character selection. It depends on the trait's heritability, the quantity of phenotypic diversity, and the selection differential used by breeders. Genetic advance was observed and expressed as a percentage of mean was observed to be high in days to 50% flowering, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), seed yield per plant, moderate for number of seeds per plant, 100 seed weight (g) and moderate for number of seeds per plant, seed width (mm), 100 seed weight (g) and low for days to maturity, seed length (mm), harvest index (%).

The present study revealed that h^2 (Broad Sense) was high for days to 50% flowering, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per plant, pod length (cm), seed width (mm), 100 seed weight (g), seed yield per plant and low for days to maturity, seed length (mm), harvest index (%). The estimations of the genotypic and phenotypic correlation coefficients for the various variables in the current investigation were also calculated and are shown in Table 3 and Table 4. It aids in indirect selection for the target traits, was obtained by the calculation of genotypic and phenotypic correlations among traits. The magnitude of genotypic correlations were higher than the phenotypic coefficient for the majority of the correlations, indicating that genetic variables had a greater influence than environmental influences. Number of seeds per plant, seed length (mm), seed width (mm) showed significant and positive correlation. Seed yield per plant showed significant and positive correlation except number of pods per plant, plant height (cm), pod length (mm), number of seeds per plant, 100 seed weight (g). Harvest index showed significant and positive correlation except days to 50% flowering. 100 seed weight (g) showed significant and positive correlation except days to 50% flowering and days to maturity as shown in Table 3. Seed yield per plant showed significant and positive correlation with all the traits studied except number of pods per plant, plant height (cm), pod length (cm), number of seeds per plant, seed length (mm), 100 seed weight (g), harvest index (%) as shown in Table 4.

Table 1: Analysis of variance for different characters of French bean

Source	Degrees of freedom	Days to 50% flowering	Number of branches per plant	Number of pods per plant	Plant height (cm)	Pod length (cm)
Replication	2	4.7820	0.1540	1.3320	0.330	0.7740
Treatment	24	226.687**	2.427**	42.538**	1907.628**	24.356**
Error	48	5.758	0.076	0.661	7.101	0.382

Source	Number of seed per plant	Seed length (mm)	Seed width (mm)	Days to maturity	100 seed weight (g)	Seed yield per plant	Harvest Index
Replication	0.2550	0.7120	0.6520	82.1490	3.0670	12.85**	6.7060
Treatment	2.402**	0.839**	1.808**	108.944**	130.544**	20.702**	28.976**
Error	0.128	0.338	0.21	41.197	10.19	1.156	12.412

** Significant at 1 percent level of significance

Table 2: Estimates of parameters of variability for various traits in French bean

Traits	Mean \pm SE(m)	Range	PCV (%)	GCV (%)	h ² (Broad Sense)	Genetic advance as % of mean 5%
Days to 50% flowering	43.61 \pm 1.39	31.00-56.34	20.44	19.68	92.75	39.04
Days to maturity	125.39 \pm 3.71	113.34-134.67	6.37	3.79	35.41	4.65
Plant height (cm)	42.92 \pm 1.54	21.24-85.30	58.97	58.64	98.89	120.13
Number of branches per plant	3.69 \pm 0.16	2.01-5.34	25.16	24.02	91.16	47.24
Number of pods per plant	10.17 \pm 0.47	7.00-20.34	37.61	36.76	95.48	73.98
Number of seeds per plant	5.53 \pm 0.21	4.27-7.27	17.03	15.75	85.53	30.00
Pod length (cm)	10.13 \pm 0.36	5.77-16.44	28.56	27.90	95.44	56.14
Seed length (mm)	10.58 \pm 0.34	9.18-11.40	6.72	3.86	33.07	4.58
Seed width (mm)	7.06 \pm 0.26	5.72-8.88	12.21	10.35	71.76	18.05
100 seed weight (g)	40.94 \pm 1.84	30.67-55.34	17.33	15.47	79.75	28.46
Seed yield per plant	15.66 \pm 0.62	10.67-21.01	17.69	16.31	84.94	30.96
Harvest Index (%)	42.87 \pm 2.03	38.17-50.47	9.88	5.48	30.79	6.27

Table 3: Estimates of Phenotypic correlation coefficient between different characters

Phenotypic Correlation Matrix												
	Days to 50% flowering	Number of branches per plant	Number of pods per plant	Plant height (cm)	Pod length (cm)	Number of seed per plant	Seed length (mm)	Seed width (mm)	Days to maturity	100 seed weight (g)	Harvest Index	Seed yield per plant
Days to 50% flowering	1	-0.0979	-0.452**	-0.855**	-0.0784	-0.2218	-0.1912	-0.1609	0.359*	-0.465**	-0.409**	0.438**
Number of branches per plant		1	0.286*	0.333*	0.235*	0.419**	0.2201	0.231*	-0.175	0.355*	0.2237	-0.143
Number of pods per plant			1	0.651**	0.755**	0.743**	0.324*	0.326*	-0.481**	0.847**	0.423**	-0.494**
Plant height (cm)				1	0.255*	0.516**	0.288*	0.338*	-0.472**	0.658**	0.536**	-0.502**
Pod length (cm)					1	0.761**	0.1726	0.0748	-0.506**	0.713**	0.0106	-0.349*
Number of seed per plant						1	0.245*	0.230*	-0.484**	0.761**	0.245*	-0.377**
Seed length (mm)							1	0.383**	-0.1218	0.348*	0.247*	-0.1483
Seed width (mm)								1	-0.0176	0.231*	0.244*	-0.1382
Days to maturity									1	-0.571**	-0.0102	0.315*
100 seed weight (g)										1	0.352*	-0.466**
Harvest Index											1	-0.2122
Seed yield per plant												1

*Significant at 5%: * $p < 0.05$ ** Significant at 1%: ** $p > 0.05$ **Table 4:** Estimates of Genotypic correlation coefficient between different characters

Genotypic Correlation Matrix												
	Days to 50% flowering	Number of branches per plant	Number of pods per plant	Plant height (cm)	Pod length (cm)	Number of seed per plant	Seed length (mm)	Seed width (mm)	Days to maturity	100 seed weight (g)	Harvest Index	Seed yield per plant
Days to 50% flowering	1	-0.1035	-0.483**	0.893**	-0.0849	-0.243*	-0.355*	-0.2222	0.690**	-0.534**	-0.713**	0.467**
Number of branches per plant		1	0.296*	0.352*	0.235*	0.469**	0.334*	0.274*	-0.314*	0.401**	0.471**	-0.1912
Number of pods per plant			1	0.672**	0.780**	0.821**	0.581**	0.412**	-0.819**	0.954**	0.790**	-0.550**
Plant height (cm)				1	0.260*	0.565**	0.545**	0.416**	-0.790**	0.743**	0.977**	-0.545**
Pod length (cm)					1	0.840**	0.271*	0.0711	-0.845**	0.807**	0.0431	-0.389**
Number of seed per plant						1	0.448**	0.302*	-0.938**	0.864**	0.590**	-0.429**
Seed length (mm)							1	0.626**	-0.183	0.744**	0.741**	-0.436**
Seed width (mm)								1	-0.1158	0.303*	0.627**	-0.2023
Days to maturity									1	-0.889**	-0.648**	0.667**
100 seed weight (g)										1	0.787**	-0.533**
Harvest Index											1	-0.503**
Seed yield per plant												1

*Significant at 5%: * $p < 0.05$;**Significant at 1%: ** $p > 0.01$

Conclusion

Plant breeders depend on the variety of crop species to develop their plants. The likelihood of obtaining the intended crop variety is improved with greater variability. For all the traits being studied, there were highly significant differences between the genotypes. The estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient variation (GCV) for all the characters. Seed yield per plant showed significant and positive correlation except number of pods per

plant, plant height (cm), pod length (mm), number of seeds per plant, 100 seed weight (g) suggesting that it would be beneficial to select for these features in order to increase the number of seeds produced per plant.

Acknowledgment

The author would like to thank NBPGR regional station Shimla for providing rajmash germplasm, DEST&CC for support in collection of traditional and local rajmash germplasm for the

study, as well as Abhilashi University for facilitating the experiment.

References

1. Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron J.* 1953;45:478-481.
2. Jhanavi DR, Patil HB, Justin P, Revanappa, Hadimani HP, Mulla SWR, *et al.* Genetic variability, heritability and genetic advance studies in French bean (*Phaseolus vulgaris* L.) genotypes. *Indian J Agric Res.* 2018;52(2):162-166.
3. Dewey DR, Lu KH. A correlation and path analysis of components of crested wheat-grass seed production. *Agron J.* 1959;51:515-518.
4. Al-Ballat IA, Al-Araby AA. Correlation and path coefficient analysis for seed yield and some of its traits in common bean (*Phaseolus vulgaris* L.). *Egypt J Hort.* 2019;46(1):41-51.
5. Johnson H, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agron J.* 1955;47:314-318.
6. Shah KN, Rana DK, Singh V. Variability and trait relation between yield and yield related traits in French bean (*Phaseolus vulgaris* L.). *Plant Arch.* 2021;21(1):1090-1097.
7. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. *Agron J.* 1949;41:353-359.
8. Searle SR. Phenotypic, genotypic and environmental correlations. *Biometrics.* 1961;17(3):474-480.
9. Singh DK, Singh DP, Singh SS. Studies of genetic variability, heritability and genetic advance for yield and related traits in French bean (*Phaseolus vulgaris* L.). *J Pharmacogn Phytochem.* 2018;7(2):236-240.
10. Sudre CP, Goncalves LSA, Rodrigues R, do Amaral Junior AT, Riva-Souza EM, dos Santos CD, *et al.* Genetic variability in domesticated Capsicum spp. as assessed by morphological and agronomic data in mixed statistical analysis. *Genet Mol Res.* 2010;9(1):283-294.
11. Toker C, Cagiran MI. Use of phenotypic correlations and factor analysis in determining characters for grain yield selection in chickpea (*Cicer arietinum* L.). *Hereditas.* 2004;140(2):226-228.
12. Yadeta B, Derbew B, Gebreselaranassie W, Fekadu M. Variability, heritability and genetic advance in hot pepper (*Capsicum annum* L.) genotypes in West Shoa, Ethiopia. *Am-Eurasian J Agric Environ Sci.* 2011;10(4):587-592.