D-5486
[1-5]

RESEARCH ARTICLE Agricultural Science Digest, Volume Issue : ()

Variability Analysis in Determinate F_4 Progenies for Yield and it's Attributes in Indian Bean [*Lablab purpureus* (L.) Sweet]

A.G. Patel, K.G. Modha, B.H. Kale, R.K. Patel

10.18805/ag.D-5486

ABSTRACT

Background: Indian bean [*Lablab purpureus* (L.) Sweet] is an important vegetable as well as split pulse crop in India. An attempt was made here to study the genetic variability, correlation and direct and indirect effects through path analysis for yield and yield attributing traits.

Methods: Total 52 genotypes were evaluated in randomized block design (RBD) with three replications during early-*rabi* season, 2018-2019. Observations were recorded on 11 quantitative traits.

Result: Significant variation existed in all the characters. Higher values of GCV and PCV were observed for pods per raceme, pods per plant and seed yield per plant. High heritability coupled with high genetic advance was observed for racemes per plant, pods per raceme, pods per plant, pod width and seed yield per plant. Seed yield per plant was highly significant and positively correlated at genotypic level with days to maturity, plant height, racemes per plant, pods per raceme, pods per plant and seeds per pod. Path analysis based on genotypic correlation revealed that high positive direct effects on seed yield per plant was registered by pod per raceme followed by racemes per plant, pod length, days to 50% flowering, plant height, pod weight and days to maturity.

Key words: Correlation, Genetic variability, Heritability, Path coefficient.

INTRODUCTION

Indian bean [*Lablab purpureus* L. (Sweet), 2n = 22] is an important vegetable as well as split pulse crop in India. The species is extremely diverse and taxonomically three subspecies are recognized mainly based on differing characteristics of pods and seeds (Verdcourt 1971; Pengelly and Maass 2001; Maass *et al.* 2005; Tefera 2006).

Improvement of specific trait through selection is totally depends upon the genetic variability present in the available germplasm. Since, many of the plant characters especially yield and its contributing traits are governed by polygenes. Moreover, knowledge of heritability indicates the extent of transmissibility of a character in future generations. Release of variability in segregating generation and its assessment is an important aspect in any crop improvement programme (Thakur *et al.* 1999). Breeding for high yield requires information on the nature and magnitude of variation in the available material. Such information in a segregating population of a cross (where selection is actually practiced) will be more meaningful and of immediate practical utility (Sawant *et al.* 1995).

The association between grain yield and its component characters was studied. Yield components have ultimate influence on yield, both directly and indirectly (Turkey, 1954). Path coefficient, which is a standard partial regression coefficient, specifies the cause and effect relationship and measures the relative importance of each variable (Wright, 1921). Therefore, correlation in combination with path coefficient analysis is an important tool to find out the direct and indirect association and quantify the direct and indirect influence of one character upon another (Dewey and Lu, 1959).

Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari-396 450, Gujarat, India.

Corresponding Author: B.H. Kale, Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari-396 450, Gujarat, India.
Email: bhushan.kale@nau.in

How to cite this article: Patel, A.G., Modha, K.G., Kale, B.H. and Patel, R.K. (2022). Variability Analysis in Determinate F_4 Progenies for Yield and it's Attributes in Indian Bean [*Lablab purpureus* (L.) Sweet]. Agricultural Science Digest. DOI: 10.18805/ag.D-5486.

Submitted: 09-09-2021 **Accepted:** 19-04-2022 **Online:** 03-05-2022

Therefore, in the present investigation, an attempt was made to study the genetic variability, correlation and path analysis for yield and yield attributing traits.

MATERIALS AND METHODS

The total 52 genotypes including two checks (GNIB-21 and GNIB-22) were raised in randomized block design with three replications during early-*rabi* season, 2018-2019 at College Farm, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat. The individual plot size was 4.0 m length and 0.60 m width. The row to row and plant to plant spacing was 60 cm and 20 cm, respectively. Observations were recorded on 11 quantitative traits *viz*., days to 50% flowering, days to maturity, plant height (cm), racemes per plant, pods per raceme, pods per plant, pod length (cm), pod width (cm), pod weight (g), seeds per pod and seed yield per plant (g). Observations were recoded

from 10 randomly selected plants per treatment for analysis, except, days to 50% flowering and days to maturity which were recorded on plot basis.

The GCV and PCV were determined as per Burton and Devane (1953). The heritability in broad sense was estimated according to method given by Allard (1960). The expected genetic advance as expressed as per cent of mean was calculated by the method suggested by Johnson *et al*. (1955). Correlation coefficients were calculated by adopting the method explained by Miller *et al.* (1958). Path analysis suggested by Wright (1921) and Dewey and Lu (1959) were adopted for portioning the genotypic correlation between variables with seed yield into direct and indirect effects of those variables on yield.

RESULTS AND DISCUSSION

Analysis of variability parameters

Analysis of variance for various characters is presented in Table 1. Analysis revealed significant progeny mean square values for all the traits in F_4 progenies. It showed the sufficient variability in material under study. Similar results were reported by Patel *et al*. (2016) and Hadavani *et al*. (2018).

In the present study, the result of measures of variability parameters is presented in Table 2 and Graph 1. Mean values revealed vast range for days to 50% flowering (51-59), days to maturity (93-97), plant height (26.23-63.58 cm), racemes per plant (2.61-7.87), pods per raceme (3.01-7.24), pods per plant (9.39-39.40), pod length (4.85-8.01 cm), pod width (0.71-2.09 cm), pod weight (0.41-0.97 g), seeds per pod (2.90-3.86) and seed yield per plant (4.62-13.19 g). Based on the mean values, the progeny D32-10-2 (13.19 g) recorded significantly higher seed yield per plant over check varieties GNIB 21 and GNIB 22. Higher values of GCV and PCVwere observed for pods per raceme (21.69% and 25.73% respectively), pods per plant (36.44% and 39.77% respectively) and seed yield per plant (22.32% and 26.06% respectively) and the less differences between GCV and PCV for these traits revealed less influences of environment on these traits so that there is great scope of improvement by applying selection on these characters. Similar results were reported for pods per plant and seed yield per plant by Choudhary *et al.* (2016). For pods per plant by Chaitanya *et al.* (2014) and Jyothireddy *et al*. (2018).

High heritability (broad sense) values of more than 60 per cent was observed for racemes per plant (69.13%), pods per raceme (71.07%), pods per plant (83.97%), pod length (76.23%), pod width (85.89%) and seed yield per plant (73.35%) indicating that the traits are generally governed by additive gene effects and improvement for these traits could be made by simple phenotypic selection. Similar outcomes were reported for racemes per plant and pods per plant by Pawar and Prajapati (2013); for racemes per plant and seed yield per plant by Asaduzzaman *et al.* (2015); for pod length, pod width, pods per plant and seed yield per plant by Hadavani *et al.* (2018).

Table 1: Result of Analysis of variance for character studied.

Source of variation	d.f.	Mean sum of square										
		DTF	DTM	PH	RPP	PPR	PPP	PL	PW	PWT	SPP	SYPP
Replication	2	13.583*	73.904**	235.967**	0.339	0.855	23.558	0.578**	0.010	0.015	0.515**	3.385
Progenies	51	9.008**	3.588*	199.164**	3.399**	3.807**	144.840**	1.120**	0.178**	0.056**	0.142**	11.768**
Error	102	4.080	2.309	42.818	0.440	0.455	8.666	0.105	0.009	0.012	0.073	1.271

** - Significant at 1% probability, * - Significant at 5.0 per cent level of probability.

Table 2: Result of measures of variability parameters of all the characters studied.

Character	Range			GCV (%)	PCV (%)	h^2(bs)(%)	GA	GAM
Days to 50% flowering	51-59	1.64	5.72	2.41	4.51	28.70	1.41	2.66
Days to maturity	93-97	0.43	2.74	0.69	1.74	15.59	0.53	0.56
Plant height (cm)	26.23-63.58	52.12	94.93	16.01	21.60	54.90	11.02	24.43
Racemes per plant	2.61-7.87	0.97	1.43	19.62	23.60	69.13	1.70	33.60
Pods per raceme	3.01-7.24	1.12	1.57	21.69	25.73	71.07	1.84	37.67
Pods per plant	9.39-39.40	45.39	54.06	36.44	39.77	83.97	12.72	68.78
Pod length (cm)	4.85-8.01	0.34	0.44	9.77	11.19	76.23	1.05	17.57
Pod width	0.71-2.09	0.06	0.07	19.50	21.04	85.89	0.45	37.23
Pod weight (g)	0.41-0.97	0.01	0.03	17.90	23.83	56.42	0.19	27.69
Seeds per pod	2.90-3.86	0.02	0.10	4.52	9.22	24.00	0.15	4.56
Seed yield per plant (g)	4.62-13.19	3.50	4.77	22.32	26.06	73.35	3.30	39.38

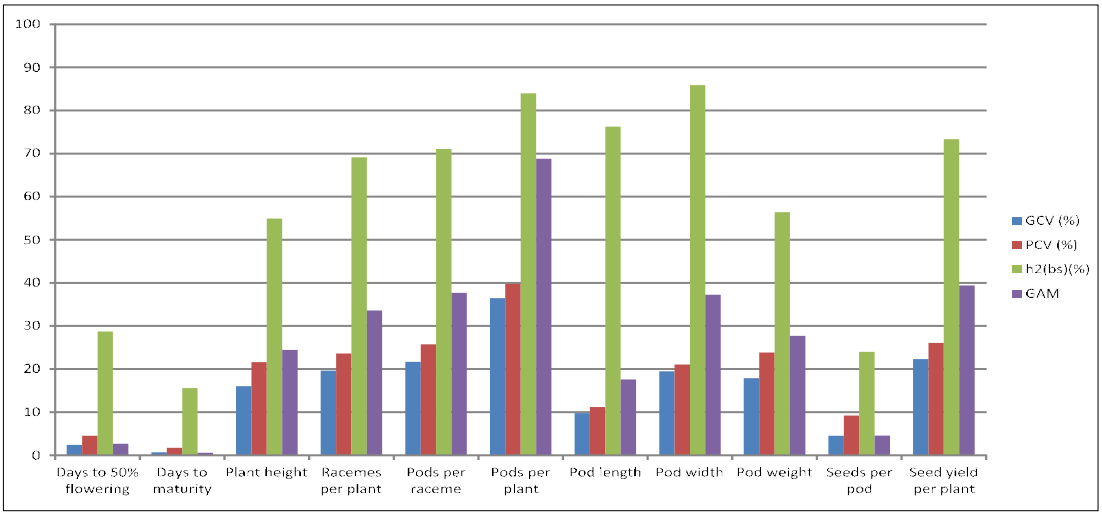
DTF = Days to 50 per cent flowering; DTM = Days to maturity; PH = Plant height; RPP = Racemes per plant; PPR = Plant per raceme PPP = Pods per plant; PL = Pod length; PW = Pod width; PWT = Pod weight; SPP = Seeds per pod; SYPP = Seed yield per plant h; h^2(bs) = Heritabilty(broad sense); GCV = Genotypic coefficient of variation; σ^2_g = Genotypic variance; GA = Genetic advance; PCV = Phenotypic coefficient of variation; σ^2_p = Phenotypic variance; GAM = Genetic advance as percent of mean.

High genetic advance as per cent mean was observed for plant height (24.43%), racemes per plant (33.60%), pods per raceme (37.67%), pods per plant (68.78%), pod width (37.23%), pod weight (27.69%) and seed yield per plant (39.38%). Similar results were observed for pod width and seed yield per plant by Hadavani *et al.* (2018); for plant height and pods per plant by Chaitanya *et al.* (2014); for pods per plant by Patel *et al.* (2016).

Heritability with genetic advance collectively, giving more detailed idea of gene action. High heritability coupled with high genetic advance as per cent of mean were perceived for racemes per plant (69.13% and 33.60% respectively), pods per raceme (71.07% and 37.67% respectively), pods per plant (83.97% and 68.78% respectively), pod width (85.89% and 37.23% respectively) and seed yield per plant (73.35% and 39.38% respectively) showing role of additive gene effects and less influence of environmental factors on the expression of these traits. Thus, improvement of these characters could be achieved through direct phenotypic selection. These results are in accordance withthe earlier finding of Choudhary *et al.* (2016) and Hadavani *et al.* (2018) for Pod per plant, pod width and seed yield per plant.

Correlation coefficient analysis

The association studies among 11 charecters (Table 3) revealed that, seed yield per plant appeared highly significant and positively correlated at genotypic level with days to maturity (0.419), plant height (0.348), racemes per plant (0.790), pods per raceme (0.743), pods per plant (0.829) and seeds per pod (0.480), which suggested, such component characters can be improved simultaneously with seed yield per plant by direct selection. Similar results were obtained for correlation of seed yield per plant with days to maturity and pods per plant by Kamble *et al.* (2015); with pods per plant by Salim *et al.* (2013). It also exhibited negative and non-significant correlation with pod width (-0.076).



Graph 1: GCV, PCV, h^2(bs) and GAM for eleven quantitative characters in F_4 progenies in Indian bean.

Table 3: Genotypic correlation coefficients of seed yield per plant with other characters in F_4 progenies in Indian bean.

Characters	DTF	DTM	PH	RPP	PPR	PPP	PL	PW	PWT	SPP	SYPP
Days to 50% flowering	1.000										
Days to maturity	0.376**	1.000									
Plant height	0.294**	0.353*	1.000								
Racemes per plant	0.218**	0.716**	-0.095^{NS}	1.000							
Pods per raceme	-0.096^{NS}	0.392**	-0.176*	0.699**	1.000						
Pods per plant	0.059^{NS}	0.651**	-0.136^{NS}	0.931**	0.922**	1.000					
Pod length	-0.390**	-0.628**	0.076^{NS}	-0.154^{NS}	-0.208**	-0.198*	1.000				
Pod width	-0.177*	-0.990**	-0.015^{NS}	-0.423**	-0.215**	-0.424**	0.451**	1.000			
Pod weight	-0.039^{NS}	-0.978**	0.447**	-0.536**	-0.572**	-0.612**	0.644**	0.698**	1.000		
Seeds per pod	0.445**	-0.333**	0.563**	-0.061^{NS}	-0.328**	-0.146^{NS}	0.803**	0.414**	0.667**	1.000	
Seed yield per plant	0.040^{NS}	0.419**	0.348**	0.790**	0.743**	0.829**	0.123^{NS}	-0.076^{NS}	0.048^{NS}	0.480**	1000

** - Significant at 1.0 per cent level of probability, * - Significant at 5.0 per cent level of probability.

DTF = Days to 50% flowering; DTM = Days to maturity; PH = Plant height; RPP = Racemes per plant; PPR = Pods per raceme; PPP = Pods per plant; PL = Pod length; PW = Pod width; PWT = Pod weight; SPP = Seeds per pod; SYPP = Seed yield per plant.

Table 4: Genotypic path coefficient analysis of component characters towards seed yield per plant in F_4 progenies.

Characters	DTF	DTM	PH	RPP	PPR	PPP	PL	PW	PWT	SPP	Correlation with seed yield per plant
Days to 50% flowering	2.557	0.030	0.368	1.484	-0.770	-0.762	-1.619	0.194	-0.010	-1.433	0.040
Days to maturity	0.961	0.080	0.441	4.862	3.134	-8.372	-2.610	1.088	-0.238	1.074	0.419**
Plant height	0.753	0.028	1.250	-0.648	-1.409	1.745	0.316	0.017	0.109	-1.813	0.348**
Racemes per plant	0.559	0.058	-0.119	6.795	5.586	-11.980	-0.638	0.465	-0.131	0.196	0.790**
Pods per raceme	-0.246	0.032	-0.220	4.747	7.995	-11.853	-0.864	0.236	-0.139	1.056	0.743**
Pods per plant	0.152	0.052	-0.170	6.328	7.367	-12.863	-0.823	0.466	-0.149	0.469	0.829**
Pod length	-0.996	-0.051	0.095	-1.043	-1.661	2.546	4.158	-0.495	0.157	-2.588	0.123
Pod width	-0.452	-0.080	-0.019	-2.875	-1.718	5.455	1.873	-1.098	0.170	-1.333	-0.076
Pod weight	-0.100	-0.079	0.559	-3.644	-4.569	7.876	2.676	-0.766	0.244	-2.149	0.048
Seeds per pod	1.138	-0.027	0.704	-0.414	-2.621	1.873	3.340	-0.454	0.163	-3.221	0.480**

** - Significant at 1.0 per cent level of probability, Residual = 0.85, Bold diagonal figures are the direct effects

DTF = Days to 50% flowering; DTM = Days to maturity; PH = Plant height; RPP = Racemes per plant; PPR = Pods per raceme; PPP = Pods per plant; PL = Pod length; PW = Pod width; PWT = Pod weight; SPP = Seeds per pod; SYPP = Seed yield per plant.

Whereas, seed yield was observed to be non-significantly associated with days to 50% flowering (0.040), pod length (0.123) and pod weight (0.048), indicated less significance of these traits from improvement point of view.

Plant height had significant positive correlation with days to 50% flowering (0.294) and days to maturity (0.353) and seed yield per plant (0.348). But, early flowering and early maturity is desirable in Indian bean. Therefore, for increasing seed yield potential, optimum plant height should be considered while selections for higher seed yield. The traits racemes per plant, pods per raceme and pods per plants were significantly and positively associated with each other, similarly, pod length, pod width, pod weight and seeds per pod were significantly and positively associated with each other suggesting such traits can be improved indirectly through direct selections for increasing seed yield.

Path coefficient analysis

The direct and indirect effects of various yield component traits on seed yield per plant are given in Table 4. The overall path analysis revealed that high positive direct effects on seed yield per plant was registered by pod per raceme (7.995) followed by racemes per plant (6.795), pod length (4.158), days to 50% flowering (2.557), plant height (1.250), pod weight (0.244) and days to maturity (0.080). Therefore, selection for such traits would bring about improvement in Indian bean. The results are in accordance with Pawar and Prajapati (2013) for racemes per plant and days to 50% flowering, Kamble *et al.* (2015) for pod length, plant height and days to maturity, Dewangan *et al.* (2018) for pods per raceme, pod length and pod weight. The highest negative direct effects on seed yield per plant was recorded by pods per plant (-12.863) followed by seeds per pod (-3.221) and pod width (-1.098) suggesting less significance of these traits during selections for higher seed yield. Pods per plant and seeds per plant showed high negative direct effects, although they rendered highly significant correlation with seed yield per plant, which might be due to positive indirect effects via other casual traits. Such traits with direct and indirect effects of varying magnitude and opposite in the direction, counterbalancing each other will not be more useful in breeding programme. In general, it was observed that all the character recorded high to very high magnitude of indirect effects on seed yield per plant via racemes per plant, pods per raceme, pods per plant and pod length. Path analysis for seed yield revealed high residual effect of 0.85, which implies that more other traits need to be included in future studies to increase per cent accountable variation in the investigations.

CONCLUSION

On the basis of overall analysis it is concluded that sufficient amount of variability is present within the material used. The overall outcome of the study identifies that the traits racemes per plant, pod per raceme and pod per plant as main yield contributing traits. Therefore, selection for such traits in F_4 as well as in subsequent generations will be easy and would bring about improvement for seed yield in Indian bean.

Conflict of interest: None.

REFERENCES

Allard,W. (1960). Principles of Plant Breeding, John Wiley and Son. Inc., New York. Chapter.19(1): 224-233.

Asaduzzaman, M., Bhuiyan, M.J.H., Hossain, M.A. and Raffi, S.A. (2015). Genetic variability, heritability and genetic advance of yield and yield contributing characters of lablab bean (*Lablab purpureus* L.). Progressive Agriculture. 26(1): 22-25.

Burton, G.W. and Devane, E.M. (1953). Estimating heritability in fall fescue (*Festuaca cirunclindcede*) from replicated clonal material. Agronomy Journal. 45(1): 478-481.

Chaitanya, V., Reddy, R.V.S.K., Kumar, P.A. (2014). Variability, heritability and genetic advance in indigenous dolichos bean [*Dolichos lablab* (L.) *Var typicus*] genotypes. Plant Archives. 14(1): 503-506.

Choudhary, J., Kushwah, S.S., Singh, O.P. and Naruka, I.S. (2016).Studies on genetic variability and character association in Indian bean [*Lablab purpureus* (L.) sweet]. Legume Research. 39(3): 336-342.

Dewangan, R., Choyal, P., Ramesh, Kerketta, A. and Godara, A. (2018). Path coefficient analysis study in dolichos bean (*Lablab purpureus* L.). International Journal of Chemical Studies. 6(4): 2494-2496.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, 51(1): 515-518.

Hadavani Janaki, K., Mehta, D.R., Raval, L.J. and Ghetiya, K.P. (2018). Genetic variability parameters in Indian bean (*Lablab purpureus* L.). Int. J. Pure App. Biosci. 6(4): 164-168.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955).Genotypic and phenotypic correlation in soybean and their implications in selection. Agronomy Journal. 47(1): 477-483.

Jyothireddy, K., Prabhakar, B.N., Saidaiah, P. and Pandravada, S.R. (2018). Genetic divergence, variability, heritability and genetic advance for growth, pod quality and yield characters in dolichos bean [(*Dolichos lablab* (L.) var. *typicus Prain*)] germplasm. Legume Research. 41: 804-809.

Kamble, S.S., Devmore, J.P., Sawardekar, S.V., Bhave, S.G. and Palshetkar, M.G. (2015). Correlation and path coefficient analysis for yield and yield components in segregating (F_4) generation of lablab bean [(*Labab purpureus* (L.) Sweet)]. International Journal of Applied Biology and Pharmaceutical Technology. (6)3: 237-240.

Maass, B.L., Jamnadass, R.H., Hanson, J. and Pengelly, B.C. (2005). Determining sources of diversity in cultivated and wild *Lablab purpureus* related to provenance of germplasm by using amplified fragement length polymorphism. Genetic Resourses and Crop Evolution. 52(6): 683-695.

Miller, P.J., Willams, J.C., Robinsons, H.F. and Comstock, R.E. (1958). Estimates of genotypic and environmental variances and covariance in upland cotton and their implications in selection. Agronomy Journal. 50: 126-131.

Patel, S., Trivedi, J., Sharma, J. and Pandey, P. (2016). Genetic variability, heritability and genetic advance in dolichos bean (*Lablab purpureus* L.). Advances in Life Science. 5(9): 3673-3679.

Pawar, R.M. and Prajapati, R.M. (2013). Genetic variability, correlation and path analysis in India bean [(*Lablab purpureus* (L.) Sweet)]. Internat. J. Agric. Sci. 9(2): 615-619.

Pengelly, B.C. and Maass, B.L. (2001).*Lablab purpureus* L. Sweet-diversity, potential use and determination of core collection of this multi-purpose tropical legume. Genetic Resources and Crop Evolution. 48(3): 261-272.

Salim, M., Hossain, S., Alam, S., Rashid, J.A. and Islam, (2013). Variability, correlation and path analysis in lablab bean (*Lablab purpureus* L.). *Bangladesh J. Agril. Res*., 38(4): 705-717.

Sawant, D.S. Patil, S.L. and Sodaye, V.G. (1995). Genetic variability and heritability in segregating generation of Rice crosses. Ann. Agric. Res. 16 (2): 201-205.

Tefera, T.A. (2006). Towards Improved Vegetable Use and Conservation of Cowpea (*Vigna unguiculata*) and Lablab (*Lablab purpureus*): Agronomic and Participatory Evaluation in North Eastern Tanzania and Genetic Diversity Study. Cuvillierverlag, Goettingen, 214 pp.

Thakur, S.K. Choubey, S.K. and Sharma, N.P. (1999). Genetic variability and character association in F_2 (Anupama × IR 36) population in rice (*Oryza sativa* L.). Agric. Sci. Digest. 19(3): 187-190.

Turkey, J.W. (1954). Causation, segregation and path analysis of causal path. Biometrics. 15: 236-258.

Verdcourt, B. (1971). *Lablab* Adans.In: Studies in the Leguminosae-Papilionoideae of the 'Flora of Tropical East Africa': IV. Kew Bull. 24: 695-699.

Wright, S. (1921). Correlation and causation. Journal of Agricultural Research. 20: 557-587.