

Appraisalment of Genetic Variability for Yield and other Quantitative Traits in Derived Germplasm of Indian Bean [*Lablab purpureus* (L.) Sweet]

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(Received 12 September 2022, Accepted 05 November, 2022)

(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: The presence of variation in a population is key to select desirable plants for further improvement. The experiment was done to assess the 135 germplasm derived from four crosses along with four checks GNIB-21, GNIB-22, V-19-154 and W-19-58 were grown in augmented block design. Analysis showed significant genotype mean square values for all the traits except pods per raceme. In the present investigation, based on *per se* performance V-19-78, V-19-107, V-19-111 and V-19-115 were identified as promising genotypes in the current study because they had higher grain yields per plant. Selection for determinate growth habit with high yield potential can help in mechanized harvesting in lablab bean. These genotypes could be further examined in order to identify attributes that lead to higher yields, early maturity and better yield. Based on all of the research, it can be said that racemes per plant is the most significant trait in Indian bean seed yield. As, this trait showed higher estimates of GCV, PCV, $h^2_{(bs)}$ and GAM.

Keywords: Augmented Block Design, Derived germplasm, Variability, Heritability, Genetic Advance, Indian bean.

INTRODUCTION

Beans are almost the ideal food, as they are high in vitamins, minerals, protein, and fibre while being low in fat. They are known as pocket of nutrients, which means they supply more nutrition per calorie. *Lablab purpureus* (L.) Sweet (Indian bean) Syn. *Dolichos lablab* L. has chromosomal numbers $2n = 22$ and is a member of the Fabaceae family. The Indian bean's genome is 367 Mb in size and contains 20,946 protein-coding genes (Missanga *et al.*, 2021).

India is primary center of origin for lablab bean and was brought to Africa from Southeast Asia near about the 8th century (Deka *et al.*, 1990) but according to Maass *et al.* (2016) lablab originated in Eastern and Southern Africa. Karnataka makes a significant contribution, making up about 90% of the nation's area and production (Padma *et al.*, 2020).

The Indian bean is split into three types in Gujarat based on morphology: "Wal" "Valor" and "Papdi". Papdi and valor are usually utilized as immature pods or seeds for vegetable applications, whereas "Wal" is used as a dry seed and dal. Despite its value as a multipurpose crop and superior drought tolerance to

common bean and cowpea (Maass *et al.*, 2010), it also has the ability to adapt in acidic and brackish soils (Mugwira and Haque 1993; Murphy and Colucci 1999). It cannot be grown in water logging conditions. The green pods are eaten after cooking and have very good nutritive value. In addition to the nutrients, it might also have trace levels of trypsin inhibitors, tannins, and phytic acid, which are antinutritional elements. The bioavailability and absorption of nutrients in legume grains are decreased by these anti-nutrients (Kilonzi *et al.*, 2017). Recent studies have suggested that the lablab carbohydrate-binding proteins, which frequently resemble insulin, might well be useful in preventing the SARS-CoV-2 and influenza viruses, providing a viable approach for treating such illnesses.

Most of the landraces or varieties of this crop are indeterminate in growth habits as well as photoperiod and temperature-sensitive. However, few photo-insensitive and determinate varieties accessible for farming. Because of the plants synchronous flowering and maturation, their definite growth patterns, and their day length insensitive flowering, intercropping and sole

cultivation are especially possible throughout the year (Keerthi *et al.*, 2014).

High phenotypic and genotypic variation in qualitative as well as in quantitative characters gives more chance to select different germplasm as per the objective of a breeding programme for improvement of a diverse group of lablab beans. Heritability is part of phenotypic variance which is due to genotypic variance. Broad sense heritability and genetic advance provide information to select a particular polygenic trait more effectively. Selection for a polygenic trait is more difficult because it is a cumulative effect of many minor genes and those minor genes are mostly located at different loci in the genome.

MATERIALS AND METHODS

The current study was conducted at College Farm, Navsari Agricultural University, Navsari during *Rabi*, 2020-21. The exploratory material consisted of 139 genotypes out of which, 135 F₆ progenies of Indian bean and 4 checks (replicated in each block). These derived F₆ progenies were acquired from the four crosses *viz.*, GNIB-21 × GP-1, GNIB-21 × GP167, GNIB-21 × GP-189 and GNIB-21 × GPKH-120. Genotypes *viz.*, GNIB-21, GNIB-22, V-19-154 and W-19-58 were used as determinate checks. One hundred and thirty-five germplasm derived from the four crosses were laid out along with four checks in Augmented Block Design where each check was replicated in five blocks. Each row comprised 13 plants of single progeny with 60 cm × 20 cm inter and intra row spacing, respectively. The progenies were randomly assigned in every block.

Mean and range were calculated for the eleven quantitative traits *viz.*, days to 50 % flowering, days to maturity, plant height (cm), racemes per plant, pods per plant, pod weight (g), pods per raceme, pod length (cm), pod width (cm), seeds per pod and seed yield per plant (g) in each derived progenies. Except for the days to 50% flowering and days to maturity, the observations were made on five randomly chosen plants from each progeny. Selected plants were tagged before the first

flower emergence. Data for days to 50 per cent flowering and days to maturity were compiled on a population basis. Data for additional characters were gathered from the five plants that were arbitrarily chosen from each line and their averages were utilized in the statistical study.

Analysis of variance of the characters was done as per the standard statistical procedure for Augment Block Design as given by Federer (1956) The approach proposed by Allard (1960) was utilized to calculate broad sense heritability (h_{bs}^2). The formula used by Johanson *et al.* (1955) projected the genetic advance for each character.

RESULTS AND DISCUSSION

Analysis of variance for different quantitative traits studied is mentioned in Table 1. Analysis showed significant genotype mean square values for all the traits in F₆ progenies except pods per raceme. It also showed sufficient variability present for all the traits among the progenies under study. A comparable outcome was also recorded by Vijayanthi *et al.* (2015) except for pods per raceme. Pods per raceme showed a non-significant mean sum of square indicates that the studied genotypes were not having the diversity. So, no further analysis is carried out for this trait.

Estimation of the component of variability for different quantitative traits was carried out and data are presented in Table 2. A wide range was demonstrated by mean values for days to fifty per cent flowering (30-47), days to maturity (83-95), plant height (27.60–69.20 cm), racemes per plant (2-13), pods per plant (9.33-25.50), pod weight (0.49-1.40 g), pods per raceme (1.67-6.00), pod length (3.50-9.84 cm), pod width (0.97-1.99 cm), seeds per pod (3.19-6.47) and seed yield per plant (3.26-12.78 g). Progenies V-19-78 (12.78 g), V-19-107 (12.34 g), V-19-111 (11.62 g), V-19-115 (10.46 g), V-19-05 (10.40 g) and V-19-16 (10.28 g) showed significantly higher seed yield per plant than all the four check varieties.

Table 1: Analysis of variance for characters under study.

Source	DF	DTF	DTM	PH	RPP	PPR	PPP	PL	PW	PWT	SPP	SYPP
Block	4	2.07 ^{ns}	1 ^{ns}	76.66 *	2.51*	3.06 ^{ns}	21.18*	0.12 ^{ns}	0.02 ^{ns}	0.0021 ^{ns}	0.14 ^{ns}	1.47 ^{ns}
Entries	138	22.82 **	20.33 **	53.72 *	3.35 **	0.84 ^{ns}	9.64 ^{ns}	1.12**	0.05 **	0.03 *	0.3 *	2.45 *
Checks	3	43.87 **	0.98 ^{ns}	154.17 **	3.40*	1.83 ^{ns}	6.26 ^{ns}	6.21**	0.58 **	0.12 **	0.35 ^{ns}	4.49 *
Genotypes	134	20.28 **	18.67 **	51.86 *	3.35 **	0.79 ^{ns}	9.76 *	0.9 **	0.04 **	0.03 *	0.29 *	2.42 *
Genotypes vs. Check	1	299.74 **	300 **	1.08 ^{ns}	4.31 *	3.55 ^{ns}	3.60 ^{ns}	15.3 **	0.28 **	0.31 **	1.78**	0.01 ^{ns}
Residuals	12	0.74	1.57	16.38	0.61	1.47	5.76	0.24	0.01	0.01	0.1	0.77

Table 2: Measures of variability parameters of all the characters.

Trait	Mean	Range		σ_g^2	σ_p^2	GCV (%)	PCV (%)	h_{bs}^2 (%)	GA	GAM
		Min.	Max.							
Days to 50 % flowering	41.43	30.00	47.00	19.54	20.28	10.67	10.87	96.34	8.95	21.60
Days to maturity	88.28	83.00	95.00	17.11	18.67	4.69	4.9	91.61	8.17	9.25
Plant height (cm)	53.32	27.60	69.20	35.48	51.86	11.17	13.51	68.42	10.17	19.07
Racemes per plant	6.04	2.00	13.00	2.74	3.35	27.39	30.27	81.89	3.09	51.13
Pods per raceme	3.69	1.67	6.00	-	-	-	-	-	-	-
Pods per plant	15.38	9.33	25.50	4.00	9.76	13.01	20.32	41.02	2.64	17.19
Pod length (cm)	6.35	3.50	9.84	0.66	0.90	12.81	14.97	73.27	1.44	22.62
Pod width (cm)	1.34	0.97	1.99	0.03	0.04	12.91	15.19	72.23	0.30	22.64
Pod weight (g)	0.98	0.49	1.40	0.01	0.03	11.85	16.56	51.14	0.17	17.48
Seeds per pod	4.17	3.19	6.47	0.19	0.29	10.50	12.96	65.67	0.73	17.56
Seed yield per plant (g)	6.87	3.26	12.78	1.65	2.42	18.68	22.64	68.03	2.18	31.78

GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; GAM = GA as per cent of mean (%); σ_g^2 = Genotypic variance; σ_p^2 = phenotypic variance; GA = Genetic advance; h_{bs}^2 = Heritability (Broad sense)

GCV and PCV values were mentioned in Fig. 1. Higher GCV and PCV values for racemes per plant (27.18% and 31.14%, respectively) indicating the greater potential for implementing the choice to improve this character in an appropriate direction. Less variation between GCV and PCV values suggested less influence of the environment on this trait and selection could be effective for this trait. Moderate estimates of GCV (18.68%) and high estimates of PCV (22.64%) were recorded for seed yield per plant. Moderate GCV and PCV values were observed for the traits viz., days to 50 % flowering (10.67% and 10.87%, respectively), plant height (11.17% and 13.51%, respectively), pod length (12.81% and 14.97%, respectively), pod width (12.91% and 15.19%, respectively), pod weight (11.85% and 16.56%, respectively) and seeds per pod (10.50% and 12.96%, respectively). This suggested that these traits will respond to selection less strongly. Low GCV and PCV values were recorded for days to maturity (10.67% and 10.87%, respectively) indicating a narrow range of Substantial variation for these characteristics and restricting the scope of selection for these traits. Jyothireddy *et al.* (2018), Ingle *et al.* (2020); Kamau *et al.* (2021) reported similar findings.

All of the traits exhibited moderate to high heritability (Fig. 2). High heritability values of more than 60 per cent were observed for days to 50 % flowering (96.34%), days to maturity (91.61%), plant height (68.42%), racemes per plant (81.89%), pod length (73.27%), pod width (72.23%), seeds per pod (65.67%) and seed yield per plant (68.03%) showing that phenotype might be a useful indicator of genotypic effect and that improvement for these traits could be achieved by straightforward phenotype selection, suggesting that these traits might be regulated by additive gene effects. Same results were also observed by Vishnu and Radhamany (2021). Moderate heritability was noted for pod weight (51.14%) and pods per plant (41.02%) indicating a moderate influence of the environmental factors in the expression of these traits showing limited scope for phenotypic

selection. Same results were also observed for pods per plant by Singh *et al.* (2015); Ingle *et al.* (2020).

High genetic advance as per cent of mean (Fig. 3) was recorded for days to 50 % flowering (21.60%), racemes per plant (51.13%), pod length (22.62%), pod width (22.64%) and seed yield per plant (31.78%). Similar results were also observed for days to 50 % flowering, racemes per plant, pod length, pod width and seed yield per plant by Peer *et al.* (2018). Moderate genetic advance as per cent of mean was observed for plant height (19.07%), pods per plant (17.19%), pod weight (17.48%) and seeds per pod (17.56%). Similar results were also observed for pods per plant by Ingle *et al.* (2020); for seeds per pod by Choudhary *et al.* (2016); Patel *et al.* (2016); Afsan and Roy (2020). Low estimates of genetic advance as per cent of mean were observed for the days to maturity (9.25%). Similar results were also found by Mohan *et al.* (2014); Ingle *et al.* (2020).

Heritability combined with genetic advance as a percent of the mean is more useful in forecasting the outcome of selection than heritability alone. The high heritability combined with high genetic advance as per cent of mean was observed for days to 50 % flowering, racemes per plant, pod length, pod width and seed yield per plant demonstrating the importance of cumulative gene effects and the reduced influence of environment on the expression of the traits. Thus, the improvement of these traits could be achieved through direct phenotypic selection. Similar results were also observed by Peer *et al.* (2018). For plant height and seeds per pod, high heritability along with moderate genetic advance was observed, indicating predominance of non-additive gene activity in regulating these variables. As a result, there is little room for improvement in these attributes. Similar results were also observed for seeds per pod by Vaijayanthi *et al.* (2015); Choudhary *et al.* (2016); Patel *et al.* (2016); Afsan and Roy (2020). Days to maturity showed high heritability with low genetic advance as per cent of mean, showing non-additive gene action and days to maturity showed moderate heritability with low genetic advance, indicating the

non-additive gene influence for this variable as well. So, these traits cannot be improved through selection. The same outcomes were also noted by Mohan *et al.* (2014). The moderate heritability along with moderate genetic advance was observed for pods per plant and

pod weight. There is only a small opportunity for improving these qualities, which points to the importance of non-additive gene action. Ingle *et al.* (2020) found the same outcome for pods per plant.

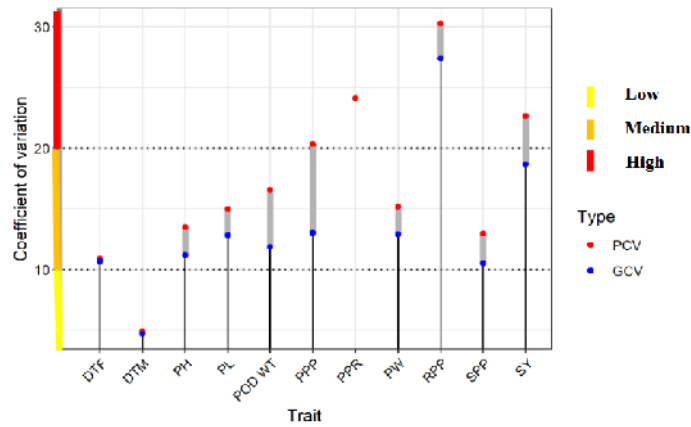


Fig. 1. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for different traits of Indian bean.

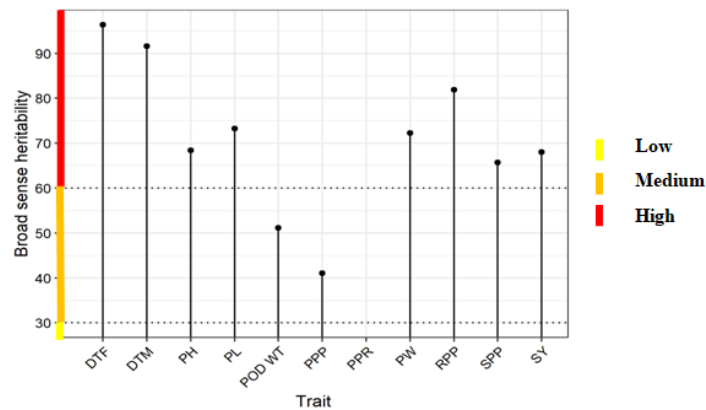
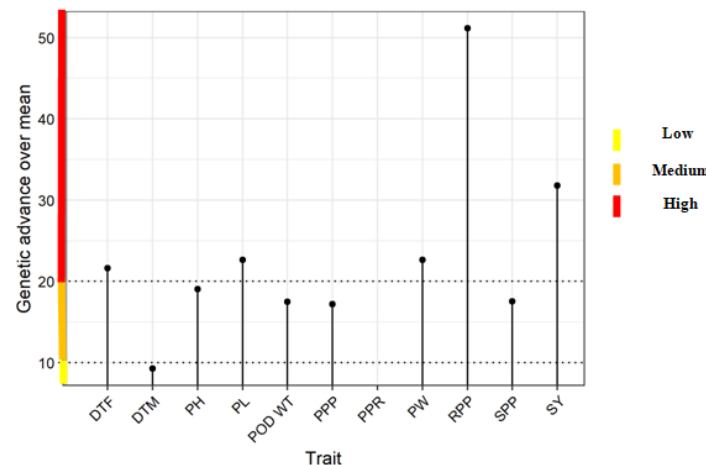


Fig. 2. Broad sense heritability for quantitative traits in F_6 progenies of Indian bean.



DTF- Days to 50% flowering
 PL – Pod length (cm)
 RPP – Racemes per plant
 SPP – Seeds per plant

DTM- Days to maturity
 POD WT – Pod weight (g)
 PPP – Pods per plant
 SY – Seed yield per plant (g)

PH – Plant height (cm)
 PW – Pod width (cm)
 PPR – Pods per plant

Fig. 3. Genetic advance as per cent of mean for quantitative traits in F_6 progenies of Indian bean.

CONCLUSION

According to the studies mentioned above, racemes per plant, pods per raceme, pods per plant and seeds per pod are the most crucial component characters for increasing grain yield per plant; as a result, these traits should be taken into consideration when choosing parents for breeding programme aimed at increasing seed yield in Indian beans.

FUTURE SCOPE

Indian bean is underutilized crop. It has tremendous variability in nature for plant growth habit, pod and seed related traits. It can survive in drought prone area and salty soil. So, it provides opportunity to breeder for developing different varietal segments having high yield with determinate growth habit and climate resilient ideotype. Besides this molecular level studies can provide information for nutritional quality and morphological traits for substantiable agriculture. Diverse genotypes with desirable traits open a broad genetic base for hybrid seed production by using economically viable seed production techniques.

Acknowledgement. The authors are grateful to the Pulse and Castor Research Station, Navsari Agricultural University, Navsari, Gujarat, India for providing the seeds of GNIB-21, GP-167, GP-1, GP-189 and GPKH-120 and advisory committee and Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari for providing the necessary resources and guidelines for the research work.

Conflict of Interest. None.

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How to cite this article: Rutvik J. Joshi, K.G. Modha, V.L. Parmar, V.B. Rana, Naresh Chaudhary, A.V. Malaviya and Naveen Y.K.V. (2022). Appraisal of Genetic Variability for Yield and other Quantitative Traits in Derived Germplasm of Indian Bean [*Lablab purpureus* (L.) Sweet]. *Biological Forum – An International Journal*, 14(4a): 109-114.