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Research Article

Genetic variability analysis for yield and yield attributes among determinate "*Wal*" type Indian bean [*Lablab purpureus* (L.) Sweet] genotypes

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Abstract

Fifty two genotypes of Indian bean were examined for the genetic variability parameters and trait correlation for 11 yield contributing traits in F_5 progenies. Analysis revealed that these genotypes had a considerable level of diversity. The magnitude of GCV and PCV was high for seed yield per plant, which indicated the potential for selection based genetic enhancement. The GCV and PCV values were moderate for pod weight, pods width and pod length. High heritability along with high genetic advance as per cent mean was recorded for pod width, pod length, pod weight and seed yield per plant. The seed yield per plant had a significant positive correlation with pod weight, plant height, pod length, pod width and seeds per pod. The overall genotypic path analysis revealed that racemes per plant exhibited the highest positive direct effects on seed yield per plant followed by direct effects of pod length, pods per raceme, pod width and pod weight. Therefore, simple selection is advised for pod length, pod width and pod weight to boost the yield of the Indian bean. Based on mean values, the progenies W-19-26, W-19-22 and W-19-25 of GNIB-21 × GP-167 among all crosses had shown significantly higher seed yield over the check varieties GNIB-21 and GNIB-22 and hence identified as elite genotypes.

Keywords: Indian bean, Variability, Correlation, Heritability, Path analysis

INTRODUCTION

Indian bean, [*Lablab purpureus* (L.) Sweet] belongs to the Fabaceae family and have varying diploid chromosome numbers 2n= 20, 22 or 24. It originated in India and introduced to Southeast Asia to Africa in the 8th century (Deka and Sarkar, 1990). It is also known as lablab bean, labian bean, Egyptian bean, hyacinth bean, field bean, Dolichos bean, poor man's bean, country bean, bonevist bean, tonga bean and butter bean. In Gujarat and Maharashtra, it is known as a '*Wal*'. Throughout the tropics and subtropics, it is grown as grain and green vegetables as well as fodder. The green and dried pods of Indian beans are enriched with nutrients like carbohydrates, proteins, fat, fibres and minerals *viz*., Ca, P and Fe (Gopalan *et al.,* 1982 and Naeem *et al.,* 2009). Seeds are rich in protein (15-25 %) as compared to pods (10-19 %) (Gopalan *et al.,* 1982). In Gujarat, many varieties of Indian beans are available for cultivation. Each of these varieties is known for its unique characteristics like pod shape, size, colour and aroma having a broad genetic base. It is photoperiod sensitive, however, rare photo-insensitive types are also available. In Gujarat, on the basis of pod characteristics, Indian bean cultivars are locally classified as *Wal* (bitter/sweet in-taste, short and flat shape, high fibre content), *Valor* (bitter or sweet in-taste, long and narrow shape, medium fibre content) and *Papdi* (sweet in-taste, short and narrow shape, less fibre content) (Kyada *et al*., 2022). Owing to its drought tolerance, it can be grown efficiently in a dry land with limited rainfall. Indian bean varieties with determinate growth habits are preferred as they have certain advantages over indeterminate types *viz.,* inter-cropping, early flowering, synchronise maturity and easy and feasible mechanical harvesting

For any genetic improvement programme, the presence of genetic variability is prerequisite in the base population. Highly heritable characters are required for the success of crop improvement programmes. The knowledge on genetic advance and heritability of the desirable traits helps plant breeders to establish accurate and appropriate breeding methodology (Dewangan *et al*., 2017). The efficiency of selection method is determined by the nature and magnitude of the interaction between heritable and non-heritable variables. Dividing the correlation coefficient into the respective direct and indirect effects would offer a more relevant explanation on the path with which the independent variables are influencing the dependent variable. Path analysis, a standardized partial regression coefficient, partitions the correlation coefficient into the component of direct and indirect effects and unravels whether the association of these characters with yields is due to their indirect effects via some other trait or traits. The path coefficient explains the cause and effect relation, and also quantifies the relative impact of all the variables (Wright, 1921). Keeping in view the importance of Indian bean and various factors affecting its yield, the present investigation was carried out with an aim to study genetic variability for yield and yield attributing traits in the Indian bean.

MATERIALS AND METHODS

The present experiment was carried out at College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari (Gujarat) during *Rabi,* 2019-20. The experimental material involved fifty-two "*Wal*" type determinate genotypes and out of which, fifty were F_5 progenies and two cultivars GNIB-21 and GNIB-22 were the check varieties. The progenies were obtained from the four crosses *i.e*., GNIB-21 × GP-1, GNIB-21 × GP-167, GNIB-21 × GP-189, and GNIB-21 × GPKH-120 (**Table 1**) and salient features of parents are furnished in **Table 2**. All 52 progenies were analyzed in a randomized

Table 1. Progenies of each cross evaluated in the present study

Cross	Number of progenies	Progenies
GNIB-21 × GP-1	7	W-19-1, W-19-2, W-19-3, W-19-4, W-19-7, W-19-11, W-19-33
GNIB-21 × GP-167	32	W-19-5, W-19-6, W-19-8, W-19-9, W-19-10, W-19-12, W-19-13, W-19-14, W-19-15, W-19-16, W-19-17, W-19-18, W-19-19, W-19-20, W-19-21, W-19-22, W-19-23, W-19-24, W-19-25, W-19-26, W-19-27, W-19-35, W-19-36, W-19-37, W-19-38, W-19-39, W-19-40, W-19-41, W-19-42, W-19-43, W-19-44, W-19-45
GNIB-21 × GP-189	11	W-19-28, W-19-29, W-19-30, W-19-31, W-19-32, W-19-34, W-19-46, W-19-47, W-19-48, W-19-49, W-19-50
GNIB-21 × GPKH-120	0	-

Table 2. Salient features of parents used in the present study

S. No.	Parents	Salient features
1.	GNIB-21	Photoperiod insensitive flowering; Determinate and pole type growth habit; No primary branches; Non-pigmented plant; White flowers; Dark green foliage; Prominent grains present inside the pods; Lowest attack of pulse beetle; C shape pods; Creamish white seeds
2.	GP-1	Photoperiod sensitive flowering; Indeterminate growth habit; Light pigmentation on flowers only; Sparsely pigmented stem; Light green, short and broad pods with 3 seeds; Dense foliage; Black seeds
3.	GP-167	Photoperiod sensitive flowering; Indeterminate growth habit; Pigmented buds and flower; Sparsely pigmented stem; Broad leaves; Dark green, long and flat pods, Creamish white bold seeds
4.	GP-189	Photoperiod sensitive flowering; Indeterminate growth habit; Darkly pigmented stem, bud, pod and flower; Purple flowers; Dark green foliage; Pigmented venation, smooth pod surface, Dark purple long narrow pods; Brown seeds with black spots
5.	GPKH-120	Photoperiod sensitive flowering; Indeterminate growth habit; Non pigmented stem, bud, pod, leaves and flower; White flowers; Light green pods with smooth surface; Mosaic susceptible; Dense canopy, Light green long and narrow pods; Creamish white wrinkled seeds

block design (RBD) with three replications. Each row was comprised of fifteen plants at a spacing of 60 cm and 20 cm between the plants within row. The crop was well grown by providing all basic agronomic and plant protection measures. Totally 11 quantitative traits *i.e.,* plant height (PH), days to 50 % flowering (DFF), days to maturity (DM), racemes per plant (RPP), pod weight (PW), pods per plant (PPP), pods per raceme (PPR), seeds per pod (SPP), pod width (PWD), pod length (PL), and seed yield per plant (SYPP) were studied. These abbreviations are used in further discussion for simplicity. Observations were recorded from 10 random plants from each progeny and each replication and their means were used in the biometrical analysis. However, days to maturity and days to 50 % flowering were evaluated on a population basis.

Analysis of Variance (ANOVA) was calculated as suggested by Panse and Sukhatme (1985). Broad sense heritability (h^2_{bs}) and the genetic advance were calculated using the method indicated by Allard (1999). Genotypic correlation coefficients were calculated using the method recommended by Miller *et al.* (1958). The path analysis was carried out according to Dewey and Lu (1959).

RESULTS AND DISCUSSION

The ANOVA for 11 quantitative characters is presented in **Table 3**. This shows significant mean square values for all the characters in F_5 progenies indicating enough variability present among the progenies for all the traits. Similar results were observed by Hadavani *et al.* (2018), Peer *et al.* (2018) and Gamit *et al.* (2020).

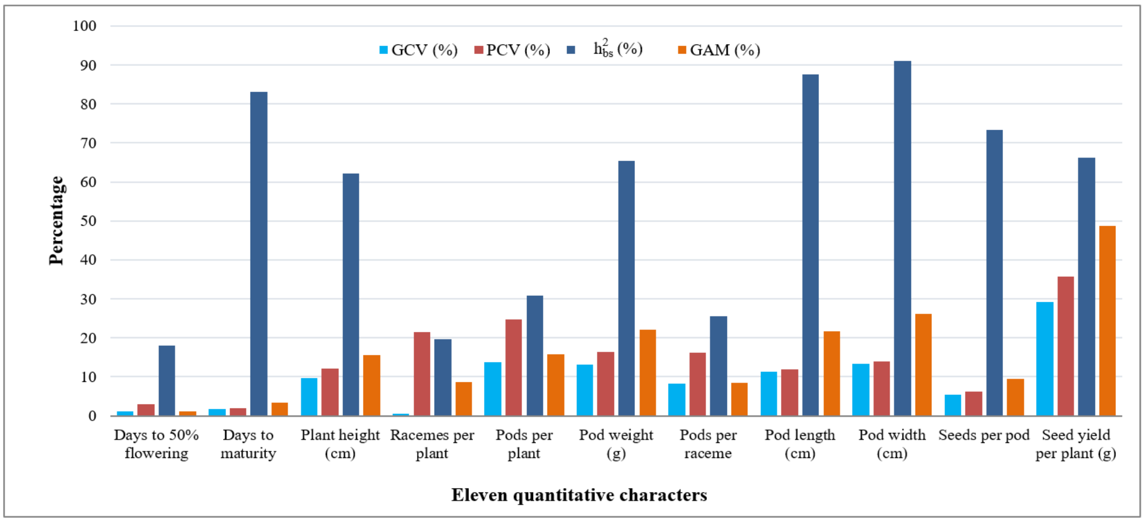
Various variability parameters are depicted in **Table 3** and **Graph 1**. The mean values indicated a vast range for DM (84.00-90.33), PH (42.93-70.42 cm), PPP (16.33-49.01), RPP (5.42-11.05), PPR (3.96-7.32), PW (0.73-1.58 g), PL (4.70-8.45 cm), PWD (1.04-2.17 cm) and SYPP (5.25-19.83 g). Based on mean values, the progenies W-19-26

Table 3. Analysis of variance for 11 quantitative characters under study

Source of variation	d.f.	Mean sum of square										
		DFF	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	SYPP
Replication	2	0.231	0.231	296.135**	3.599	180.349**	0.379**	5.381**	0.744**	0.014	0.002	8.408
Progenies	51	2.218*	7.274**	118.004**	3.897**	87.031**	0.094**	1.318**	1.469**	0.171**	0.149**	49.214**
Error	102	1.335	0.459	19.851	2.252	37.291	0.014	0.649	0.066	0.005	0.016	730.33

** - Significant at 1.0 % level of probability, * - Significant at 5.0 % level of probability

DFF=Days to 50% flowering
DM=Days to maturity
PH=Plant height (cm)
RPP=Racemes per plant
PPP=Pods per plant
PW=Pod weight (g)
PPR=Pods per raceme
PL=Pod length (cm)
PWD=Pod width (cm)
SPP=Seeds per pod
SYPP=Seed yield per plant (g)



Graph 1. Graphical representation of genetic variability parameters for eleven quantitative characters in F_5 progenies

GCV (%) = Genotypic coefficient of variation
PCV (%) = Phenotypic coefficient of variation
GAM (%) = GA as per cent of mean
h^2_{bs}(%) = Heritability (Broad sense)

(19.83 g), W-19-22 (19.45 g) and W-19-25 (19.42 g) of GNIB-21 × GP-167 cross among all crosses had shown significantly higher seed yield over the check varieties GNIB-21 (6.86 g) and GNIB-22 (10.05 g) and hence identified as elite genotypes.

Progenies exhibited higher values for GCV and PCV for SYPP (29.12 % and 35.79 %, respectively). The narrow gap between GCV and PCV indicated less influence of environment on traits *viz*., DM, PWD, PL and SPP unveiling the scope of improving these characters by selection (**Table 4**). PPP (13.77 % and 24.82 %, respectively), PW (13.22 % and 16.33 %, respectively), PL (11.24 %and 12.01 %, respectively) and PWD (13.33 % and 13.96 %, respectively) had moderate GCV and PCV values, which indicated that these traits would show less response to selection. Moreover, the magnitude of GCV and PCV values were low for DFF (1.23 % and 2.90 %, respectively), SPP (5.40 % and 6.31 %, respectively) and DM (1.76 % and 1.93 %, respectively) except PH (9.62 % and 12.19 %, respectively). PPR (8.19 % and 16.21 %, respectively) showed moderate PCV values stipulating a narrow range of variability for this trait, which restricts the scope of selection for it. The RPP (0.51 % and 21.48 %, respectively) showed lower GCV and higher PCV values. Similar results are also there in earlier studies for DFF and DM by Asaduzzaman *et al.* (2015); SYPP by Peer *et al.* (2018); PL Choudhary *et al.* (2016); PWD by Noorjahan *et al.* (2019); PW and SPP by Afsan and Roy (2020).

In addition, it indicated moderate to high heritability (broad sense) for all the quantitative traits studied **Table 4**). High heritability values for DM (83.17 %), PH (62.24 %), PW (65.52 %), PL (87.57 %), PWD (91.09 %), SPP (73.31 %) and SYPP (66.19 %) indicated that these traits are under little influence of environment, so phenotype could be a good indicator of genotypic effect and traits could be improved by simple phenotypic selection. The PPP had a moderate heritability (30.78 %) suggesting a medium influence of environment on the expression of this trait and limited scope for phenotypic selection. Low heritability values were depicted by DFF (18.05 %), RPP (19.58 %) and PPR (25.56 %) indicating the major effect of environmental effects on the total phenotypic variation. So, direct selection for these traits is not suggested. Similar results were observed for PH (92.60 %), DM (97.00 %) and SYPP (83.50 %) by Hadavani *et al.* (2018) in 50 genotypes; PWD (85.90 %) and PL (97.50 %) by Noorjahan *et al.* (2019) in 31 genotypes; pods per plant (49.83 %) by Singh *et al.* (2015) in 24 genotypes, and SPP (93.68 %) and PW (95.77 %) by Afsan and Roy (2020) in 11 genotypes.

A high magnitude of genetic advance as per cent of mean (GAM) was found for SYPP (48.80 %), PW (22.03 %), PL (21.67 %) and PWD (26.20 %) (**Table 4**). Moderate GAM was observed for PH (15.63 %) and PPP (15.73 %), while low estimates of GAM were recorded by DM (3.30 %), DFF (1.08 %), RPP (8.66 %), PPR (8.53 %) and SPP (9.53 %). Similar results were recorded for days to maturity and DFF by Mohan *et al.* (2014); PL, PWD and PW by Noorjahan *et al.* (2019a); SPP by Gupta *et al.* (2010) and SYPP by Peer *et al.* (2018).

Generally, heritability coupled with GAM is more desirable than heritability alone in predicting the response to selection. PW (65.52 % and 22.03 %, respectively), PL (87.57 % and 21.67 %, respectively), PWD (91.09 % and 26.20 %, respectively) and SYPP (66.19 % and 48.80 %, respectively) manifested high heritability coupled with high GAM pointing out the role of additive gene effects. Thus, improvement of these traits could be achieved through direct phenotypic selection. High heritability along with moderate GAM was recorded for PH (62.24 % and 15.63

Table 4. Genetic variability parameters of quantitative characters studied

Character	Range		σ^2_g	σ^2_p	GCV (%)	PCV (%)	h^2_{bs}	GAM (%)
	Minimum	Maximum						
Days to 50 % flowering	42.33	46.00	0.29	1.63	1.23	2.90	18.05	1.08
Days to maturity	84.00	90.33	2.27	2.73	1.76	1.93	83.17	3.30
Plant height (cm)	42.93	70.42	32.72	52.57	9.62	12.19	62.24	15.63
Racemes per plant	5.42	11.05	0.55	2.80	0.51	21.48	19.58	8.66
Pods per plant	16.33	49.01	16.58	53.87	13.77	24.82	30.78	15.73
Pod weight (g)	0.73	1.58	0.03	0.04	13.22	16.33	65.52	22.03
Pods per raceme	3.96	7.32	0.22	0.87	8.19	16.21	25.56	8.53
Pod length (cm)	4.70	8.45	0.47	0.53	11.24	12.01	87.57	21.67
Pod width (cm)	1.04	2.17	0.05	0.06	13.33	13.96	91.09	26.20
Seeds per pod	3.21	4.51	0.04	0.06	5.40	6.31	73.31	9.53
Seed yield per plant (g)	5.25	19.83	14.01	21.18	29.12	35.79	66.19	48.80

GCV (%) = Genotypic coefficient of variation
PCV (%) = Phenotypic coefficient of variation
h^2_{bs} (%) = Heritability (Broad sense)
GAM (%) = GA as percent of mean

%, respectively) stipulating that this trait is governed by non-additive gene effects and there is a limited scope of selection for improvement. High heritability with low GAM was observed for SPP (73.31 % and 9.53 %, respectively) and DM (83.17 % and 3.30 %, respectively) which is indicative of non-additive genes. So, it is not possible to improve these traits by simple phenotypic selection. Moderate heritability with moderate GAM was observed for PPP (30.78 % and 15.73 %, respectively). Hence, selection would be fairly effective for the improvement of this trait. Low heritability with low GAM was observed for DFF (18.05 % and 1.08 %, respectively), RPP (19.58 % and 8.66 %, respectively) and PPR (25.56 % and 8.53 %, respectively) indicating higher environmental influence, hence little gain is expected through simple selection for these traits. A similar result was observed for heritability and GAM for SYPP (94.20 % and 68.33 %), PWD (95.33 % and 24.67 %), PL (98.90 % and 65.89 %) and PW (99.19 % and 68.17 %) by Peer *et al.* (2018) in 29 genotypes; DM (93.00 % and 3.07 %) by Mohan *et al.* (2014) in 57 genotypes and SPP (85.54 % and 8.77 %) by Gnanesh *et al.* (2006) in 64 genotypes.

The correlation study revealed that SYPP had a significant positive genotypic correlation with PH (0.357**), PW (0.653**), PL (0.274*), PWD (0.699**) and SPP (0.480**), which indicated that it is possible to improve these traits simultaneously with SYPP through direct phenotypic selection (**Table 5**). While it had a non-significant positive correlation with RPP (0.086) which showed less significance of this trait for yield improvement. Similar results were observed for PW by Ali *et al.* (2005) and PH and PL by Choudhary *et al.* (2016). PH had a positive non-significant correlation and negative significant correlation with DM (0.187) and DFF (-0.417**), respectively, which suggested that simultaneous selection for more PH and SYPP may result in early flowering via indirect selection. RPP and PWD had a positive significant association with SPP (0.589** and 0.378**, respectively). SPP was significantly and negatively correlated with PPR (-0.018) (**Table 5**).

The genotypic path analysis unveiled that the highest positive direct effects on SYPP were imposed by RPP (2.132) followed by PL (0.934), PPR (0.664), PWD (0.610) and PW (0.046) (**Table 6**). Hence, selection for such characters will be easy in Indian beans. Similar results were also recorded for RPP and PWD by Magalingam *et al.* (2013); PWD and PL by Singh *et al.* (2011) and PPR by Ravinaik *et al.* (2014). The highest negative direct effect on SYPP was recorded by PPP (-2.339) followed by PH (-1.068), SPP (-0.874), DFF (-0.755) and DM (-0.576) suggesting less importance of these traits in selection for higher seed yield. Similar results were also recorded for DFF and SPP by Kamble *et al.* (2015); DM by Singh *et al.* (2015), and PPP and PH by Ravinaik *et al.* (2014). PH imposed the highest positive indirect effect *via* PPP on SYPP. PPP and SPP exhibited the highest positive indirect effect on SYPP *via* RPP. PW, PWD and PL exhibited a positive direct effect on SYPP along with high significant and positive association with SYPP. Therefore, these can be regarded as the most important yield attributing characters. In path analysis, a high residual effect of 0.577 was observed which indicates that more yield related traits are necessary to be included in future studies to cover all of the available variations.

The study indicated that abundant variability was present among the genotypes for all the characters. The progenies W-19-26, W-19-22 and W-19-25 had shown significantly higher seed yield over the check varieties and hence identified as elite genotypes. The magnitude of GCV and PCV was high for seed yield per plant, which indicated the potential for selection based genetic enhancement. High heritability along with high GAM was recorded for pod width, pod length, pod weight and seed yield per plant. The seed yield per plant had a significant positive correlation with pod weight, plant height, pod length, pod

Table 5. Genotypic correlation coefficients of seed yield per plant with other characters in F_5 progenies

Character	DFF	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	SYPP
DFF	**1.000**										
DM	-0.189	**1.000**									
PH	-0.417**	0.187	**1.000**								
RPP	-0.273	0.205	0.171	**1.000**							
PPP	0.073	-0.268	-0.603**	0.491**	**1.000**						
PW	-0.219	-0.189	0.094	-0.189	-0.056	**1.000**					
PPR	0.481**	-0.425**	-0.845**	-0.054	0.726**	0.058	**1.000**				
PL	0.167	-0.022	-0.006	-0.235	0.093	0.548**	0.017	**1.000**			
PWD	-0.376**	0.126	0.441**	-0.042	-0.165	0.620**	-0.314*	0.529**	**1.000**		
SPP	-0.489**	0.329*	0.301*	0.589**	-0.018	0.254	-0.376**	0.222	0.378**	**1.000**	
SYPP	-0.288*	-0.162	0.357**	0.086	-0.068	0.653**	-0.210	0.274 *	0.699**	0.480**	**1.000**

** - Significant at 1.0 % level of probability, * - Significant at 5.0 % level of probability

Table 6. Genotypic path coefficient analysis of component characters towards seed yield per plant in F_5 progenies

Character	DFF	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	Correlation with seed yield per plant
DFF	-0.755	0.109	0.445	-0.581	-0.170	-0.010	0.319	0.156	-0.229	0.428	-0.288 *
DM	0.143	-0.576	-0.200	0.437	0.627	-0.009	-0.283	-0.021	0.008	-0.288	-0.162 NS
PH	0.315	-0.108	-1.068	0.365	1.411	0.004	-0.561	-0.006	0.269	-0.263	0.357 **
RPP	0.206	-0.118	-0.183	2.132	-1.148	-0.009	-0.036	-0.220	-0.025	-0.515	0.086 NS
PPP	-0.055	0.154	0.644	1.046	-2.339	-0.003	0.482	0.087	-0.100	0.015	-0.068 NS
PW	0.165	0.109	-0.100	-0.403	0.131	0.046	0.039	0.512	0.378	-0.222	0.653 *
PPR	-0.363	0.245	0.903	-0.116	-1.699	0.003	0.664	0.016	-0.191	0.328	-0.210 NS
PL	-0.126	0.013	0.006	-0.501	-0.217	0.025	0.011	0.934	0.322	-0.194	0.274 *
PWD	0.284	-0.007	-0.471	-0.086	0.385	0.028	-0.208	0.494	0.610	-0.330	0.699 **
SPP	0.369	-0.190	-0.321	1.255	0.041	0.012	-0.250	0.207	0.230	-0.874	0.480 *

** - Significant at 1.0 % level of probability, * - significant at 5.0 % level of probability, Residual = 0.577, Bold diagonal figures are the direct effects

width and seeds per pod. The overall genotypic path analysis revealed that racemes per plant exhibited the highest positive direct effects on seed yield per plant followed by direct effects of pod length, pods per raceme, pod width and pod weight. The proximity of GCV and PCV estimates, high genetic advance as per cent mean, high heritability, positive and significant correlation and the positive direct effect were observed for pod weight, pod width and pod length. So, these traits would be advantageous in a further breeding program for the improvement of seed yield in Indian beans.

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