

Genetic Variability and Correlation Study in Determinate Type Progenies of Indian Bean [*Lablab purpureus* (L.) Sweet]

ABSTRACT

Aims: In India, the Indian bean is a popular vegetable and legume crop. An attempt was made to analyze the variability, correlation as well as direct-indirect effects using path analysis for yield and its sub-characters.

Place and Duration of Study: Navsari Agricultural University, Navsari, Gujarat. In *Rabi* 2019-20.

Methodology: The investigation was conducted using 55 genotypes in a randomized block design using three replications. Total of eleven quantitative traits were studied and data was collected from ten random plants from each genotype.

Results: ANOVA depicted sufficient variability present among the genotypes for all traits. Plant height, racemes per plant, pods per raceme, pod weight, pods per plant, pod width, and seed yield per plant showed moderate to high GCV (**Genotypic coefficient of variation**) and PCV (**Phenotypic coefficient of variation**), moderate to high heritability, and moderate to high genetic advance as a per cent of mean. Plant height, racemes per plant, pods per plant, pod weight, and pods per raceme were significantly and positively associated with seed yield per plant at the genotypic level. Pods per plant had the most favorable direct effects (0.736) on seed yield per plant, subsequently by pod weight, seeds per pod, pods per raceme, pod length, pod width, plant height and days to maturity.

Conclusion: It is concluded that sufficient amount of variability is present within the material under study. The selection for pods per plant, pods per raceme, pod weight, pod length, pod width, plant height, seeds per pod and days to maturity would be easy and useful in bringing about improvement of seed yield in Indian bean.

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

1. INTRODUCTION

Indian bean [*Lablab purpureus* (L.) Sweet] ($2n=22$) belongs to the family Fabaceae (Subfamily Papilionaceae) and is frequently also referred as lablab bean, labia bean, egyptian bean, field bean, hyacinth bean, dolichos bean and poor man's bean [2, 15]. It is one of the earliest cultivated legume plants and is now cultivated in tropical areas of Asia and Africa [4]. In tropical areas, Indian bean can be grown as a stand-alone crop, as a catch crop, or in combination with other crops like finger millet, peanuts, castor, maize, bajra, or sorghum [15]. Moreover, it has ability to fix nitrogen in the soil using symbiotic bacteria [17]. It is rich source of protein which ranges from 20 to 28 per cent in seed [10]. The pods are high in carbohydrates, fats, proteins and fibres, as well as minerals including Ca, P and Fe [10]. Green pods are being used as a vegetable, while mature and dried seeds can be used as pulses [12].

Furthermore, there are very few photo-insensitive and determinate cultivars available for cultivation [9]. Because of these features, crops can be grown in any season and multiple seasons per year can be taken [9].

In Gujarat, based general observations on pod characteristics, Indian bean genotypes are locally classified as “*Wal*” (short and flat shape, bitter in test, high fibre content), “*Valor*” (long and narrow shape, bitter/sweet in test, medium fibre content) and “*Papdi*” (short and narrow shape, sweet in test, less fibre content). Interestingly, till to date there is no determinate “*Valor*” type variety available for cultivation in Gujarat [9].

Knowledge of genetic variability is crucial for developing high-yielding cultivars by a systematic breeding effort [1]. Heritability is also required to determine the trait transmissibility to the following generation [1]. Direct selection for yield would be useless because it is quantitative in nature and has a high environmental influence [1]. So, the understanding of degree of association of yield with its sub-characters, as well as among them, would be useful to select for high yield based on visual selection of yield associated traits. Path coefficient analysis is being used by breeders to divide the correlation coefficient as direct and indirect effects, which will assist them to select for crucial quantitative traits that will result in a high yield. So, the present investigation was conducted to understand the variability parameters among the ‘*Valor*’ type Indian bean genotypes and to study the association and effects of various quantitative traits on seed yield and among themselves.

2. MATERIAL AND METHODS

The experiment was conducted during *Rabi* 2019-20, at College Farm, Navinchandra Mafatlal College of Agriculture, Navsari Agricultural University, Navsari (Gujarat). Fifty-five ‘*Valor*’ type genotypes were used in the study, fifty-three of which were F_5 progenies and two of which were control varieties (GNIB-21 and GNIB-22). All 53 F_5 progenies (Shown in Table 1 with mean data of each trait) were obtained from three crosses *i.e.*, GNIB-21 \times GP-1, GNIB-21 \times GP-167 and GNIB-21 \times GP-189. Parents of these crosses are obtained from Department of Genetics and Plant Breeding, Navinchandra Mafatlal College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India. All fifty-five genotypes were analysed in a randomised block design having three replications. Each row had 15 single progeny plants with a spacing of 60 cm x 20 cm. In every replication, the progenies were assigned to the plots at random. To avoid damage and border effect, the experiment was enclosed by one guard row. All of the recommended agronomic techniques as well as the necessary crop protection measures were implemented on time to ensure a successful crop harvest. The soil was prepared by deep ploughing followed by harrowing and levelling. The crop was supplied with 10-20-00 NPK Kg/ha. The irrigation was given at every 2 week intervals and regular weeding was done as per the requirements. Pests such as whitefly, aphids and heliothis were controlled by appropriate insecticide spray. During the trial, total of eleven quantitative characters *viz.*, days to 50% flowering (from date of sowing when fifty percent of plants of progeny showed flowering), days to maturity (from the date of sowing to the date when fifty per cent of the plants of the progeny showed dried brown pods), plant height (cm) (from base to the tip of main shoot at physiological maturity), racemes per plant (from main axis at maturity), pod length (cm), pod width (cm) (both pod length and width averaged from three randomly selected pods after harvesting), pods per raceme (from three randomly selected racemes per plant), pods per plant, pod weight (g) (average weight of ten randomly selected pods after harvesting), seeds per pod (average of three randomly selected pods) and seed yield per plant (g) (average yield of all selected plants) were examined. Before the first flower appeared, ten plants were marked randomly from each progeny rows. Days to 50% flowering and days to maturity were recorded on a population basis. Except for these two traits, the data were collected from ten plants selected randomly from each progeny in each replication and their means were used in the statistical analysis. This type of observations was recorded previously by [6].

The data were subjected to analysis of variance [11], and to biometrical analysis to estimate the heritability (broad sense) (h_{bs}^2), genetic advance, correlation [18] and path coefficients [5] using Rstudio [16] via the variability R package [14].

3. RESULTS AND DISCUSSION

3.1 Variability parameters

Analysis of variance revealed substantial amount of variability present among the progenies for all the characters (Table 2), which is comparable with the findings of Patel *et al.* [12]. A large range of variation was observed based on mean performance for days to 50% flowering (38-46), days to maturity (84-94.67), plant height (30.17-66.14 cm), racemes per plant (4.08-12.90), pods per plant (12.44-35.24), pod weight (0.68-1.11 g), pods per raceme (2.11-6.04), pod length (5.87-9.67 cm), pod width (1.08-1.93 cm), seeds per pod (3.50-4.39) and seed yield per plant (7.78 to 22.09 g). Based on mean performance, the progenies NV-14 (22.09 g), NV-26 (21.17 g) and NV-1 (20.95 g) exhibited significantly higher seed yield per plant than both the control varieties GNIB-21 and GNIB-22 (14.29 g and 16.40 g, respectively) and identified as elite genotypes (Table 1).

Among the characters studied, higher GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation) was recorded for pods per plant (22.91 % and 25.54 %, respectively) indicating high available variability for improvement of this character (Table 3 and Figure 1). Racemes per plant (19.19 % and 23.67 %, respectively) and seed yield per plant (16.18 % and 20.78 %, respectively) showed moderate GCV and high PCV estimates, indicating an environmental effect on this trait and these traits are less responsive to selection. Moderate GCV and PCV estimates were recorded for plant height (11.22 % and 15.49 %, respectively), pod weight (11.72 % and 14.05 %, respectively), pods per raceme (17.14 % and 19.52 %, respectively), and pod width (12.84 % and 13.44 %, respectively). Low GCV and PCV were recorded for days to 50% flowering (2.31 % and 2.83 %, respectively), days to maturity (1.67 % and 1.95 %, respectively) and seed per pod (4.15 % and 5.70 %, respectively), apart from pod length (9.79 % and 11.71 %, respectively), which showed moderate PCV. The Low and Moderate GCV estimates for these traits indicated a limited variability for these traits and the extent of response to selection for these characters would be limited. These results were in accordance with previous work for pods per plant [12], seed yield per plant and racemes per plant [13].

The heritability of all of the variables ranged from moderate to high (Table 3 and Figure 1). Pod width (91.36 %), pods per plant (80.48 %), pods per raceme (77.13 %), days to maturity (72.98 %), racemes per plant (65.78 %), days to 50% flowering (66.60 %), pod length (69.92 %), pod weight (69.68 %) and seed yield per plant (60.67 %) had high heritability values, indicating that these traits are largely governed by additive gene effects and these traits could be improved by selection. Peer *et al.* [13] also found high heritability for these traits except for days to maturity. Plant height (52.48 %) and seeds per pod (53.07 %) had moderate heritability, indicating influence of environment on these traits, limiting the potential for phenotypic selection. Hadavani *et al.* [7] found similar results for seeds per pod.

Racemes per plant (32.07 %), pods per plant (42.35 %), pod weight (20.16 %), pods per raceme (31.01 %), pod width (25.29 %) and seed yield per plant (25.97 %) showed high genetic advance as percent of mean (Table 3 and Figure 1). Plant height (16.75 %), and pod length (16.87 %) showed moderate genetic advance as per cent of mean. Similar trends were followed by Patel *et al.* [12] for racemes per plant and pods per raceme, and by Hadavani *et al.* [7] for pods per plant and seed yield per plant. The traits days for 50% flowering (3.88 %), days to maturity (2.94 %) and seeds per pod (6.24 %), found to have low genetic advance as per cent of mean. Gnanesh *et al.* [6] obtained a similar trend for seed per pod.

Heritability expressed with genetic advance as per cent of mean provides more information regarding gene action, environmental influence, and crop improvement plan. As a result, high heritability along with high genetic advance was depicted for raceme per plant (65.78 % and 32.07 %, respectively), pods per plant (80.48 % and 42.35 %, respectively), pod weight (69.68 % and 20.16 %, respectively), pods per raceme (77.13 % and 31.01 %, respectively), pod width (91.36 % and 25.29 %, respectively) and seed yield per plant (60.67 % and 25.97 %, respectively), indicating the role of additive gene action and less environmental

Table 1: Mean values of fifty three progenies and two checks for various quantitative traits

Sr. No.	Progenies	DFE	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	SYPP
1	NV-1	41.67	88.00	51.04	7.31	32.49	0.99	5.30	6.97	1.17	3.86	20.95
2	NV-2	42.00	88.00	54.42	5.77	23.71	1.05	3.66	7.03	1.35	3.89	17.32
3	NV-3	42.00	88.67	55.04	7.43	22.08	0.81	4.91	7.15	1.35	4.15	13.49
4	NV-4	41.33	87.67	56.46	8.66	29.53	0.73	6.04	7.66	1.43	3.81	16.11
5	NV-5	45.33	87.00	56.70	7.56	24.96	0.88	4.99	7.83	1.27	3.83	16.17
6	NV-6	41.00	87.33	58.24	8.28	23.80	0.83	4.12	8.48	1.57	4.14	14.58
7	NV-7	41.33	86.67	65.08	10.88	31.12	0.86	5.84	6.61	1.08	3.91	18.20
8	NV-8	46.00	87.00	58.71	12.90	29.29	0.80	4.95	8.76	1.81	4.11	16.26
9	NV-9	42.00	86.67	57.63	7.37	25.33	0.70	5.07	6.30	1.38	3.96	14.30
10	NV-10	41.67	86.67	58.67	6.58	22.60	0.93	5.47	8.10	1.66	3.60	15.63
11	NV-11	41.00	87.00	56.31	8.32	31.83	0.78	4.75	7.85	1.65	4.00	17.41
12	NV-12	41.67	87.33	52.22	7.61	30.61	0.74	5.82	7.84	1.67	3.75	16.34
13	NV-13	42.33	87.00	51.51	6.88	24.39	0.99	5.12	7.65	1.52	3.86	16.75
14	NV-14	41.67	87.67	60.08	8.26	29.71	0.81	4.84	8.20	1.55	4.14	22.09
15	NV-15	41.00	87.00	56.77	6.99	31.72	0.99	4.99	8.60	1.42	3.50	20.59
16	NV-16	42.00	88.33	58.45	7.17	29.10	0.98	5.33	7.52	1.31	3.99	19.73
17	NV-17	42.00	88.33	54.00	7.96	26.10	0.72	5.89	6.98	1.32	3.91	13.99
18	NV-18	42.67	88.33	57.19	7.45	27.33	0.85	4.96	7.71	1.27	3.77	16.76
19	NV-19	41.00	86.67	58.29	7.92	27.41	1.04	5.13	5.87	1.20	4.03	19.11
20	NV-20	41.67	86.33	58.23	7.34	23.63	0.86	4.94	8.03	1.34	3.99	15.03
21	NV-21	43.00	87.33	60.74	7.72	24.91	0.95	4.98	8.55	1.27	3.97	16.81
22	NV-22	43.00	87.67	59.25	7.17	25.29	1.11	4.82	8.27	1.37	3.87	18.74
23	NV-23	42.00	88.33	58.14	8.09	32.47	0.84	5.37	8.65	1.38	3.56	18.45
24	NV-24	41.33	88.00	63.90	7.98	30.55	0.69	5.47	9.47	1.34	3.67	15.64
25	NV-25	41.00	88.00	66.14	9.29	29.54	0.94	5.30	7.60	1.34	4.03	18.66
26	NV-26	42.00	87.33	57.10	8.00	35.24	0.99	5.65	7.96	1.23	3.75	21.17
27	NV-27	41.67	87.00	51.29	7.88	25.46	0.91	4.40	8.59	1.37	3.80	16.68
28	NV-28	42.00	86.33	50.67	5.00	13.91	1.06	4.02	7.34	1.43	3.67	12.51
29	NV-29	41.67	88.33	48.19	7.11	17.00	1.02	3.71	9.67	1.76	3.88	18.65
30	NV-30	43.00	87.33	43.68	9.42	19.22	0.93	4.30	9.26	1.93	4.11	14.66

Table 1 continue...

Sr. No.	Progenies	DFE	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	SYPP
31	NV-31	42.00	87.67	30.17	4.97	12.44	0.85	3.17	8.03	1.54	4.00	12.75
32	NV-32	41.33	88.00	49.00	7.44	23.29	0.84	4.76	7.42	1.40	3.68	14.26
33	NV-33	41.00	94.67	46.58	6.88	22.74	1.09	4.54	7.06	1.27	3.70	17.00
34	NV-34	42.00	93.67	50.81	8.55	34.99	0.68	4.97	7.63	1.52	3.96	17.35
35	NV-35	41.33	87.67	45.00	7.50	25.11	0.77	4.51	8.35	1.33	3.95	7.78
36	NV-36	41.67	87.67	38.61	7.64	23.63	0.90	3.81	7.85	1.76	4.01	15.13
37	NV-37	42.33	87.67	52.18	7.80	23.73	1.09	5.57	8.77	1.20	4.02	17.39
38	NV-38	41.00	86.67	56.39	12.00	25.61	0.88	3.89	8.53	1.29	3.93	16.54
39	NV-39	42.00	86.67	58.87	8.52	24.56	0.88	3.96	8.83	1.28	4.00	15.79
40	NV-40	42.67	84.33	58.56	10.03	27.49	0.91	3.74	8.77	1.91	3.91	17.37
41	NV-41	41.67	84.00	63.67	6.95	25.63	0.79	4.02	7.52	1.43	4.34	14.67
42	NV-42	41.00	87.33	52.60	5.08	14.06	1.03	4.21	8.28	1.30	4.14	16.61
43	NV-43	42.00	87.67	54.94	7.17	28.83	0.80	4.56	8.91	1.43	4.04	16.70
44	NV-44	42.00	87.33	49.41	7.02	15.28	0.80	3.91	8.30	1.43	4.39	17.60
45	NV-45	41.67	88.00	55.78	5.67	20.46	0.76	3.96	8.10	1.42	4.11	12.48
46	NV-46	41.67	88.00	54.67	8.68	15.56	0.99	3.99	8.00	1.38	3.94	12.01
47	NV-47	41.67	87.67	49.61	5.33	13.09	0.91	3.29	7.99	1.39	4.02	10.82
48	NV-48	42.00	88.00	49.83	7.23	23.38	0.82	4.08	7.05	1.35	3.60	14.60
49	NV-49	42.33	88.67	38.94	4.08	12.56	0.84	2.11	7.49	1.35	3.86	8.25
50	NV-50	41.67	88.00	57.22	6.34	18.31	1.01	3.10	7.30	1.37	4.09	14.19
51	NV-51	42.00	87.67	57.18	8.11	19.00	0.81	3.97	7.64	1.37	4.13	11.91
52	NV-52	41.67	88.67	55.20	6.72	25.33	0.95	3.67	7.79	1.44	3.80	17.01
53	NV-53	41.33	88.33	50.29	6.11	16.20	0.72	3.34	7.71	1.35	4.05	17.44
54	GNIB 21	38.00	87.67	42.32	7.16	23.36	0.82	4.97	6.12	1.09	4.18	14.29
55	GNIB 22	42.67	86.67	42.82	5.99	22.91	0.98	4.89	5.96	1.17	4.13	16.40

Table 2: Result of Analysis of variance for characters under study

Source of variation	d.f.	Mean sum of square										
		DDF	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	SYPP
Replication	2	1.6424*	0.0788	86.037	2.3901	2.816	0.008	0.277	0.6540	0.0020	0.078*	1.532
Progenies	54	3.2790**	7.2346**	142.072**	7.3961**	100.791**	0.037**	2.019**	2.029**	0.101**	0.104**	24.419**
Error	108	0.4696	0.7948	32.939	1.0932	7.541	0.0047	0.181	0.254	0.0031	0.0236	4.3392

** - Significant at 1% level of probability, * - Significant at 5.0 % level of probability

DDF=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)

Table 3: Result of measures of variability parameters of all the characters studied

Character	Range		GCV (%)	PCV (%)	h_{bs}^2 (%)	GA	GAM
	Min.	Max.					
Days to 50% flowering	38	46	2.31	2.83	66.60	1.62	3.88
Days to maturity	84	94.67	1.67	1.95	72.98	2.57	2.94
Plant height (cm)	30.17	66.14	11.22	15.49	52.48	9.00	16.75
Racemes per plant	4.08	12.9	19.19	23.67	65.78	2.42	32.07
Pods per plant	12.44	35.24	22.91	25.54	80.48	10.30	42.35
Pod weight (g)	0.68	1.11	11.72	14.05	69.68	0.17	20.16
Pods per raceme	2.11	6.04	17.14	19.52	77.13	1.41	31.01
Pod length (cm)	5.87	9.67	9.79	11.71	69.92	1.32	16.87
Pod width (cm)	1.08	1.93	12.84	13.44	91.36	0.35	25.29
Seeds per pod	3.5	4.39	4.15	5.70	53.07	0.24	6.24
Seed yield per plant (g)	7.78	22.09	16.18	20.78	60.67	4.15	25.97

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

GAM = GA as per cent of mean (%)

GA = Genetic advance

h_{bs}^2 = Heritability (Broad sense)

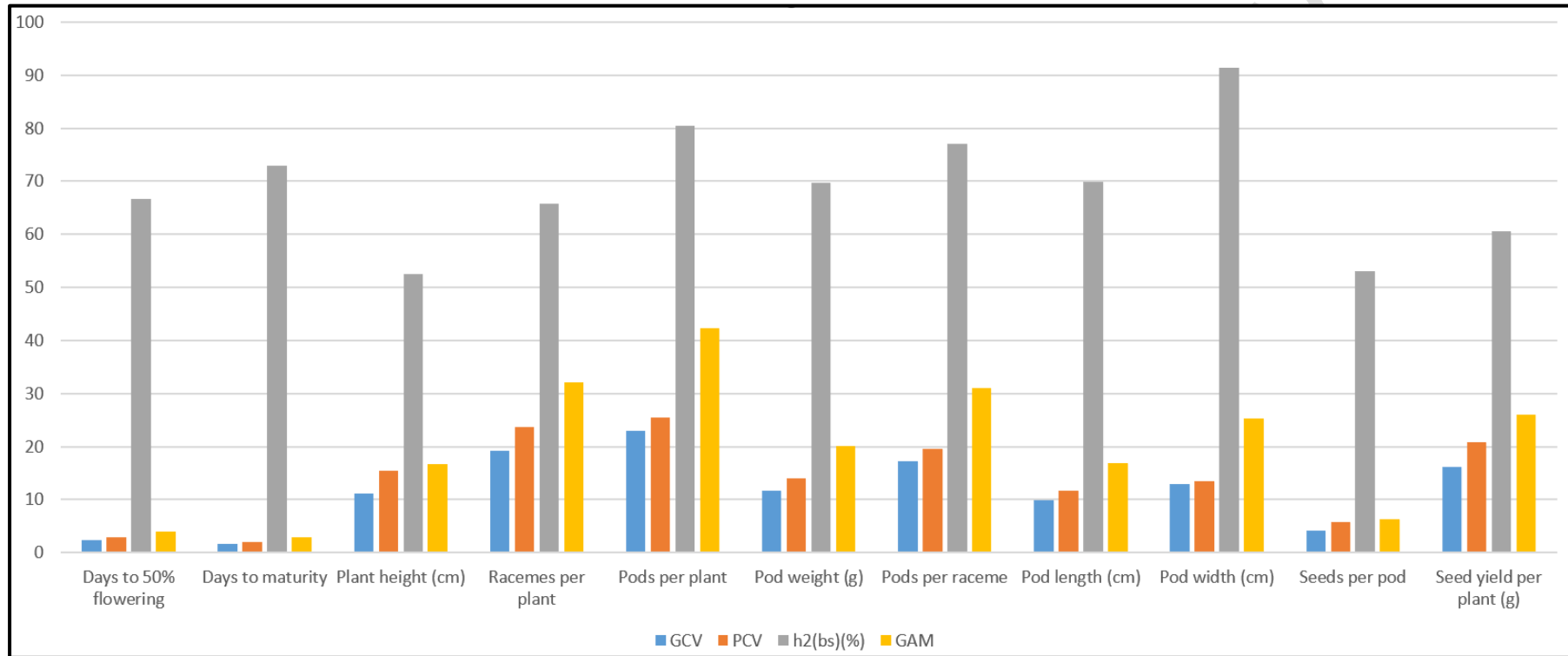


Figure 1. GCV, PCV, h^2_{bs} and GAM for eleven quantitative characters

GCV (%) = Genotypic coefficient of variation

PCV (%) = Phenotypic coefficient of variation

GAM = GA as per cent of mean (%)

h^2_{bs} (%) = Heritability (Broad sense)

UNDEF

influence on these traits. As a result, direct phenotypic selection could be effective to improve these characters. The trait pod length had high heritability and moderate genetic advance as per cent of mean (69.92 % and 16.87 %, respectively), indicating non-additive gene action for these traits. High heritability with low genetic advance as a per cent of mean were reported for days of 50% flowering (66.60 % and 3.88 %, respectively) and days to maturity (72.98 % and 2.94 %, respectively), indicating less environmental influence on this trait but manifested presence of non-additive gene action in the expression of this character and implying a decreased possibility of improvement by simple selection. Plant height exhibited moderate heritability and moderate genetic advance as per cent of mean (52.48 % and 16.75 %, respectively) indicating that less improvement is expected by selection. For seed per pod (53.07 % and 6.24 %, respectively), moderate heritability was observed with low genetic advance as per cent of mean, showing non-additive gene effect and selection for this trait would not be useful.

3.2 Genotypic correlation study

Out of ten independent traits, Plant height (0.431**), racemes per plant (0.309**), pods per plant (0.607**), pod weight (0.304**) and pods per raceme (0.521**) were significantly and positively associated with seed yield per plant, indicating that these characters can be used simultaneously to enhance seed yield per plant (Table 4). Similar trend was followed by Patel *et al.* [12] except for pod weight. Days to maturity (0.035) and pod length (0.078) had a non-significant and positive correlation, implying that these variables are less important for enhancing seed yield. Plant height was negatively and significantly correlated to days to maturity (-0.294*), implying that simultaneous improvement for early maturity via seed yield per plant could be useful while direct selection for plant height is possible.

Racemes per plant had a positive and significant association with pod length (0.280*), whereas pod length had a positive and significant relationship with pod width (0.558**), indicating that while direct selection for racemes per plant is possible, simultaneous improvement of pod length and pod width with seed yield per plant is also possible. Pods per plant (0.766** with pods per raceme, 0.586** with racemes per plant), pods per raceme (0.436** with racemes per plant), and racemes per plant were all found to be significantly and positively associated, and also had significant positive association with seed yield per plant, indicating that such characters can help selection for each other as well as for high seed yield. Seeds per pod, interestingly, did not show positive and significant correlation with any of the characters, indicating that this trait could not be increased directly or indirectly with seed yield per plant.

3.3 Genotypic path analysis

Days to 50 % flowering and racemes per plant exhibited negative direct effects on seed yield per plant, while all other traits showed positive direct effects (Table 5). This indicates that selection for later traits in F₅ progenies and following generations will be simple and useful for improving the indian bean, and less significance of former two traits in selection for higher seed yield. Pods per plant had the highest positive direct effect (0.736) and significant contribution to yield. Similar results were observed by Kamble *et al.* [8] for days to 50 % flowering, days to maturity, pods per plant, racemes per plant, plant height and pod length; Anburani and Shalini [3] for pod weight and pods per raceme.

The pods per raceme exhibited highest positive indirect effects through pods per plant, while seeds per pod registered highest negative indirect effects *via* pods per plant on seed yield per plant. Racemes per plant had high negative direct effect in contrast to positive significant correlation with seed yield per plant. It suggests that the indirect effects created this correlation, with the pods per plant contributing the most to it. In this case selection for racemes per plant will not be more useful in breeding program, and selection for pods per plant would be suggested.

For seed yield, path coefficient analysis found a residual effect of 0.362, implying that more variables should be included in future studies to account for all the available variation.

Table 4: Genotypic correlation coefficients of seed yield per plant with other characters

Characters	DFE	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	SYPP
Days to 50% flowering	1.000										
Days to maturity	-0.120	1.000									
Plant height (cm)	0.113	-0.294*	1.000								
Racemes per plant	0.224	-0.166	0.503**	1.000							
Pods per plant	0.003	0.053	0.550**	0.586**	1.000						
Pod weight (g)	0.081	0.018	-0.019	-0.207	-0.212	1.000					
Pods per raceme	0.021	0.022	0.463**	0.436**	0.766**	-0.111	1.000				
Pod length (cm)	0.305*	-0.121	0.118	0.280*	-0.015	-0.020	-0.136	1.000			
Pod width (cm)	0.317*	-0.149	-0.131	0.237	-0.061	-0.163	-0.236	0.558**	1.000		
Seeds per pod	-0.003	-0.224	-0.096	0.084	-0.328*	-0.214	-0.328*	-0.108	0.049	1.000	
Seed yield per plant (g)	-0.016	0.035	0.431**	0.309*	0.607**	0.304*	0.521**	0.078	-0.038	-0.169	1.000

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

Table 5: Genotypic path coefficient analysis of sub-characters towards seed yield per plant

Characters	DFE	DM	PH	RPP	PPP	PW	PPR	PL	PWD	SPP	Correlation with SYPP
Days to 50% flowering	-0.121	-0.009	0.013	-0.057	0.002	0.044	0.005	0.057	0.051	-0.001	-0.016
Days to maturity	0.014	0.080	-0.035	0.042	0.039	0.010	0.005	-0.022	-0.024	-0.075	0.035
Plant height (cm)	-0.013	-0.023	0.119	-0.129	0.405	-0.010	0.115	0.022	-0.021	-0.032	0.431**
Racemes per plant	-0.027	-0.013	0.060	-0.256	0.432	-0.113	0.108	0.052	0.038	0.028	0.309*
Pods per plant	-0.0001	0.004	0.065	-0.150	0.736	-0.116	0.191	-0.002	-0.009	-0.110	0.607**
Pod weight (g)	-0.009	0.001	-0.002	0.053	-0.156	0.548	-0.027	-0.003	-0.026	-0.072	0.304*
Pods per raceme	0.002	0.001	0.055	-0.111	0.564	-0.061	0.249	-0.025	-0.038	-0.110	0.521**
Pod length (cm)	-0.037	-0.009	0.014	-0.071	-0.011	-0.011	-0.034	0.186	0.090	-0.036	0.078
Pod width (cm)	-0.038	-0.011	-0.015	-0.060	-0.045	-0.089	-0.058	0.104	0.161	0.016	-0.038
Seeds per pod (g)	0.0001	-0.017	-0.011	-0.021	-0.241	-0.118	-0.081	-0.020	0.007	0.335	-0.169

** - Significant at 1.0 per cent level of probability, * - significant at 5.0 per cent level of probability, Residual = 0.326, Bold diagonal figures are the direct effects

4. CONCLUSION

It is concluded that sufficient amount of variability is present within the material under study. As per the correlation and path analysis, selection for pods per plant, pods per raceme, pod weight, pod length, pod width, plant height, seeds per pod and days to maturity would be easy and useful in bringing about improvement in improvement of seed yield in Indian bean. In addition, the identified elite genotypes need to be assessed over space and time for confirmation of performance.

REFERENCES

1. Allard RW, Principles of Plant Breeding. John Wiley and Sons, New York; 1999.
2. Al-Snafi AE. The pharmacology and medical importance of Dolichos lablab (Lablab purpureus)-A review. IOSR Journal of Pharmacy. 2017; 7(2): 22-30.
3. Anburani A, Shalini, TB. Path co-efficient analysis in dolichos bean [*Dolichos lablab* (Roxb.) L. var. *typicus*]. The Asian Journal of Horticulture. 2013;8(2):440-443.
4. Cook BG, Pengelly BC, Brown SD, Donnelly JL, Eagles DA, Franco MA, Hanson J, Mullen BF, Partridge IJ, Peters M, Schultze-Kraft R. Tropical forages: an interactive selection tool. *Lablab purpureus*; 2005.
5. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 1959;51: 515-518.
6. Gnanesh BN, Sekhar MR, Reddy KR, Eswarareddy NP. Genetic variability, character association and path analysis of pod yield and its component characters in field bean (*Lablab purpureus* L. sweet). GEOBIOS. 2006;33: 163-168.
7. Hadavani K, Mehta DR, Raval LJ, Ghetiya KP. Genetic Variability Parameters in Indian bean (*Lablab purpureus* L.). International Journal of Pure Applied Bioscience. 2018;6(4): 164-168.
8. Kamble SS, Devmore JP, Sawardekar SV, Bhawe SG, Palshetkar MG. Correlation and path coefficient analysis for yield and yield components in segregating (F₄) generation of lablab bean (*Lablab purpureus* L. Sweet). International Journal of Applied Biology and Pharmaceutical Technology. 2015;6(3): 237-240.
9. Kyada AD, Kale BH, Jwala Pranati, Patel GM, Patel DP, Prajapati MR, Modha KG, Patel RK. Genetic variability, character association and path coefficient analysis in determinate F₅ progenies of Indian bean [*Lablab purpureus* (L.) Sweet]. Electronic Journal of Plant Breeding. 2022;13(2): 319-324.
10. Naeem M, Shabbir A, Ansari AA, Aftab T, Khan MMA, Uddin M. Hyacinth bean (*Lablab purpureus* L.)-An underutilised crop with future potential. Scientia Horticulturae. 2020; 272.
11. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi; 1978.
12. Patel AG, Modha KG, Kale BH, Patel RK. Variability Analysis in Determinate F₄ Progenies for Yield and it's Attributes in Indian Bean [*Lablab purpureus* (L.) Sweet]. Agricultural Science Digest. 2022; DOI: 10.18805/ag.D-5486.

13. Peer SS, Reddy PSS, Sadarunnisa S, Reddy DS, Pandravada S R. Genetic variability and heritability for yield and yield attributes in field bean (*Lablab purpureus* L.) genotypes. International Journal of Current Microbiology and Applied Sciences. 2018;7(3): 2131-2137.
14. Popat R, Patel R, Parmar D. variability: Genetic Variability Analysis for Plant Breeding Research. R package version 0.1.0. 2020; <https://CRAN.R-project.org/package=variability>
15. Raghu BR, Samuel DK, Mohan N, and Aghora TS. Dolichos bean: An underutilized and unexplored crop with immense potential. International Journal of Recent Advances in Multidisciplinary Research. 2018; 5(12): 4338-4341.
16. R Core Team R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. 2021; URL <https://www.R-project.org/>.
17. Sheahan CM. Plant Guide for Lablab (*Lablab Purpureus*). USDA-Natural Resources Conservation Service, Cape May Plant Materials Center. 2012; Cape May, NJ 08210.
18. Singh RK, Chaudhry BD. Biometrical Methods In Quantitative Genetic Analysis. Kalyani Publishers, NewDelhi; 1979.