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RESEARCH ARTICLE

Estimation of genetic parameters and variance components in biparental progenies of lablab bean (*Lablab purpureus* L.)

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Abstract

The existing variation in the lablab bean is limited primarily owing to its self-pollination. Hence, bi-parental mating was attempted in the F_3 generation of a cross between Arka Swagat × S.16. A study was conducted using 32 biparental progenies (BP_1), derived from a North Carolina Design II (NCD II) mating design to evaluate genetic variability, heritability and gene action for yield and related traits in lablab bean (*Lablab purpureus* L.) under a randomized block design with two replications. Analysis of variance revealed significant differences among sets for key traits, including number of flowers per inflorescence, pod width, number of pods per plant, shelling percentage and pod fresh weight, indicating substantial genetic variability. The genetic analysis indicated that pod yield per plant exhibited the highest estimates for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad-sense) and genetic advance as percent of mean (GAM). Similarly, high values for these parameters were observed for the number of pods per plant and the number of flowers per inflorescence. Shelling percentage and pod width exhibited moderate to high GCV, PCV, heritability and GAM, suggesting good scope for selection. Traits such as the number of inflorescences per plant and primary branches per plant showed moderate heritability but lower GAM, indicating a limited response to selection. In contrast, the number of seeds per pod, pod fresh weight and pod dry weight were characterized by low heritability and low GAM, reflecting a greater influence of non-additive gene effects and environmental factors. Narrow-sense heritability was highest for shelling percentage, pod yield per plant, number of flowers per inflorescence, pod width and number of pods per plant, whereas moderate narrow-sense heritability was recorded for the number of primary branches per plant, seeds per pod, pod fresh weight and pod dry weight. The average degree of dominance exceeded unity for all traits, indicating the presence of partial to overdominance gene action in the inheritance of the traits studied. Overall, pod yield per plant and its major contributing traits emerged as reliable selection criteria for genetic improvement in lablab bean.

Keywords: biparental mating; dolichos bean; gene action; genetic advance; heritability; lablab bean; variability

Introduction

Dolichos or lablab bean (*Lablab purpureus* L.) (2n = 2x = 22), commonly known as Indian bean, hyacinth bean, sem and simba, belongs to the family Fabaceae and is one of the prominent vegetable crops widely used in Indian cuisine (1). It is native to the Indian subcontinent (2). The pod are nutritionally rich, containing protein (0.81-5.92 g 100 g^{-1}), vitamin C (2.49-7.87 mg 100 g^{-1}), phenol (0.84-3.17 mg g^{-1}), calcium (3.45-39.51 ppm), iron (8.80-34.32 ppm), copper (1.10-11.88 ppm), manganese (4.14-26.27 ppm), zinc (25.30-57.50 ppm), phosphorous (16.24-50.21 %) and potassium (8.65-75.19 %) (3). Among the legumes, Indian bean possesses considerable pharmaceutical and therapeutic value, as it constitutes include anthocyanins, predominantly in purple pod types, which act as potent antioxidants and ascorbic acid, which is used to prevent and treat scurvy, a disease caused by vitamin C deficiency, in both modern and traditional systems of medicine (4).

It is considered a multipurpose crop, as it is used for vegetable production, forage, weed control, soil improvement and soil conservation (5). The productivity potential of lablab bean remains low, as only a limited number of improved varieties have been developed and the crop is highly photosensitive. Hence, there is a pressing need to develop and promote high-yielding dolichos bean varieties in the state. The natural selection over the years in legumes operated towards increasing the potential for survival and wider adoption at the cost of yield traits (6). Further, the genes contributing to higher yield seem to be scattered in the natural

population. Therefore, it is advocated that extensive hybridization involving a larger number of parents of diverse origin should be adopted to synthesise broad based gene pool (6, 7).

Breeding programs for vegetable-type lablab bean varieties should prioritize a defined set of agronomic and quality traits. An ideal phenotype should combine high yield, short duration from planting to harvest, prolific pod bearing and photo-insensitivity to ensure stable and reliable production. From a consumer perspective, selection should favour pods with fleshy and tender pod walls and moderate seed size, thereby aligning varietal development with the market preferences.

Biparental mating refers to crossing among randomly selected plants in F_2 or subsequent generation of a cross in a predetermined manner. The approach was first proposed and systematically described in classical genetic studies (8). It is an important method of concentrating favourable genes in a population. Biparental mating causes forced recombination and breakdown of tight linkages, mostly in the repulsion phase. As a consequence, rare recombinants which remain restricted due to linkage disequilibrium are exposed in the population. It is a useful system of mating for rapid generation of variability. Biparental mating could also be of great use in creating new populations with high frequencies of rare recombinants. Rare recombinants usually being raised by traditional breeding approach when desired genes are unfavourably linked and could not understood properly in small segregating populations. It also avoids the early fixation of genes in a homozygous state and provides a greater variability for selection to be effective for a longer period.

The yield potential in dolichos beans has remains largely static over the years. Therefore, the biparental mating approach was adopted in the present investigation to assess the pattern of variability among biparental progenies (BP_1) and to exploit this variability for yield improvement.

Materials and Methods

Location of the experiment

The experiment was carried out at Central Horticultural Experiment Station (CHES), ICAR- Indian Institute of Horticultural Research (IIHR), Aiginia, Bhubaneswar, Odisha, India (22 0 15' N and 85 0 15' E, 25.5 m above mean sea level). The soils of the experimental site were of a red laterite type, slightly acidic, with a low water-holding capacity and poor nutrient status.

Experimental material and mating design

In the F_3 generation of a cross (Arka Swagat × S.16) of 2 set of 4 male and 4 female, bi-parental mating was performed in North Carolina Design-II (NCD-II) format. The crosses were performed with four randomly selected males and female parents in two sets. In each set, each female was crossed with all the males. The evaluation of the 32 BP_1 was carried out for the quantitative traits.

Season and year of the experiment

The crosses for the BP_1 were made on rabi 2023-24 and the resulting BP_1 were raised during rabi, 2024-25. The seeds were sown in the last week of September and the first week of October during the 2024-25 season.

Experimental design

The 32 bi-parental progenies were laid out in a randomised block design (RBD) with two replications. The seeds were sown at a spacing of 90 × 60 cm. The spacing was wider than the recommended spacing to facilitate easy and accurate observation of individual progeny plants, as closer spacing leads to intertwining of vines of adjacent plants, thereby hindering precise observations on individual plants.

Statistical analyses

The statistical analyses for each observed trait under the study were carried out utilising R, OPSTAT and GRAPES software packages. MS Excel was used for data preparation, organization and preliminary calculations. Analysis of variance (ANOVA) based on the NCD-II was used to estimate the genetic effects for the BP_1, whereas ANOVA under a RBD was used for the estimation of genetic parameters and correlation analyses.

Estimation of genetic variability parameters for BP_1

Genotypic variance and phenotypic variance: Phenotypic and genotypic components of variance were estimated by using the below given formulas (9):

$$\text{Genotypic variance } (\sigma g^2) = \frac{\text{MSS due to genotypes - MSS due to error}}{\text{Number of replications}} \quad \text{(Eqn. 1)}$$

Phenotypic variance = Genotypic variance (s_g^2) + Error variance (s_e^2)

Where, MSS = mean sum of square.

Coefficient of variability: Both phenotypic and genotypic coefficients of variability for all characters were estimated by using the below given formulas (10):

$$\text{Phenotypic coefficient of variability (PCV \%) } = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100 \quad \text{(Eqn. 2)}$$

$$\text{Genotypic coefficient of variability (GCV \%)} = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100 \quad \text{(Eqn. 3)}$$

The PCV and GCV estimated as follows (11): low: <10 %; moderate: 10-20 %; high: >20 %.

Heritability in broad sense (h^2_{bs}): The broad sense heritability (h^2_{bs}) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance (12).

$$\text{Heritability } (h^2_{bs}) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100 \quad \text{(Eqn. 4)}$$

The heritability estimates can be placed in the following categories (13): low: <30 %; moderate: 30-60 %; high: >60 %.

Genetic advance (GA): The expected genetic advance for each character was estimated by using the below given formula (14):

$$GA = h^2_{(bs)} \times s_p \times K \quad \text{(Eqn. 5)}$$

Where,

$h^2_{(bs)}$ = Heritability estimate in broad sense

s_p = Phenotypic standard deviation of the trait

K = Selection intensity constant which is 2.06 at 5 % selection intensity

Genetic advance was classified as low (<10 %), moderate (10 -20 %) and high (>20 %). Further, the genetic advance as % of mean was computed by using the following formula.

$$\text{Genotypic advance as \% of mean (GAM)} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100 \quad \text{(Eqn. 6)}$$

Results

Analysis of the variation of biparental mating (NCD-II)

The analysis of variance for the biparental mating (BPM) ANOVA revealed significant differences among the sources of variation for several traits in the segregating material (Table 1). Significant mean sum of squares due to sets were observed for the number of flowers per inflorescence, pod width, shelling % and pod fresh weight. Replications showed significant differences for the number of flowers per inflorescence, pod width, number of pods per plant, shelling % and pod fresh weight.

Among males within sets, significant differences were observed for the number of flowers per inflorescence, pod width, number of pods per plant, pod yield per plant, shelling % and pod fresh weight. Females within sets exhibited significant variation for the number of flowers per inflorescence, pod width, number of pods per plant, pod yield per plant, number of seeds per pod, shelling %, pod fresh weight and pod dry weight. The interaction between females and males within sets was significant for the number of primary branches per plant, number of inflorescences per plant, the number of flowers per inflorescence, pod width, number of pods per plant, shelling % and pod fresh weight.

Genetic parameters among BP_1 for various traits

Estimates of genetic parameters revealed substantial variability among the genotypes for most traits (Table 2). Pod yield per plant showed the highest GCV (40.74 %), PCV (49.64 %), heritability (67.37 %) and GAM (68.88 %). Number of pods per plant and number of flowers per inflorescence also recorded high GCV (37.31 and 31.95, respectively), PCV (48.36 and 41.01), heritability (59.53 and 60.67 %) and GAM (59.30 and 51.26 %). Shelling percentage and pod width also exhibited moderate to high GCV (30.85 and 30.48), PCV (38.27 and 42.23), heritability (65.00 and 52.09 %) and GAM (51.24 and 45.32 %). Number of inflorescences per plant and the number of primary branches per plant showed moderate heritability values (39.66 and 42.55 %) with lower GAM (27.86 and 29.24 %). In contrast, traits such as the number of seeds per pod, pod fresh weight and pod dry weight showed low heritability (19.92, 5.39 and 21.14 %, respectively) and low GAM (11.50, 3.04 and 14.62 %).

Genetic components and the narrow-sense heritability of various traits among the BP_1

Analysis of genetic components revealed considerable variability for all traits (Table 3). Narrow-sense heritability was highest for shelling percentage (71.61 %), pod yield per plant (70.27 %), number of flowers per inflorescence (69.95 %), pod width (64.76 %) and number of pods per plant (65.12 %), while moderate heritability was recorded for number of primary branches per plant (50.83 %), number of seeds per pod (32.08 %), pod fresh weight (27.22 %) and pod dry weight (33.32 %). Additive variance was greater than dominance variance for traits such as pod yield per plant (additive variance: 143103.62; dominance variance: 35579.07), number of pods per plant (2658.61; 963.95) and shelling percentage (610.03; 174.13), while dominance variance exceeded additive variance for pod fresh weight (2.683; 5.318) and pod dry weight (0.439; 0.535). The ratio of additive to dominance variance was high for pod yield per plant (4.02), shelling percentage (3.50), number of flowers per inflorescence (2.88) and number of pods per plant (2.76). The average degree of dominance was greater than one for all the traits, indicating overdominance.

Table 1. Bi-parental mating (NCD-II) ANOVA of various characters

		MSS											
SV	**Df**	**DG**	**SD**	**NPBP**	**NIP**	**NFI**	**DFF**	**DFH**	**PL**	**PW**	**NPP**	**PYP**	**NSP**
Sets	1	1.000	0.442	1.563	49.000	30.250*	189.06	150.063	1.005	2.739*	2425.56*	4128.06	0.900
Replications	2	0.621	1.475	0.855	45.858	15.672*	132.46	156.245	1.338	1.375*	1577.30*	10345.94	0.475
Males in sets	6	2.000	5.420	1.240	83.458	18.375*	374.41	334.906	4.386	1.209*	2996.66*	148489.91*	1.149
Females in sets	6	4.500	15.256	7.250	637.500	47.625*	838.42	1048.917	14.653	2.874*	9521.92*	509423.58*	3.508*
Females × males in sets	18	1.763	19.400	1.060*	102.98*	3.742*	352.69	840.827	13.922	0.277*	942.06*	42749.51	0.990
Residuals	30	1.017	11.541	0.579	58.730	1.200	202.78	494.080	8.264	0.075	460.08	24959.98	0.562
SV	**Df**	**SL**	**SW**	**ST**	**100SW**	**SP**	**PFW**	**PDW**	**MP**	**PIP**	**PS**	**CAR**	**PHE**
Sets	1	1.703	0.001	0.003	0.325	732.90*	25.398*	0.647	122.004	0.233	0.336	2.031	0.770
Replications	2	1.749	0.881	0.569	8.319	377.06*	12.805*	0.338	97.957	0.548	4.399	1.517	0.779
Males in sets	6	0.913	1.993	0.323	26.284	635.38*	7.023	1.192	100.763	3.035	16.310	2.446	0.623
Females in sets	6	7.482	4.821	2.568	258.735	2114.36*	12.734*	1.789*	199.113	3.155	33.457	4.757	3.910
Females × males in sets	18	14.879	7.970	4.079	109.256	154.82*	4.513*	0.612	509.538	2.874	57.550	5.370	1.746
Residuals	30	8.811	4.723	2.410	64.999	67.75*	1.854	0.345	299.192	1.688	34.236	3.121	0.996

DG - days to germination, SD - stem diameter (mm), NPBP - number of primary branches per plant, NIP - number of inflorescence per plant, NFI - number of flowers per inflorescence, DFF - days to first flowering, DFH - days to first harvest , PL - pod length (cm), PW - pod width (cm), ANPP - average number of pods per plant, PYP - pod yield per plant (g), SP - shelling percentage (%), PFW - pod fresh weight (g), PDW (g) - pod dry weight (g), NSPP - number of seeds per pod, SL - seed length (cm), SW - seed width (cm), ST - seed thickness (cm), 100 SW (g) -100 seed weight (g), MP - moisture percentage (%), PIP-protein in pods (mg per 100 mg), PMS - protein in mature seed (mg per 100 mg), CAR - carbohydrate (mg per 100 mg) and PHE - phenol (mg per 100 mg).

Table 2. Genetic parameters among bi-parental progenies for various traits

Traits	Mean	GCV	PCV	H_2	GAM
NPBP	3.22	79.36	97.34	81.53	91.91
NIP	29.31	741.14	941.50	78.72	91.46
NFI	6.88	286.72	304.19	94.26	128.53
PW (cm)	1.71	75.41	79.79	94.51	132.47
ANPP	80.59	4494.85	5065.72	88.73	144.21
PYP (g)	555.72	32153.44	36644.91	87.74	146.07
NSP	3.09	49.29	67.47	73.06	69.95
SP (%)	46.93	1670.76	1815.12	92.05	117.35
PFW (g)	6.96	114.88	141.51	81.18	75.02
PDW (g)	2.06	47.36	64.12	73.86	84.55

NPBP - number of primary branches per plant, NIP - number of inflorescences per plant, NFI - number of flowers per inflorescence, PW - pod width (cm), ANPP - average number of pods per plant, PYP - pod yield per plant (g), NSP - number of seeds pod, PFW - pod fresh weight (g) and PDW (g) - pod dry weight (g).

Table 3. Components of variance and narrow sense heritability of various traits

Traits	Environmental	F × M	Males	Females	Additive variance	Dominant variance	Additive/ dominance Ratio	Average degree of dominance	Narrow sense heritability
NPBP	0.579	0.240	0.023	0.774	1.593	0.962	1.656	4.622	50.834
NFI	1.200	1.271	1.829	5.485	14.629	5.083	2.878	1.179	69.952
PW	0.075	0.101	0.116	0.325	0.882	0.405	2.177	1.319	64.761
ANPP	460.08	240.99	256.82	1072.48	2658.61	963.95	2.76	1.37	65.12
PYP	24959.98	8894.77	13217.55	58334.26	143103.62	35579.07	4.02	1.16	70.27
NSP	0.562	0.214	0.020	0.315	0.669	0.855	0.783	4.641	32.077
SP	67.75	43.53	60.07	244.94	610.03	174.13	3.50	1.20	71.61
PFW	1.854	1.329	0.314	1.028	2.683	5.318	0.504	2.911	27.222
PDW	0.345	0.134	0.073	0.147	0.439	0.535	0.822	1.920	33.316

NPBP - number of primary branches per plant, NIP - number of inflorescence per plant, NFI - number of flowers inflorescence, PW - pod width (cm), ANPP - average number of pods per plant, PYP - pod yield per plant (g), NSP - number of seeds per pod, PFW - pod fresh weight (g) and PDW (g) - pod dry weight (g).

Discussion

Analysis of the variation of biparental mating (NCD-II)

The significant mean sum of squares observed through NCD II ANOVA for sets in traits such as number of flowers per inflorescence, pod width, number of pods per plant, shelling percentage and pod fresh weight suggested the presence of differential performance between the two mating sets, likely attributable to variation in the genetic backgrounds of the parents involved in each set and the presence of diverse alleles within the population.

However, the more critical genetic effects were revealed through the partitioning of variance among males and females within sets. The significant differences among males within sets were observed for several yield related traits including number of flowers per inflorescence, pod width, number of pods per plant, pod yield per plant, shelling percentage and pod fresh weight point towards the influence of additive genetic variance contributed by the male parents. This suggests that selection among male lines could be effectively utilised for the improvement of these traits. Similarly, females within sets exhibited significant variance for a wider range of traits, including pod dry weight and number of seeds per pod, indicating that female lines might also contribute substantially to both additive and non-additive genetic variance.

The significant female × male interaction effects observed for traits such as number of primary branches per plant, number of inflorescences per plant, number of flowers per inflorescence, pod width, number of pods per plant, shelling percentage and pod fresh weight reflected the presence of dominance and/or epistatic interactions. Overall, the findings suggested that the biparental mating approach under NCD II had effectively partitioned the genetic variance, facilitating the identification of traits governed by additive and non-additive effects. Similar results were observed significant variation between the biparental F_3 progenies in dolichos bean for pods per plant and pod yield per plant and comparable observations have also been documented in black gram (15, 16).

Genetic parameters among BP_1 for various traits

Pod yield per plant exhibited the highest values for all the genetic parameters assessed, GCV, PCV, heritability and GAM, suggesting that it was under strong additive genetic control and could be effectively improved through phenotypic selection. Similarly, the number of pods per plant and number of flowers per inflorescence also recorded high GCV, PCV, heritability estimates and GAM values, reinforcing their suitability for selection in early generations. The moderate to high heritability in these traits, coupled with high genetic advance, points towards the influence of additive gene action, facilitating reliable selection outcomes. Shelling percentage and pod width demonstrated moderately high heritability, along with high GCV and GAM. These traits were also promising candidates for selection, given their reasonably high genetic variability and potential gain under selection pressure.

Moderate heritability but relatively lower GAM of number of inflorescences per plant indicated that although genetic factors are partially involved in the expression of these traits, the expected response to selection may be moderate and might require more than one cycle of selection for noticeable improvement. The high discrepancy between PCV and GCV in these traits reflected a strong influence of environmental factors, suggesting that selection based on phenotype alone would be less effective.

An increase in phenotypic variance was observed in progenies obtained from biparental mating in the F_2 generation of garden pea for pod yield per plant, number of pods per plant and number of seeds per pod. Similarly, an increase in genetic variance of BP_1 for pod yield per plant and plant height in cross I and for number of pods per plant in both crosses, has been reported previously (17).

Genetic components and the narrow-sense heritability of various traits among the BP_1

The analysis of genetic components revealed substantial variability for all traits, indicating the scope for effective selection in BP_1 of lablab bean. Higher narrow-sense heritability estimates of shelling percentage, pod yield per plant, number of flowers per inflorescence, pod width and number of pods per plant suggested that these traits were largely governed by additive gene action and could be improved through selection in further generations. Moderate narrow-sense heritability of the number of primary branches per plant, number of seeds per pod, pod fresh weight and pod dry weight reflected the possible influence of both additive and non-additive gene effects, making the realisation of complete genetic gains through selection difficult.

High additive component of variance over dominance variance for key yield-contributing traits, which had high narrow-sense heritability, such as pod yield per plant, number of pods per plant, shelling percentage, pod width and number of flowers per inflorescence, further confirmed their possible improvement through selection. In contrast, dominance variance was greater for pod fresh weight and pod dry weight, suggesting a stronger role of dominance effects in their inheritance. Interestingly, the average degree of dominance exceeded unity for all the traits, indicating overdominance. This suggested that while additive effects were important for many traits, non-additive gene effects also played a substantial role, which may be exploited through hybridisation strategies.

Corroborating our findings higher additive component and narrow sense heritability for pods per plant and yield per plant in BP_1 were identified in dolichos bean have also reported higher magnitudes of additive variance in chickpea (15, 18-20). Contrastingly, another study reported higher magnitude of dominance genetic variance than the additive genetic variance for traits such as days to 50 % flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, number of pods per plant, seed diameter, seed yield per plot, biological yield per plot and harvest index, except for 100 seed weight, which had higher additive variance, in chickpea among a biparental mating progeny (19). In their experiment, all the traits exhibited low to moderate narrow sense heritability. In black gram, the dominance variance was high for pods per plant, while additive variance was high for 100-seed weight and number seeds per pod in NCD - III crosses. Very high narrow sense heritability for pods per plant and 100 seed weight was observed previously (16).

Conclusion

The NCD II biparental mating analysis revealed substantial genetic variability among lablab bean progenies for major yield and morphological traits. Significant variation among sets, males, females and their interactions reflected diverse parental backgrounds and effective allelic recombination. Although environmental effects were observed, genetic factors contributed predominantly to observed trait variability. Additive genetic effects from both male and female lines indicated strong selection potential, while significant female × male interactions suggested the presence of non-additive gene action. Overall, NCD II efficiently partitioned genetic components, supporting the application of pedigree and recurrent selection for the improvement of pod yield and associated traits.

In BP_1, high additive genetic variance and narrow-sense heritability for pod yield per plant, number of pods per plant, shelling percentage, pod width and number of flowers per inflorescence confirmed their amenability to improvement through selection. These findings elucidate the capacity of biparental mating to enhance genetic variation and trait improvement in self-pollinated crops such as lablab bean.

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Authors' contributions

The research was conceptualized by KKM, SKD and AVK, who also designed the experiments. Experimental materials were contributed by AVK and KKM. The field and laboratory experiments, along with data collection, were carried out by KKM, AVK and SKD. Data analysis and technical guidance were provided by KKM, AVK, MD and PT. The manuscript was prepared by KKM, AVK, SKD, PT, GSS and SS, while modifications, revisions and overall coordination were undertaken by KKM, AVK, MD, PT and SKD. All the authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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