

MORPHOLOGICAL EVALUATION OF RECOMBINANT INBRED LINE POPULATION FOR GENETIC PARAMETERS IN

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Abstract

The present study comprised of 154 RILs developed from four different crosses in Indian bean. This RIL population was evaluated in augmented design along with five different checks during kharif-rabi 2021-22 to study variability parameters. Analysis of variance unveiled significant genotypic mean square values for all six traits in present study indicating presence of sufficient variability in RIL population. High estimates of GCV and PCV were observed for plant height, racemes per plant, pods per plant and seeds per pod. Less difference between GCV and PCV values for these traits indicated less environmental influence. Moreover, higher magnitude of broad sense heritability coupled with higher genetic advance was observed for all the traits except seeds per pod indicated involvement of additive gene effects and less impact of environment. Thus, there is ample scope for improvement of these traits through simple selection.

Keywords: Variability, Augmented design, Recombinant Inbred Lines, Indian bean

Introduction

Indian bean [*Lablab purpureus* (L.) Sweet] is a food-grain legume and predominantly a self pollinated crop with chromosome number $2n = 22$ (Goldblatt, 1981). The genome size of Indian bean is 367 Mb and number of protein coding genes are 20,946 (Missanga, Venkataramana, and Ndakidemi 2021). It is a minor pulse crop belonging to family Fabaceae and tribe phaseoleae. Indian bean is evidenced to be originated in Indian subcontinent (Nene 2006). However, some reports also showed its origin in Eastern and Southern Africa (Maass 2016). Some of the frequent names used for Indian bean are lablab bean, field bean, hyacinth bean, dolichos bean, carpet legume and poor man's bean (Magoon, Singh, and Mehra 1974). In Gujarat Indian bean is popular as "Papdi, Valor and Wal". The name "Lablab" is an Arabic or Egyptian name describing the dull rattle of the seed inside the dry pod. It is a multi-purpose crop grown as vegetable (immature soft green pods and immature grains) and dried seeds are used as split pulse. Being a legume, it fixes atmospheric nitrogen, hence famous as intercrop to enrich soil fertility. It is used as fodder, forage and cover crop (Magoon, Singh, and Mehra 1974). This crop is grown either as a sole crop or intercropped with finger millet, groundnut, castor, corn, pearl millet and sorghum (Keerthi et al. 2014). Indian bean is a good source of vegetable proteins because its seeds and pods contain 20-28 % protein (Devaraj 2016; Habib et al. 2017) and therefore could be a part of major protein source in human diet for the vegetarian population.

Success of crop improvement programme in any crop depends upon the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. Variability in the population especially for the character, for which improvement is sought, is a pre-requisite for successful selection (Tyagi and Khan 2008). The seed yield is a complex and multiplicative character, which is highly influenced by environmental variations. The assessment of the variation in the yield determining quantitative traits of crop has become primary interest in the improvement of yield which could be achieved through directional selections for yield and its contributing traits (Akbar and Kamran 2006). It has been found that yield contributing traits have reliable and predictable effect on grain yields in legumes such as mung bean, pea and pigeon pea (Tyagi and Khan 2008). It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters

using suitable parameters like genetic co-efficient of variability (GCV), heritability estimates (H) and genetic advance (GA). Thus, present study focuses on morphological evaluation of F_7 RILs of Indian bean for quantitative yield attributing traits.

Materials and method

Experimental material consisted 160 genotypes (154 RILs and 5 checks) of Indian bean. F_7 RILs were developed through SSD method from four different determinate $\times$ indeterminate crosses viz., GNIB-21 $\times$ GP-1, GNIB-21 $\times$ GP-167, GNIB-21 $\times$ GP-189 and GNIB-21 $\times$ GPKH-120. Four parents viz., GNIB-21, GP-1, GP-189, GPKH-120 and a released variety GNIB-22 were used as checks. For morphological evaluation, 154 RILs derived from above mentioned crosses along with checks were laid out with checks in Augmented Block Design in kharif-rabi, 2021-2022 at Navsari Agricultural University, Navsari, Gujarat. Each check was replicated in five blocks. Single row comprised 10 plants with 90 cm and 45 cm inter and intra row spacing, respectively. The progenies were randomly assigned to each block. All the recommended agronomic practices along with necessary plant protection measures were followed timely for raising the healthy crop. Mean performances of various morphological traits like days to first raceme emergence, growth habit, plant height (cm), racemes per plant, pods per plant, seeds per pod and seed yield per plant (g) were evaluated for each RIL populations. All the traits except days to first raceme emergence was recorded at physiological maturity.

Statistical analysis

Analysis of variance of the characters was done as per standard statistical procedure for Augmented Design given by Federer (1956). The genotypic and phenotypic coefficient of variation were estimated as per the formula suggested by Burton (1952). GCV and PCV were classified as suggested by Burton and Devane (1953). Broad sense heritability was estimated as per the formula given by Allard (1960). The range of heritability in broad sense was classified as suggested by Johnson et al. (1955). Genetic advance as well as genetic advance as per cent of mean for each character were worked out as per the formula given by Johnson et al. (1955). R STUDIO software was used for the above mentioned statistical analysis.

Result and Discussion**Analysis of variance (ANOVA)**

Analysis of variance revealed significant genotypic mean square values for all the traits in RIL population (Table 1). This represents

the presence of sufficient variability among this population which allows efficient selection among the population for improvement of any traits under the study. Similarly, the mean square due to genotypes vs. check was significant for all the traits except plant height and seeds per pod, indicating thereby that the test entries were significantly different from checks except for these two traits (Table 1). However, the adjusted block effects were non-significant for all the traits indicating homogeneity of evaluation blocks. Similar outcomes were reported by Saba *et al.* (2017).

Estimation of genetic variability

Various measures of variability were calculated for the six quantitative traits (Table 2). Frequency distributions, genotypic and phenotypic coefficients of variation, broad sense heritability and genetic advance as per cent of mean of traits under study are represented in graphical form in Fig. 1 to Fig. 9.

Days to first raceme emergence

The variation in number of days to raceme emergence ranged from 34.50 to 84.40 days with mean of 58.99 days (Table 2, Fig. 1). The genotypic variance and phenotypic variance for this trait were 88.98 and 130.95, respectively. Days to first raceme emergence showed a moderate level of GCV (15.99 %) and PCV (10.80 %). A high level of heritability (67.95 %) and high level of genetic advance as per cent of mean (27.19 %) were recorded for this trait (Table 2).

Growth habit

RILs varied in growth habit for determinacy and indeterminacy. Total 55 lines showed indeterminate growth habit and 68 lines showed determinate growth habit.

Plant height (cm)

Plant height ranged from 15.00 cm to 166.40 cm with mean of 59.98 cm in RILs (Table 2, Fig. 2). Genotypic variance and phenotypic variance obtained were 955.45 and 1058.25, respectively. For this trait, high GCV (51.54 %) and PCV (54.24 %) were observed. Additionally, high level of broad sense heritability (90.29 %) coupled with high GAM (101.02 %) was observed for plant height (Table 2).

Racemes per plant

Number of racemes per plant ranged from 2 to 29 with mean of 8.76 (Table 2, Fig. 3). Genotypic and phenotypic variance for this trait were 23.41 and 8.76, respectively. Magnitude of GCV (53.02 %) and PCV (55.25 %) were high for this trait. Additionally, this trait described higher degree of broad sense heritability (92.09 %) and GAM (104.97 %) (Table 2).

Pods per plant

Pods per plant in RILs ranged from 3.00 to 55.60 with mean of 19.90 (Table 2, Fig. 4). The values of genotypic and phenotypic variance were recorded as 126.82 and 119.49, respectively. For this trait, higher GCV (54.94 %) and PCV (56.6 %) were observed. Simultaneously, high broad sense heritability (94.24 %) and genetic advance as percent of mean (110.02 %) were recorded (Table 2).

Seeds per pod

This trait exhibited the mean of 3.42 among the RILs ranging from 3.00 to 4.20 (Table 2, Fig. 5). It showed the genetic variance of 0.11 and phenotypic variance of 0.91. GCV and PCV were recorded 9.74 % (low) and 12.59 % (moderate), respectively. Although, broad sense

heritability (59.96 %) and GAM (15.56 %) both were classified under moderate category (Table 2).

Seed yield per plant

Seed yield for RIL population ranged from 1.66 g to 44.44 g with mean yield of 12.64 g (Table 2, Fig. 6). Genotypic variance and phenotypic variance were measured 50.81 and 57.94, respectively. GCV (56.38 %) and PCV (60.20 %) were recorded high for this trait. Similarly, higher estimates of broad sense heritability (87.70 %) and genetic advance as percent of mean (108.92 %) were observed (Table 2).

In present study, high GCV and PCV were observed for plant height, racemes per plant, pods per plant and seeds per pod. Higher values of GCV and PCV for these traits indicated the greater scope of improving this character by applying the selection in an appropriate direction. Moreover, less difference between estimates of GCV and PCV indicated less influence of the environment and simple selection could be effective for these traits. Similar outcomes were previously reported by some researchers (Afsan and Roy 2019; Eliezah *et al.* 2021; Ingle *et al.* 2020). Moderate values of GCV and PCV were observed for days to first raceme emergence. Similar outcomes for days to first flowering was observed by Nadeem *et al.* (2020). However, seeds per pod showed lower magnitudes of GCV and moderate PCV. Similar results were also obtained by Gamit *et al.* (2020) and Eliezah *et al.* (2021).

Coefficient of variation only describe variation present in genotypes, it does not partition variation into heritable and non-heritable variation. Whereas, heritability shows heritable variation only. Thus, not the magnitude of coefficient of variation but extent of heritability, a heritable variation is what which matters the most to attain desired improvement through selection. Broad sense heritability is the ratio of genetic variance to total variance or phenotypic variance. It includes all three types of genotypic variances *i.e.* additive, dominance and epistatic, confirmation of any one gene effect is not possible to find out as it includes both fixable and non-fixable variances unless couples with genetic advance. Heritability and genetic advance collectively, give thorough indication of gene action, extent of environmental influence and effective improvement strategies. In accordance to that, higher magnitude of broad sense heritability coupled with higher genetic advance was observed for all the traits *viz.*, days to first raceme emergence, plant height, racemes per plant, pods per plant and seed yield per plant indicating role of additive gene effects and less environmental influence. Thus, improvement of these traits can be achieved by simple selection. Similar outcomes were also observed in previous studies (Afsan and Roy 2019; Gamit *et al.* 2020; Ingle *et al.* 2020; Nadeem *et al.* 2020). Seeds per pod described moderate estimates for both, broad sense heritability as well as genetic advance which can be the resultant effect of non-additive gene effects. Thus, this trait could be exploited through manifestation of dominance and epistatic components through recurrent selection as hybrid development is difficult due to cleistogamous nature of Indian bean. These findings are similar to Ingle *et al.* (2020).

Table 1: Analysis of variance for six quantitative traits of RIL population

Source	df	DTRE	PH	RPP	PPP	SPP	SYP
Block	3	47.53 ^{ns}	146.16 ^{ns}	1.48 ^{ns}	0.98 ^{ns}	0.07 ^{ns}	17.21 ^{ns}
Entries	158	150.32 ^{**}	1116.54 ^{**}	23.49 ^{**}	151.1 ^{**}	0.18 [*]	81.56 ^{**}
Check	4	671.37 ^{**}	3619.52 ^{**}	24.32 ^{**}	275.29 ^{**}	0.14 ^{ns}	156.12 ^{**}
Genotypes	153	130.95 [*]	1058.25 ^{**}	23.41 ^{**}	126.82 ^{**}	0.19 [*]	57.94 ^{**}
Genotypes vs. Check	1	1028.92 ^{**}	23.27 ^{ns}	33.37 ^{**}	3367.95 ^{**}	0.01 ^{ns}	3397.86 ^{**}
Block	3	47.53 ^{ns}	146.16 ^{ns}	1.48 ^{ns}	0.98 ^{ns}	0.07 ^{ns}	17.21 ^{ns}
Residuals	12	41.97	102.79	1.85	7.34	0.07	7.13

df : degree of freedom PPP : Pods per plant ** : Significance at 1% level of probability
DTRE : Days to first raceme emergence SPP : Seeds per pod ns : Non-significance
PH : Plant height (cm) SYP : Seed yield per plant (g)
RPP : Racemes per plant * : Significance at 5% level of probability

Table 2 : Measures of variability parameters of all the characters

Traits	Range		Mean	GV	PV	GCV (%)	PCV (%)	h _{bs} ² (%)	GA	GAM (%)	CV (%)
	Min.	Max.									
Days to first raceme emergence	34.50	84.40	59.99	88.98	130.95	15.99	19.40	67.95	16.04	27.19	11.11
Plant height (cm)	15.00	166.40	59.98	955.45	1058.25	51.54	54.24	90.29	60.59	101.02	16.85
Racemes per plant	2.00	29.00	8.76	21.56	23.41	53.02	55.25	92.09	9.19	104.97	15.73
Pods per plant	3.00	55.60	19.90	119.49	126.82	54.94	56.60	94.24	21.89	110.02	12.87
Seeds per pod	3.00	4.20	3.42	0.11	0.91	9.74	12.59	59.93	0.53	15.56	7.96
Seed yield per plant (g)	1.66	44.44	12.64	50.81	57.94	56.38	60.20	87.70	13.77	108.92	19.30

GV : Genotypic variance PV : Phenotypic variance GCV : Genotypic coefficient of variation
PCV : Phenotypic coefficient of variation h_{bs}² : Broad sense heritability GA : Genetic advance
GAM : Genetic advance as percent of mean CV : Coefficient of variation

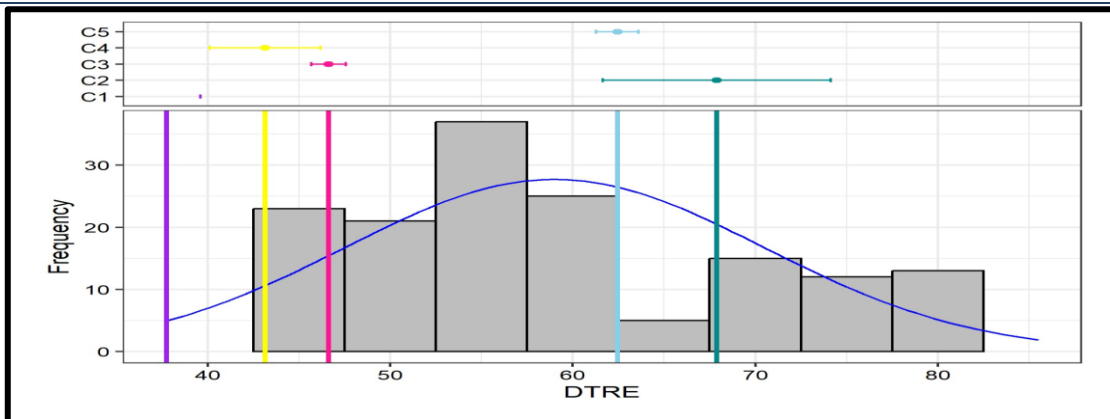


Figure 1: Frequency distribution for days to first raceme emergence (DTRE) in RIL population and checks

C1 : GNIB-21, C2 : GP-1, C3 : GP-189, C4 : GNIB-22, C5 : GPKH-120

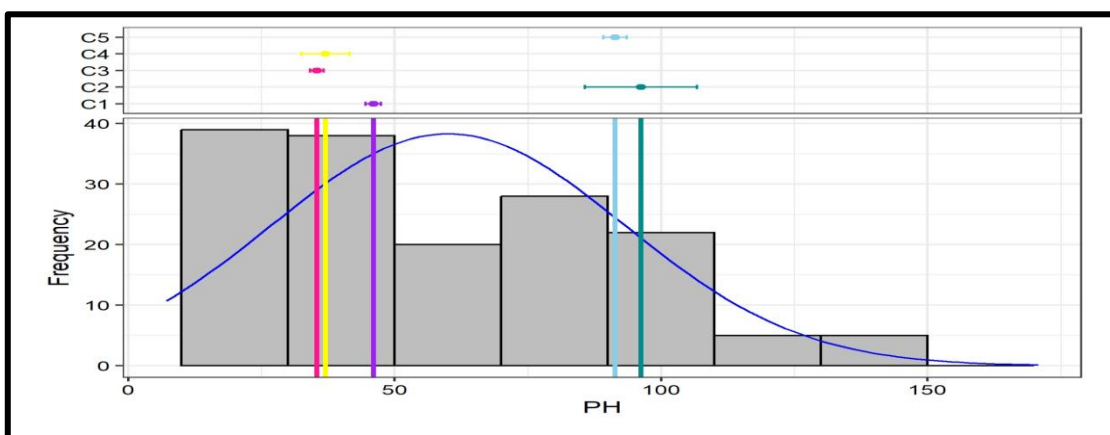


Figure 2: Frequency distribution for plant height (PH) (cm) in RIL population and checks

C1 : GNIB-21, C2 : GP-1, C3 : GP-189, C4 : GNIB-22, C5 : GPKH-120

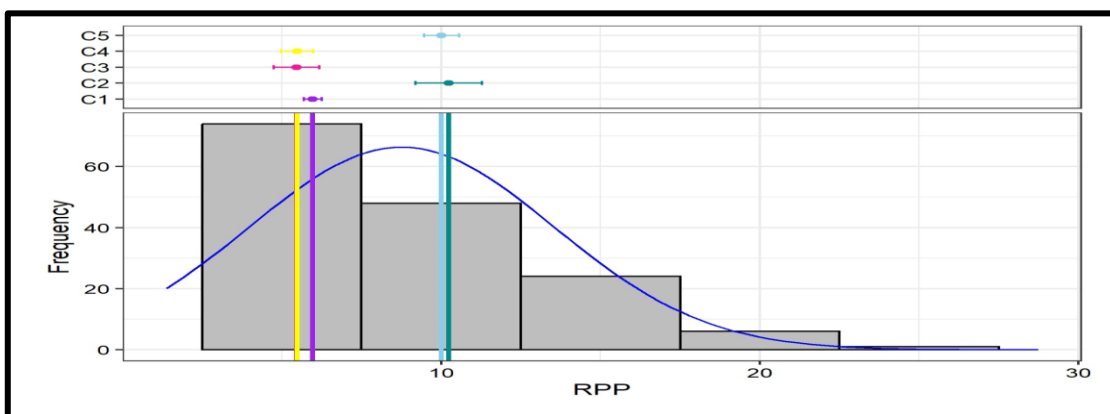


Figure 3: Frequency distribution for racemes per plant (RPP) in RIL population and checks

C1 : GNIB-21, C2 : GP-1, C3 : GP-189, C4 : GNIB-22, C5 : GPKH-120

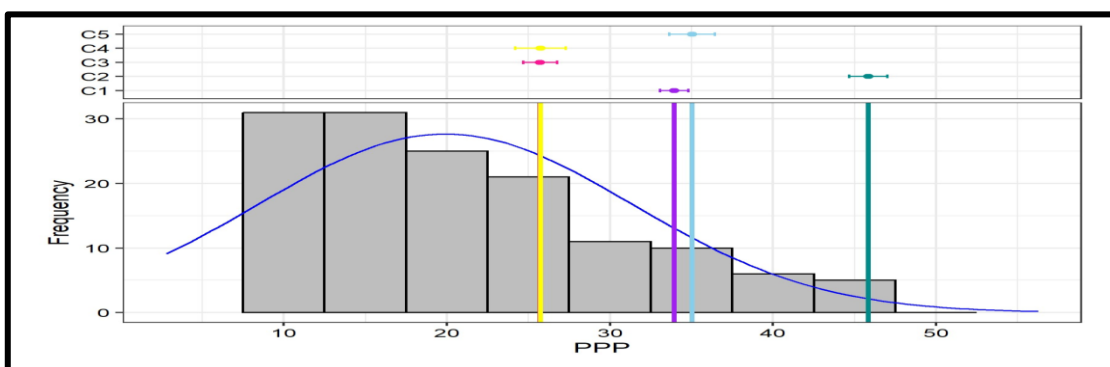


Figure 4: Frequency distribution for pods per plant (PPP) in RIL population and checks

C1 : GNIB-21, C2 : GP-1, C3 : GP-189, C4 : GNIB-22, C5 : GPKH-120

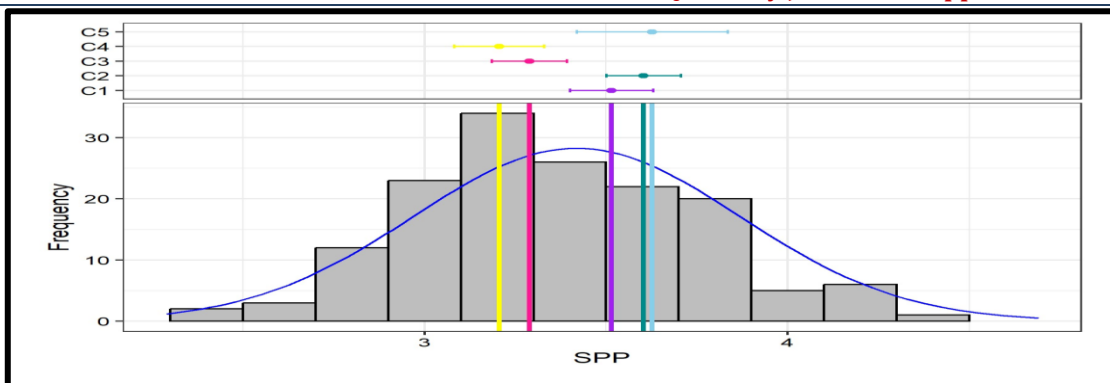


Figure 5: Frequency distribution for seeds per pod (SPP) in RIL population and checks

C1 : GNIB-21, C2 : GP-1, C3 : GP-189, C4 : GNIB-22, C5 : GPKH-120

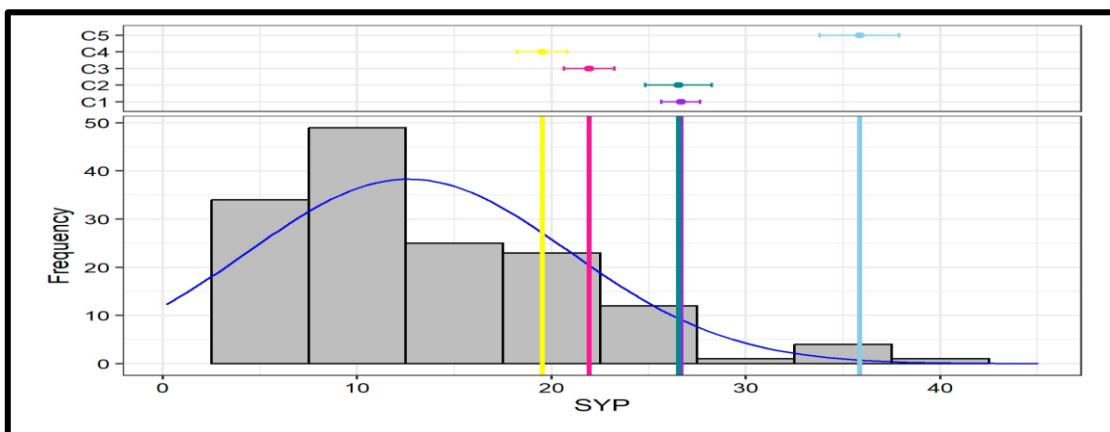


Figure 6: Frequency distribution for seed yield per plant (SYP) (g) in RIL population and checks

C1 : GNIB-21, C2 : GP-1, C3 : GP-189, C4 : GNIB-22, C5 : GPKH-120

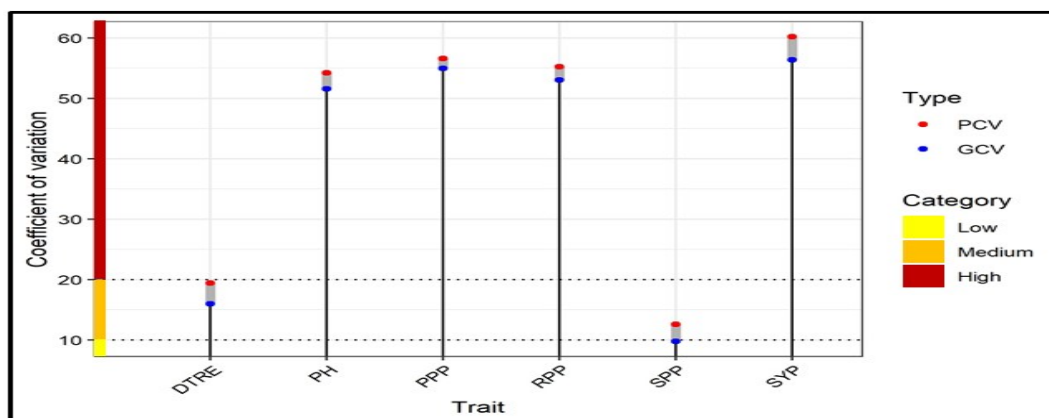


Figure 7: Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for various traits of Indian bean

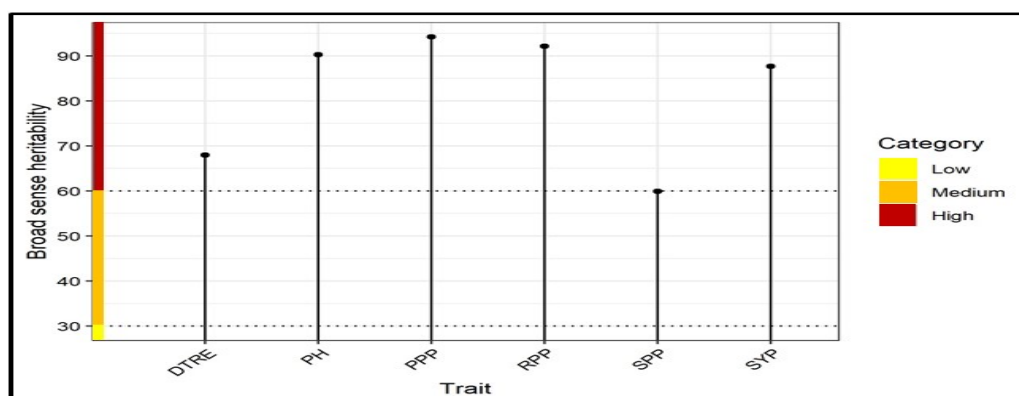


Figure 8: Broad sense heritability for quantitative traits in RILs of Indian bean

DTRE - Days to first raceme emergence RPP - Racemes per plant
PH - Plant height (cm) SPP - Seeds per pod
PPP - Pods per plant SYP - Seed yield per plant (g)

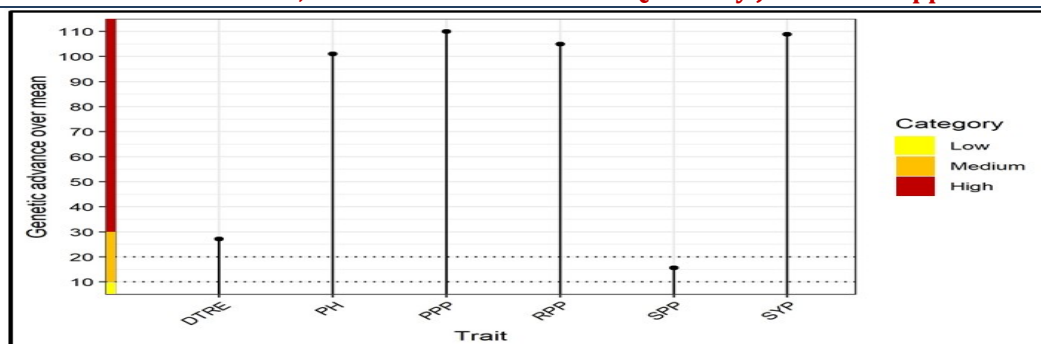


Figure 9: Genetic advance as percent of mean for quantitative traits in RILs of Indian bean

DTRE - Days to first raceme emergence RPP - Racemes per plant
 PH - Plant height (cm) SPP - Seeds per pod
 PPP - Pods per plant SYP - Seed yield per plant (g)

Conclusion

Evaluation of 154 RILs in present study indicated wide range of variability for various quantitative traits under study in Indian bean. As per the results obtained in this study, high broad sense heritability coupled with high genetic advance was observed for days to first raceme emergence, plant height, racemes per plant, pods per plant and seed yield per plant indicating role of additive gene effects and less influence of environment. Thus, improvement of these traits could be achieved by simple selection in appropriate direction. Seeds per pod described moderate estimates for both, broad sense heritability as well as genetic advance which can be resultant effect of non-additive gene effects. Thus, this trait could be exploited through manifestation of dominance and epistatic component through recurrent selection.

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