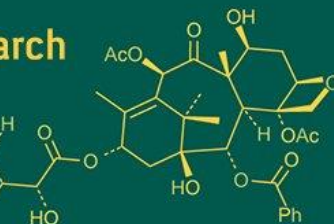
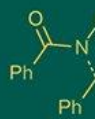


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(7): 1933-1937
www.biochemjournal.com
Received: 20-05-2026
Accepted: 24-06-2026

R Kirankumar
Department of Genetics and
Plant Breeding, College of
Agriculture, University of
Agricultural Sciences, GKVK,
Bengaluru, Karnataka, India

MD Valeeta
¹Department of Plant
Biotechnology, College of
Agriculture, UAS, GKVK,
Bengaluru, Karnataka, India
²Department of
Biotechnology, St. Joseph's
University, Lalbagh Road,
Bengaluru, Karnataka, India

M Byregowda
AICRP on Pigeonpea, ZARS,
UAS, GKVK, Bengaluru,
Karnataka, India

S Ramesh
Department of Genetics and
Plant Breeding, College of
Agriculture, University of
Agricultural Sciences, GKVK,
Bengaluru, Karnataka, India

Assessment of genetic variability, heritability and genetic advance among determinate F₄ progenies in Dolichos bean (*Lablab purpureus* L. var. *typicus*)

R Kirankumar, MD Valeeta, M Byregowda and S Ramesh

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i7Sw.9340>

Abstract

Dolichos bean (*Lablab purpureus* L. var. *typicus*) is an economically important vegetable legume cultivated for its tender green pods. The success of crop improvement depends on the availability of genetic variability and the identification of heritable traits that facilitate effective selection. The present study was undertaken to assess genetic variability, heritability, and genetic advance for yield and its associated traits in F₄ progenies of dolichos bean. The experimental material comprised 281 F₄ progenies derived from ten determinate × indeterminate crosses along with two check varieties, Arka Jay and Avami. The experiment was conducted during Kharif 2018-19 at the Zonal Agricultural Research Station, University of Agricultural Sciences, GKVK, Bengaluru, using an augmented design. Observations were recorded on eight quantitative traits, and the data were analyzed for analysis of variance (ANOVA), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, and genetic advance as *per cent* of mean (GAM). ANOVA revealed highly significant differences among F₄ progenies for all traits, indicating substantial genetic variability. PCV estimates were consistently higher than GCV estimates, suggesting varying degrees of environmental influence on trait expression. Narrow differences between PCV and GCV for fresh pod yield plant⁻¹, fresh pods plant⁻¹, plant height, and days to 50% flowering indicated greater genetic control of these traits. Broad-sense heritability ranged from 15.89% to 89.79%, with the highest estimates recorded for fresh pod yield plant⁻¹, followed by plant height and fresh pods plant⁻¹. High heritability coupled with high GAM for fresh pods plant⁻¹ and fresh pod yield plant⁻¹ indicated the predominance of additive gene action, suggesting that these traits can be effectively improved through direct phenotypic selection. The identified variability provides valuable breeding material for developing high-yielding dolichos bean cultivars.

Keywords: Dolichos bean, F₄ progenies, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance

1. Introduction

Dolichos bean (*Lablab purpureus* L. var. *typicus*) is one of the important legume vegetable crop grown throughout India for its tender green pods especially in Madhya Pradesh, Uttar Pradesh, Tamil Nadu, Andhra Pradesh, Maharashtra, Gujarat and Karnataka. Botanically, it belongs to family Fabaceae with chromosome number 2n=2x=22. Evidently, it is originated in India. Dolichos bean is synonymously known as Indian bean, Egyptian bean, Hyacinth bean, Field bean, Sem, Bonavist bean etc. "Dolichos" is a Greek word meaning "long" and "lablab" is derived from Egyptian or Arabic language to mean "dull rattle of the seed inside the dry pod" (Chaudhury, 1972) [6]. Botanists identify two types of Dolichos bean based on the angle of attachment of seeds to the suture of the pods (Magoon *et al.* 1974) [12]. The *Lablab purpureus* L. var. *typicus* is commonly used for green vegetable and *Lablab purpureus* L. var. *lignosus* is used as a pulse. Longer, flat, and more tapering pods with long axis of seeds parallel to the suture of the pod are the attribute of *Lablab purpureus* var. *typicus*. It finds predominant usage as fleshy and soft whole pods and is often trained due to its twinning habit. *Lablab purpureus* var. *lignosus* is bushy type annual plant. Pods are comparatively shorter and more abruptly truncated and long axis of the seeds is perpendicular to the suture of the pod. It is cultivated for fresh immature seeds used as a vegetable and to a rarely as pulse. The foliage of the crop provides green manure, silage and hay.

Corresponding Author:
R Kirankumar
Department of Genetics and
Plant Breeding, College of
Agriculture, University of
Agricultural Sciences, GKVK,
Bengaluru, Karnataka, India

Crop improvement is a dynamic process focussing on the changing needs and the emerging problems in crop productivity. Availability of naturally existing or generated genetic variability is a prerequisite for any crop improvement as it provides a wide scope for breeder to select. The fruitfulness of selection depends on the variability and its nature, extent, and magnitude. The degree of heritability is another facet of effectiveness of selection. Existing variability has been exploited to the maximum possible extent by selection; thus, there is a need to generate variability afresh by crossing superior diverse genotypes.

Yield is a complex trait controlled by polygenes and to the significant extent by environment. There are ample proofs to show that selection directly for yield in plants is not so effective. The knowledge on existing variability and degree of relationship between economical traits viz., fresh pod yield and its component traits and their relative contribution to fresh pod yield is essential for effective selection. Estimates like heritability and genetic advance are reliable genetic parameters for breeders to impose selection.

Heritability is an important aspect of the genetic constitution of the breeding material, which has a close relevance on the response to selection. "Heritability is the transmissibility of characters from parents to off-springs". It is of great significance in selection as it reflects the reliability of phenotypic value as guide to breeding value. Heritability is a useful indicator of the advance that can be expected by practising selection on the resilient population. However, a measure of heritability alone does not give the information about the expected gain in the next generation, while consideration of genetic advance in conjunction with heritability is more precise. Thus, high yield can be achieved by selection for those characters that have high heritability and genetic advance.

2. Material and Methods

2.1 Experimental site

The experiment was carried out during *Kharif*-2018-19 in the experimental plot of Zonal Agricultural Research Station (ZARS), University of Agricultural Sciences (UAS), Gandhi Krishi Vignana Kendra (GKVK), Bengaluru. The experimental plots are located at an altitude of 930 m above mean sea level (MSL) 12° 58' North and 77° 35' East latitude and longitude, respectively.

2.2 Experimental Material

The material for the study consisted of progenies of 281 selected F₃ determinate selections of *Lablab purpureus* L. var typicus and two checks (Arka Jay and Avami). These F₄ progenies were derived from ten determinate × indeterminate crosses out of 21 crosses made (Table 1).

Table 1: List of ten determinate × indeterminate crosses

Sl. No.	Coded cross No.	Crosses	No. of selected plants in F ₃
1	1	Arka Jay × GLP 44	36
2	2	Arka Jay × GLP 45	24
3	4	Arka Jay × GLP 67	56
4	5	Arka Jay × GLP 68	26
5	6	Arka Jay × GLP 71	15
6	15	Arka Amogh × GLP 45	20
7	16	Avami × GLP 67	13
8	18	Avami × GLP 69	14
9	20	Avami × GLP 72	32
10	21	Avami × GLP 73	45

2.3 Evaluation of experimental material

Progenies of F₃ determinate selections along with two checks (Arka Jay and Avami) were sown at GKVK, Bengaluru during *kharif*-2018-19 following Augmented design (Federer, 1956) [8] in six compact blocks. Each block consisted of 47 determinate F₃ progenies, two checks (replicated thrice) and four border entries. Each entry in each block was sown in a single row of 4 m length, with a spacing of 0.45 m between rows and 0.3 m between plants within a row. A basal dose of 25:50:25 Kg NPK ha⁻¹ was applied to the experimental plot. Recommended agronomic and plant protection practices were followed to raise a healthy crop.

2.4 Data collection

Observations were recorded on 10 randomly selected plants in each entry on eight quantitative characters namely, Plant height (cm), Days to 50% flowering, Racemes plant⁻¹, Raceme length (cm), Primary branches plant⁻¹, Fresh pods plant⁻¹, Fresh pod length (cm) and Fresh pod yield plant⁻¹ (g).

2.5 Statistical analysis

The statistical analysis was carried out using the adjusted trait means of 281 F₄ progenies. Mean values of the 10 randomly selected plants in F₄ progenies and checks were used for statistical analysis. ANOVA was performed following Augmented design (Federer, 1956) [8] using SAS version 9.3 software to examine statistical significance or otherwise of the differences among F₄ progenies. Adjusted quantitative trait means of 281 F₄ progenies were used for estimating eight quantitative traits mean, absolute range (highest - lowest trait mean), standardized range, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability (broad sense) and expected genetic advance as per cent of mean (GAM).

3. Results and Discussion

3.1 Analysis of variance

Exploitation of natural genetic variability is a short-term strategy to meet immediate requirement of the farmers, consumers and end-users. In the past, selection by farmers and/or plant breeders in the available natural genetic variability has resulted in significant genetic improvement in crop productivity. However, continued crop genetic improvement to meet medium- and long-term requirements requires generation of variability induced through deliberately planned crosses among the genotypes harbouring desired combination of traits. Analysis of variance (ANOVA) is a diagnostic tool and a pre-requisite step for preliminary detection of genetic variability in the working genetic material (Govindaraju *et al.*, 2015; Hawkes, 1991) [9, 10].

ANOVA (Table 2) revealed significant variability among F₄ progenies for all the traits. Significant mean squares due to checks for most of the traits suggested considerable variability between the checks for most of the traits. Significant mean squares attributable to 'F₄ progenies vs checks' suggested that F₄ progenies as a unit differed substantially from checks for all traits except raceme length (Table 2). The photograph (Plate 1) is a testimony to considerable variability for pod traits among the 281 F₄ progenies.



Plate 1: Variability for pod traits among the 281 F₄ progenies of the ten crosses

3.2 Genetic variability among F₄ progenies

Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV)

As expected, the magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. The estimates of PCV ranged from 1.78 to 11.72 *per cent* (Table 3; Figure 1). The estimates of PCV were moderate for racemes plant⁻¹ (11.72), compared to those of fresh pods plant⁻¹ and primary branches plant⁻¹ (Table 3; Figure 1). These results were in line with the findings of Chaitanya *et al.* (2014) [4], Sharma *et al.* (2014) [14] and Verma *et al.* (2014) [16].

The estimates of GCV values ranged from 0.99 to 9.42 *per cent* (Table 3; Figure 1). The estimates of GCV were lower for fresh pods plant⁻¹ (9.42) compared to those of fresh pod yield plant⁻¹, racemes plant⁻¹, raceme length, primary branches plant⁻¹, plant height, fresh pod length, and days to 50% flowering (0.99) (Table 3; Figure 1). Similar results were obtained by Chaitanya *et al.* (2014) [4], Sharma *et al.* (2014) [14] and Asaduzzaman *et al.* (2015) [1].

The magnitudes of PCV were higher than those of GCV for all the traits (Table 3; Figure 1). Narrow difference between the estimates of PCV and GCV suggested limited influence of weather variables and edaphic factors on the expression of all the traits except racemes plant⁻¹, raceme length, and primary branches plant⁻¹ (Table 3; Figure 1). These results were in harmony with those of Basu *et al.* (1999) [3] and Chattopadhyay and Dutta (2010) [5]. The narrow differences between PCV and GCV estimates suggests effectiveness of selection of desired genotypes for all the traits under study.

Wider difference between the estimates of PCV and GCV for racemes plant⁻¹, raceme length, and primary branches plant⁻¹ indicating larger influence of environment on the expression of these traits. Similar findings were reported by Bahadur *et al.* (2013) [2], Chaitanya *et al.* (2014) [4] and Asaduzzaman *et al.* (2015) [1].

3.3 Heritability (broad sense)

Heritability provides information regarding the amount of transmissible genetic variation. It also determines response to selection. High heritability estimates are helpful in making selection of superior genotypes apparently from phenotypic performance. In the present study, heritability values ranged from 15.89 to 89.79 *per cent*. The estimates of heritability were high for fresh pod yield plant⁻¹ followed by plant height and fresh pods plant⁻¹ (Table 3; Figure 2). High heritability indicates the effectiveness of selection for these traits. These results were in conformity with those of Magalingam *et al.* (2013) [11], Chaitany *et al.* (2014) [4], Verma *et al.* (2014) [16] and Singh *et al.* (2015) [15]. The estimates of heritability were moderate for fresh pod length, raceme length, racemes plant⁻¹ and days to 50% flowering (Table 3; Figure 2). These findings were in agreement with the findings of Savitha (2008) [13].

3.4 Genetic Advance

The estimates of expected GAM ranged from 4.43 to 29.26 *per cent*. The expected GAM was least for days to 50% flowering and highest for racemes plant⁻¹ followed by primary branches plant⁻¹ and fresh pods plant⁻¹ (Table 3; Figure 2). These results are in accordance with the findings of Magalingam *et al.* (2013) [11], Sharma *et al.* (2014) [14] and Singh *et al.* (2015) [15]. The estimates of expected GAM were moderate for fresh pod yield plant⁻¹ followed by raceme length and fresh pod length (Table 3; Figure 2). These results were in conformity with the findings of Magalingam *et al.* (2013) [11]. The estimates of expected GAM were low for plant height followed by days to 50% flowering. These findings were in agreement with the results of Das *et al.* (2015) [7] and Singh *et al.* (2015) [15].

High heritability coupled with high expected GAM indicated effectiveness of selection for the improvement of fresh pods plant⁻¹ and fresh pod yield plant⁻¹. These results are in line with the findings of Magalingam *et al.* (2013) [11], Sharma *et al.* (2014) [14] and Singh *et al.* (2015) [15].

Table 2: Analysis of variance of Dolichos bean F₄ progenies for quantitative traits

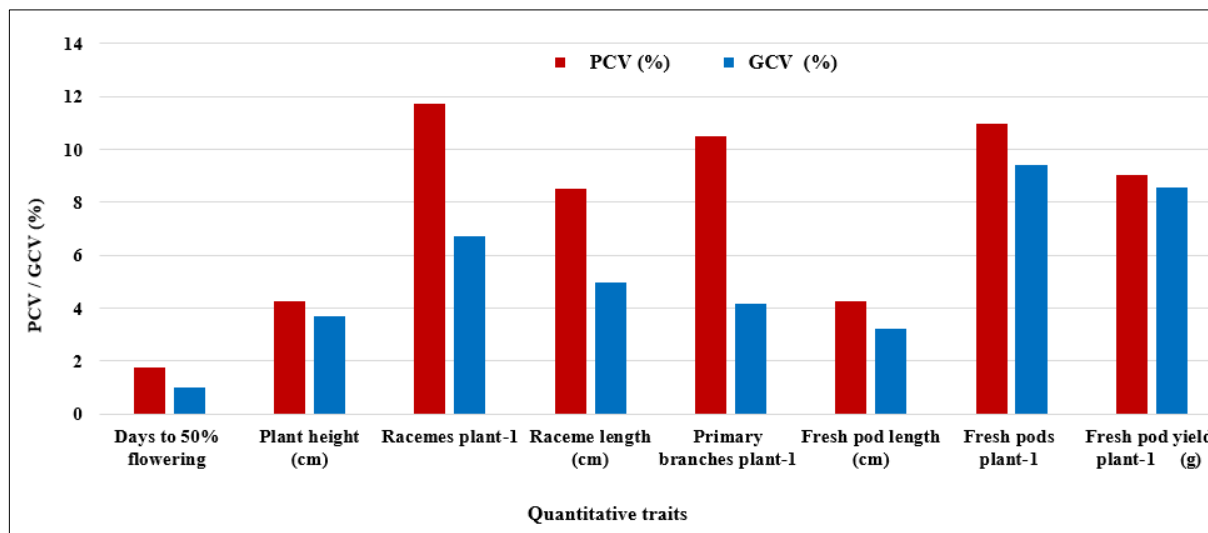
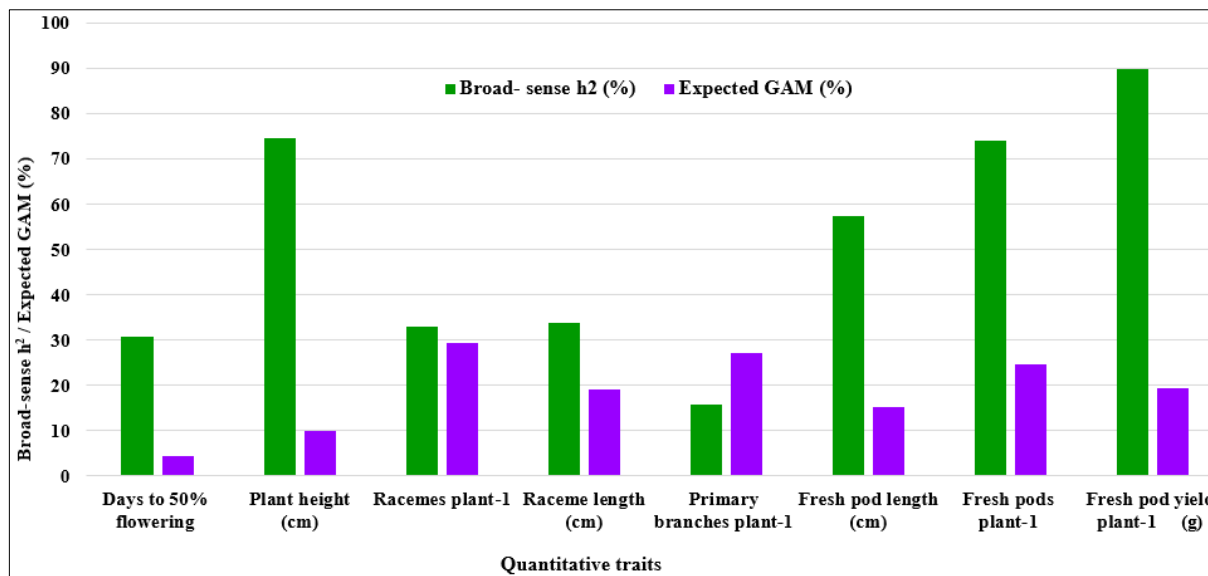
Sources of variation	Degrees of freedom	Mean sum of squares							
		Days to 50% flowering	Plant height (cm)	Racemes plant ⁻¹	Raceme length (cm)	Primary branches plant ⁻¹	Fresh pod length (cm)	Fresh pods plant ⁻¹	Fresh pod yield plant ⁻¹ (g)
Blocks	5	3.18 *	18.87 **	2.54 *	18.13	0.21	0.85 *	62.62	212.49 *
Entries (F ₄ progenies + checks)	282	3.38 **	124.55 **	4.35 **	21.94 **	0.35 **	1.67 **	198.23 **	1288.96 **
F ₄ progenies	280	3.29 **	117.25 **	3.72 **	21.10 **	0.34 **	1.63 **	196.55 **	1281.56 **
Checks	1	5.44 **	1735.00 **	182.56 **	277.39 **	0.05	4.09 **	66.23 **	1065.15 **
F ₄ progenies vs. checks	1	24.82 **	554.61 **	2.27 *	0.33	3.32 **	11.04 **	774.50 **	3604.27 **
Error	29	0.36	2.17	0.38	2.07	0.08	0.06	3.77	8.04

*Significant @ P=0.05 level; **Significant @ P=0.01 level

Table 3: Descriptive statistics for eight quantitative traits of Dolichos bean

Sl. No.	Traits	Mean $\pm$ SE	Range		Standardized range	Coefficient of variability		Broad-sense h^2 (%)	Expected GAM (%)
			Min	Max		PCV (%)	GCV (%)		
1	Days to 50% flowering	40.74 $\pm$ 0.76	36.78	47.94	0.27	1.78	0.99	30.86	4.43
2	Plant height (cm)	68.68 $\pm$ 1.85	26.23	96.36	1.02	4.26	3.68	74.65	9.86
3	Racemes plant ⁻¹	6.41 $\pm$ 0.77	2.31	12.48	1.59	11.72	6.72	32.88	29.26
4	Raceme length (cm)	20.72 $\pm$ 1.81	8.37	37.56	1.41	8.53	4.96	33.86	19.20
5	Primary branches plant ⁻¹	2.88 $\pm$ 0.35	1.09	4.53	1.20	10.50	4.19	15.89	27.15
6	Fresh pod length (cm)	9.09 $\pm$ 0.32	6.01	17.41	1.25	4.28	3.24	57.35	15.13
7	Fresh pods plant ⁻¹	34.73 $\pm$ 2.44	5.89	112.95	3.08	10.96	9.42	73.98	24.70
8	Fresh pod yield plant ⁻¹ (g)	98.26 $\pm$ 3.57	26.82	287.36	2.65	9.03	8.56	89.79	19.52

SE- Standard Error, PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, GAM- Genetic advance as% of mean

**Fig 1:** Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) for eight quantitative traits of Dolichos bean**Fig 2:** Broad-sense heritability (%) and Expected Genetic advance as% of mean for eight quantitative traits of dolichos bean

Conclusion

Highly significant mean sum of squares indicated substantial variability not only among the F₄ progenies but also their significant differences with check varieties for most of the quantitative traits as indicated by ANOVA which is a diagnostic tool for detection of variability. Absolute range and standardized range showed that F₄ progenies have got high variation for fresh pods plant⁻¹ followed by fresh pod yield plant⁻¹, racemes plant⁻¹, raceme

length, fresh pod length, primary branches plant⁻¹ and plant height and least variation for days to 50% flowering. Wider difference between the PCV and GCV was reported for racemes plant⁻¹, raceme length, and primary branches plant⁻¹ indicating larger influence of environment on the expression of these traits. While narrow difference between PCV and GCV was recorded for days to 50% flowering, plant height, fresh pod length, fresh pods plant⁻¹ and fresh pod yield plant⁻¹ representing marginal influence of environment on the

expression of these traits. Hence, there is an ample scope for improvement of these traits. The high heritability estimates were reported for fresh pod yield plant⁻¹ followed by plant height, and fresh pods plant⁻¹ indicating the effectiveness of selection. High heritability coupled with high GAM were reported for fresh pods plant⁻¹ and fresh pod yield plant⁻¹ indicated the presence of larger number of fixable additive factors which help in improvement of these traits through simple selection procedures.

5. Credit authorship contribution statement

R. Kirankumar: Conceptualization, Material preparation, Investigation, Methodology, data collection & field experiments, Data curation, Writing - review & editing, Writing - original manuscript. M. D. Valeeta: Data curation, analysis of data and tabulation of results. M. Byregowda: Supervision, Conceptualization, Methodology, Data curation. S. Ramesh: Supervision, Conceptualization, Methodology, Data curation.

6. Declarations

- **Conflict of interest:** Authors of this manuscript declare that we have no conflict of interest
- **Consent for publication:** All the authors have provided their consent for publication of this manuscript
- **Ethical approval:** This manuscript does not contain studies performed by any of the authors involving human or animals

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