www.ThePharmaJournal.com

The Pharma Innovation

Variability, heritability (h^2_b) and genetic advance studies in dolichos bean (*Lablab purpureus* L.) genotypes

Syeda Nabeela Thasneem, M Sreenivas, K Nagaraju, P Saidaiah and SR Pandravada

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(12): 6005-6008

www.thepharmajournal.com
Received: 01-10-2022
Accepted: 05-11-2022

Syeda Nabeela Thasneem
M.Sc. Scholar, Department of Vegetable Science, SKLTSHU, Mojerla, Telangana, India

M Sreenivas
Assistant Professor, Department of Plantation, Spices, Aromatic and Medicinal crops, SKLTSHU, Rajendranagar, Hyderabad, Telangana, India

K Nagaraju
Assistant Professor, Department of Vegetable Science, SKLTSHU, Mojerla, Telangana, India

P Saidaiah
Associate Professor, Department of Genetics and Plant Breeding, SKLTSHU, Mojerla, Telangana, India

SR Pandravada
Principal Scientist, National Bureau of plant genetic resources, Rajendranagar, Hyderabad, Telangana, India

Corresponding Author:
Syeda Nabeela Thasneem
M.Sc. Scholar, Department of Vegetable Science, SKLTSHU, Mojerla, Telangana, India

Abstract

The present experiment was conducted to study variability, heritability and genetic advance in dolichos bean (*Lablab purpureus* L.) genotypes. It was carried out during *Rabi* season, in the year 2021-22. The study was under taken on 45 genotypes of Dolichos Bean using randomized block design (RBD) with two replications. High genetic variability was observed for the characters *viz.*, number of pods per plant, 100-seed fresh weight, pod length, pod width, pod yield per plant and reducing sugars and indicates the significance of these characters to be used for selecting superior genotypes. High heritability coupled with high genetic advance as per cent of mean was observed in characters *viz.*, vine length, number of primary branches per plant, number of pods per plant, pod yield per plant, 100-seed fresh weight, pod length, pod width, seed length, seed width, days to 50% flowering, days to first harvest, reducing sugars and total sugars.

Keywords: *Lablab purpureus*, GCV, PCV, genetic advance, heritability

Introduction

Dolichos bean, also known as Indian bean, Hyacinth bean, sem, Egyptian kidney bean, bonavist bean, avarai, and avari chikkudu, is one of the most well-known traditional vegetables that is widely grown in India. Archaeo-botanical discoveries in India between 2000 and 1700 BC at Heller, the earliest Iron-Age site in Karnataka and 1200-300 BC at the Veerapuranam excavation site in Andhra Pradesh attest to its Indian provenance (Fuller, 2003) [9]. It is a great crop to grow in arid regions with little rainfall. The crop prefers a season that is moderately cool, with sowing taking place in July and August and fruiting begins in winter. The pods are naturally abundant in minerals including Ca, P, and Fe as well as carbohydrates, proteins, fats, and fibre (Naeem *et al*., 2009) [8]. It may be a herbaceous perennial but is grown as an annual with races that are bushy, upright, or climbing. It is a good nitrogen fixer and is occasionally used as a cover crop or for animal fodder. Short day and long day varieties are both available, and it is photosensitive. The selection of superior genotypes and the enhancement of yield attributes require genetic variability, heritability and genetic advance in order to improve a crop. The development of breeding in beans is influenced by the kind, degree, and interactions of phenotypic and genotypic variation in yield and yield-attributing traits. Heritability of a metric character is a parameter of particular importance to breeders because it measures the degree of similarity between the parents and the off-springs and its magnitude indicates how effectively a genotype can be identified by its phenotypic expression, while genetic advancement assists in applying the necessary selection pressure (Burton *et al*., 1953) [3]. The present investigation was therefore aimed to study variability, heritability and genetic advance among 45 genotypes of dolichos bean.

Material and Methods

The present experiment was carried out during the period from November 2021 to March 2022 at PG Research Block, College of Horticulture, Mojerla. The experimental material for this study comprised of 45 different genotypes of dolichos bean obtained from NBPGR *i.e*, IC-261004, IC-261005, IC-261010, IC-261311, IC-372119, IC-382830, IC-384066, IC-412977, IC-413709, IC-413710, IC-426632, IC-426957, IC-426966, IC-426970, IC-426980, IC-426983, IC-426987, IC-426988, IC-426991, IC-426694, IC-427414, IC-427417, IC-427423, IC-427424, IC-427425, IC-427428, IC-427429, IC-427436, IC-427456, IC-427462,

IC-446561, IC-446566, IC-446568, IC-446571, IC-446573, IC-446574, IC-446575, IC-446581, IC-446583, IC-446584, IC-446585, IC-446587, IC-546387, IC-598467 including Arka Adarsh which is used as a standard check. Eight plants of each genotype were included in each of the two replications of the experiment which used a Randomized Block Design. The plants were trained to pandal at a spacing of 0.5 m between plants and 2.0 m between rows. The data was collected on five arbitrarily chosen equally competitive plants in each genotype in each replication for recording observation on 16 characters *viz*., vine length (cm), number of primary branches per plant, days to 50% flowering, days to first harvest, number of pods per plant, pod length (cm), pod width (cm), number of seeds per pod, seed length (cm), seed width (cm), 100- seed fresh weight (g), 100- seed dry weight (g), pod yield per plant (g), protein content (%), reducing sugars (%), total sugars (%) and their mean was obtained.

Estimating variability in a population is an effective tool for the breeder to design the selection procedures more accurately for identifying superior genotypes. Variability helps to choose the potential genotype, since it indicates the extent of recombination for implementing effective selection. The magnitude of phenotypic and genotypic coefficients of variation has been assessed to know the real worth of the source material.

Genotypic coefficient of variation would be a useful tool for the assessment of variability, since it depends upon the heritable portion of the total variability (Allard, 1960) [1]. Heritability estimates give a measure of transmission of characters from one generation to another, thus giving an idea of heritable portion of variability and enabling the plant breeder in isolating the elite genotype in the crop. The heritability expresses the portion of total variances that was attributed to the average effect of genes and that determines the degree of resemblance between parents and off springs. It also expresses the reliability of phenotypic values as a guide to the breeding value.

Heritability in broad sense is the portion of genotypic variance to phenotypic variance, which indicates the relative success of selection. It is useful in selection of elite genotype from diverse genetic population. High heritability estimates are helpful in selecting superior genotypes on the basis of performance of quantitative characters. Heritability coupled with genetic advance is an important selection parameter. Johnson *et al*. (1955) [7] reported that heritability along with genetic gain is more useful than the heritability alone, in predicting the resultant effect for selecting the best individuals. He categorized the heritability values, as the values greater than 60 per cent indicate the high heritability, the values ranged between 30 to 60 per cent indicate the moderate heritability, while the values less than 30 per cent indicate the low heritability. Similarly, the values greater than 20 per cent indicate high genetic advance, the values ranged between 10 to 20 per cent indicate moderate genetic advance, while the values less than 10 per cent indicate low genetic advance.

The simple measure of variability like mean, range and the major components of variability such as phenotypic and genotypic coefficients of variation (PCV and GCV), heritability in broad sense (h^2_b), genetic advance and genetic advance as per cent of mean were furnished in Table 1. All the sixteen characters under study exhibited high variability as evident from the estimates of mean, range, coefficients of variation, heritability and genetic advance.

Results

The Analysis of variance revealed significant differences among the genotypes with respect to all the characters studied. Highly significant differences among the genotypes were observed indicating the presence of sufficient amount of variability among genotypes studied.

Vine length was recorded with high phenotypic and genotypic variances of 1804.62 and 1536.37 respectively, coupled with moderate PCV and GCV of (11.59 and 10.69% respectively). This trait showed high heritability (85.10%), high genetic advance (74.50) and high GA as per cent of mean (20.33%).

Number of primary branches per plant showed low phenotypic and genotypic variances of 0.25 and 0.22 respectively along with moderate PCV (13.76%) and GCV (12.92%). This trait showed high heritability (88.30%) but low genetic advance (0.91) and high GA as per cent of mean (25.01%) were also recorded.

Days to 50% flowering recorded high phenotypic (127.67) and genotypic (121.32) variances, moderate PCV (15.23%) and moderate GCV (14.85%). The high heritability (95.00%), high genetic advance (22.12) and high GA as per cent mean (29.82%) estimates were observed for this trait.

High phenotypic and genotypic variances (136.03 and 128.86 respectively) with moderate PCV (11.49%), GCV (11.18%), high heritability (94.70%), high genetic advance (22.76) and high GA as per cent of mean (22.42%) estimates were observed for days to first harvest.

Number of pods per plant showed high phenotypic and genotypic variances (595.77 and 568.74 respectively) with high PCV (37.19%) and GCV (36.33%). High heritability (95.50%), high genetic advance (48.00) and high GA as per cent of mean (73.13%) estimates were recorded for this trait.

Pod length recorded low phenotypic and genotypic variances (4.75 and 3.58 respectively) with high PCV (22.80%) and moderate GCV (19.81%) values, high heritability (75.50%), low genetic advance (3.39) and high GA as per cent of mean (35.47%).

Pod width showed low phenotypic and genotypic variances (0.36 and 0.29) along with high PCV (32.85%) and GCV (29.73%). The character also showed high heritability (81.90%), low genetic advance (1.01) as well as high GA as per cent of mean (55.41%).

Low phenotypic and genotypic variances (0.31 and 0.18 respectively) with moderate PCV (12.17%), low GCV (9.31%), high heritability (58.50%), low genetic advance (0.67) and moderate GA as per cent of mean (14.68%) estimates were observed for number of seeds per pod.

Seed length recorded low phenotypic and genotypic variances (0.01 and 0.01) in dolichos bean genotypes with moderate PCV (13.15%) and GCV (12.46%). Seed length also showed high heritability (89.80%) but low genetic advance (0.22) and high GA as per cent mean (24.33).

Low phenotypic (0.02) and genotypic (0.01) variances and moderate PCV (13.89%) and GCV (12.75%) were recorded for seed width. High heritability (84.30%), low genetic advance (0.21) and high GA as per cent mean (24.12%) estimates were observed for this trait.

100-seed fresh weight showed high phenotypic and genotypic variances (226.86 and 210.36 respectively) with high PCV and GCV (24.58% and 23.66%). This trait also recorded high heritability (92.70%), high genetic advance (28.77) and high

GA as per cent of mean (46.94%).

With regard to 100-seed dry weight, low phenotypic and genotypic variance (9.42 and 7.46 respectively) with moderate PCV (10.47%) and low GCV (9.32%), high heritability (79.20%), low genetic advance (5.01) and moderate GA as percent mean (17.08%) were registered.

With respect to pod yield per plant, high phenotypic and genotypic variance (15349.08 and 10547.08), high PCV (38.73%) and GCV (37.80%), high heritability (68.80%), high genetic advance (241.88) and high GA as per cent of mean (70.32%) estimates were observed.

Protein content recorded low phenotypic and genotypic variances (1.49 and 1.42 respectively) with low PCV (6.92%) and low GCV (6.75%). The high heritability (95.30%), low genetic advance (2.39) and moderate GA as per cent of mean (13.59%) were also reported for this trait.

Reducing sugars showed low phenotypic and genotypic variances (0.03 and 0.03 respectively) with high PCV (22.06%) and GCV (21.60%). High heritability (95.80%), low genetic advance (0.36) and high GA as per cent of mean (43.56%) estimates were also recorded for this trait.

Total sugars showed low phenotypic and genotypic variances (0.03 and 0.03 respectively) with moderate PCV (15.35%) and GCV (15.04%). High heritability (96.10%), less genetic advance (0.32) and high GA as per cent mean (30.39%) estimates were observed for this trait.

Table 1: Estimation of variability, heritability and genetic advance as percent of mean for sixteen characters in forty-five genotypes of Dolichos bean

S. No	Characters	Range		Mean	Variance		PCV (%)	GCV (%)	H^2 (bs)%	Genetic advance	GA as percent of mean
		Minimum	Maximum		Phenotypic	Genotypic					
1	Vine length (cm)	217.50	429.35	366.547	1804.62	1536.37	11.59	10.69	85.10	74.50	20.33
2	Number of primary branches per plant	2.88	4.77	3.642	0.25	0.22	13.75	12.92	88.30	0.91	25.01
3	Days to 50% flowering	51.06	102.50	74.188	127.67	121.32	15.23	14.85	95.0	22.12	29.82
4	Days to first harvest	82.96	135.92	101.526	136.03	128.86	11.49	11.18	94.70	22.76	22.42
5	Number of pods per plant	43.00	149.50	65.639	595.77	568.75	37.19	36.33	95.50	48.00	73.13
6	Pod length (cm)	4.86	13.47	9.554	4.75	3.58	22.80	19.81	75.50	3.39	35.47
7	Pod width (cm)	0.79	4.74	1.813	0.36	0.29	32.85	29.73	81.90	1.01	55.41
8	Number of seeds per pod	3.20	5.70	4.560	0.31	0.18	12.17	9.31	58.50	0.67	14.68
9	Seed length (cm)	0.62	1.15	0.890	0.01	0.01	13.15	12.46	89.80	0.22	24.33
10	Seed width (cm)	0.63	1.12	0.869	0.02	0.01	13.89	12.75	84.30	0.21	24.12
11	100-seed fresh weight (g)	34.10	85.25	61.297	226.86	210.36	24.58	23.66	92.70	28.77	46.94
12	100-seed dry weight (g)	22.93	34.35	29.312	9.42	7.46	10.47	9.32	79.20	5.01	17.08
13	Pod yield per plant (g)	189.45	702.67	343.985	15349.08	10547.08	38.73	37.80	68.80	241.88	70.32
14	Protein content (%)	14.54	20.29	17.616	1.49	1.42	6.92	6.75	95.30	2.39	13.59
15	Reducing sugars (%)	0.41	1.26	0.820	0.03	0.03	22.06	21.60	95.80	0.36	43.56
16	Total sugars (%)	0.71	1.50	1.062	0.03	0.03	15.35	15.04	96.10	0.32	30.39

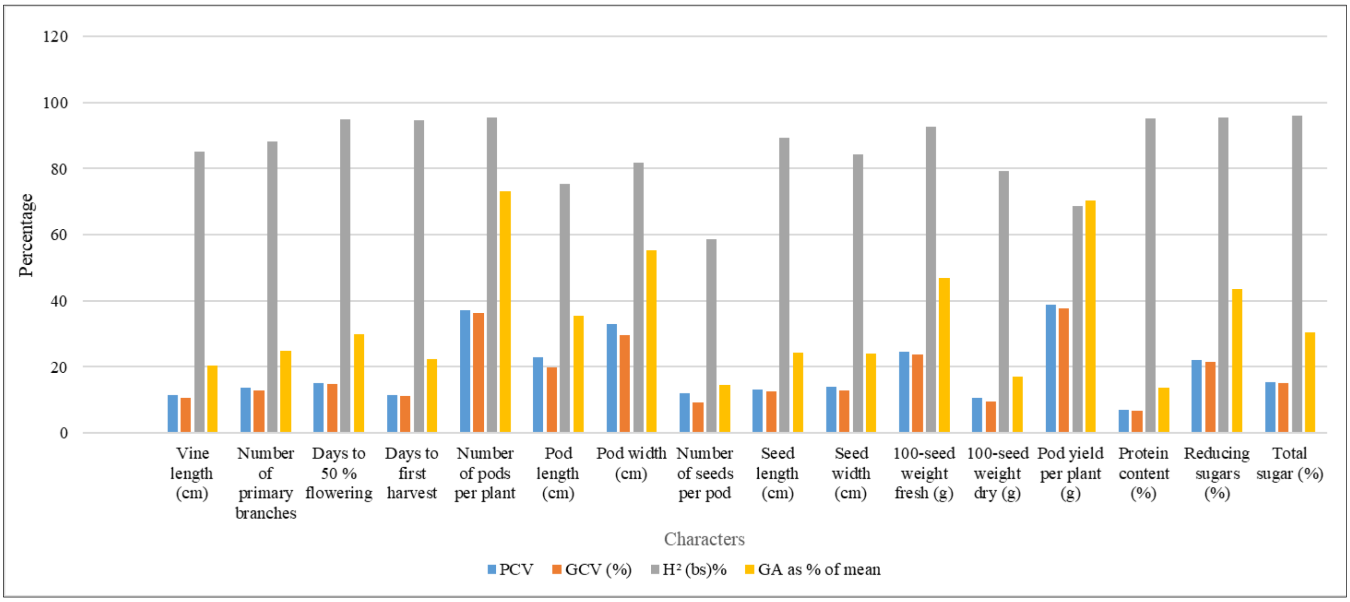

Fig 1: Genetic parameters for 16 characters in dolichos bean genotypes

Conclusion

The study revealed that PCV was higher than the corresponding GCV for all the characters indicating that all characters had interacted with environment to some degree. In the present study the high genetic variability observed for the characters *i.e.*, number of pods per plant, pod yield per plant, 100-seed fresh weight, pod length, pod width, reducing sugars and indicates the significance of these characters to be used for selecting superior genotypes.

The difference between PCV and GCV values were minimum, indicating that the traits under study were less influenced by environment and these characters could be improved by following phenotypic selection.

In the present study, the heritability in broad sense was found to be high for all the characters. High heritability estimates indicated the presence of large number of fixable additive genes and hence these traits can be improved by selection.

High heritability coupled with high genetic advance as per cent of mean indicates operation of additive gene action which was observed in characters *viz*., vine length, number of primary branches per plant, number of pods per plant, pod yield per plant, 100-seed fresh weight, pod length, pod width, seed length, seed width, days to 50% flowering, days to first harvest, reducing sugars and total sugars. These results are in accordance with Das *et al.* (2015) [5], Afsan *et al*. (2020) [2], Chauhan *et al*. (2021) [4], Sahu *et al*. (2018) [10], Reddy *et al.* (2018) [11] and Raj *et al*. (2021) [12].

Hence, directional selection for these traits in genetically diverse material could be effective for desired genetic improvement. Moderate genetic advance as per cent of mean with high or moderate heritability suggests the action of both additive and non-additive genes thereby favorable influence of environment in the expression.

An essential factor that aids the breeder in selecting a selection programme is genetic advance, which calculates the degree of gain in a trait gained under a specific selection pressure (Hamdi *et al*., 2003) [6]. A trait's high heritability and genetic advance imply that it is controlled by additive gene action, which makes it the best trait for selection.

Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes.

Acknowledgement

The author expresses sincere thanks to M. Sreenivas, K. Nagaraju, P. Saidaiah, S.R. Pandravada. I am highly thankful to College of Horticulture, Mojerla, SKLTSHU, for providing all facilities to complete this endeavor.

References

1. Allard RW. Principles of plant breeding. John Willey and sons Inc, London; c1960. p. 83-108.
2. Afsan N, Roy AK. Genetic variability, heritability and genetic advance of some yield contributing characters in lablab bean (*Lablab purpureus* L. Sweet). Journal of Bio-Science. 2020;28:13-20.
3. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. Agronomy journal. 1953;45(10):478-481.
4. Chauhan S, Kundu S. Estimation of genetic variability, heritability and genetic advance for yield and yield attributing traits in dolichos bean (*Lablab Purpureus* L.). International Journal of Environment, Agriculture and Biotechnology. 2021;6:4.
5. Das I, Shende VD, Seth T, Yadav Y, Chattopadhyay A. Genetic analysis and interrelationships among yield attributing traits in pole and bush type dolichos bean (*Lablab purpureus* L.). Journal Crop and Weed. 2015;11(2):72-77.
6. Hamdi A, El-Chareib A, Shafey SA, Ibrahim MAM. Genetic variability, heritability and expected genetic advance for earliness and seed yield from selections in lentil. Egyptian journal of agriculture Research. 2003;81(1):125-137.
7. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. Agronomy journal. 1955;47(7):314-318.
8. Naeem M, Khan MMA, Siddiqui MH. Triacontanol stimulates nitrogen-fixation, enzyme activities, photosynthesis, crop productivity and quality of hyacinth bean (*Lablab purpureus* L.). Scientia horticulturae. 2009;121(4):389-396.
9. Fuller DQ. African crops in prehistoric South Asia: a critical review. Food, fuel and fields: Progress in African archaeobotany. 2003, 239-271.
10. Sahu S, Bahadur V. Genetic analysis of dolichos bean (*Lablab purpureus* L.) genotypes for horticultural traits. J Pharmacogn. Phytochem. 2018;7(4):3112-3116.
11. Reddy KJ, Prabhakar BN, Saidaiah P, Pandravada SR. Study of different qualitative traits in dolichos bean (*Dolichos lablab* L., Var. *typicus Prain*) Germplasm. International Journal of Current Microbiology and Applied Sciences. 2018;7(10):358-364.
12. Raj N, Anitha P, Pradeepkumar T, Jose D, Beena VI, John CL. Genetic divergence analysis in dolichos bean (*Lablab purpureus* var. *typicus*). Research Journal of Agricultural Sciences. 2021;12(1):195-199.