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ASSESSMENT OF GENETIC DIVERGENCE IN DOLICHOS BEAN (*Lablab purpureus* Var. *Typicus* PRAIN) FOR YIELD AND QUALITY TRAITS

J. Spandana^{1*}, Smt. Krishna Veni², P. Saidaiah³, P. Pranusha⁴ and S. Mallesh⁵

¹Department of Vegetable Science, Post Graduate Institute for Horticultural Sciences, Sri Konda Laxman Telangana Horticultural University (SKLTGHU), Mulugu, Siddipet, Telangana, India-502279

²MAPRS, Rajendranagar, Department of Plantation, Spices, Medicinal and Aromatic crops, SKLTGHU, Hyderabad, Telangana, India-500030

³Professor and Technical Secretary to Vice Chancellor, Admin. Office, Department of Genetics and Plant Breeding, Sri Konda Laxman Telangana Horticultural University (SKLTGHU), Mulugu, Siddipet, Telangana, India-502279

⁵Department of Plant Physiology ICAR-NBPGR, Regional Station, Rajendranagar, Hyderabad, Telangana, India-500030

⁴HRS, Department of Vegetable Science, SKLTGHU, Adilabad, Telangana, India

*Corresponding author E-mail: jakkulaspandana75@gmail.com

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ABSTRACT

The present experiment was conducted to study genetic divergence, variability, heritability and genetic advance in dolichos bean (*Lablab purpureus* L. var. *typicus* Prain) genotypes. It was carried out during *Kharif* season, in the year 2025-26 at ICAR-NBPGR Regional Station, Rajendranagar, Hyderabad. The study was under taken on 22 genotypes of Dolichos bean using randomized block design (RBD) with three replications. The twenty-two genotypes were classified into five distinct clusters according to the relative magnitude of D^2 values. The highest number of genotypes (12) appeared in cluster I. Cluster III exhibited the maximum intra cluster distance ($D^2=91.03$). The maximum inter cluster distance observed between II and V ($D^2=958.39$) and the minimum inter cluster distance observed between IV and V ($D^2=80.64$). Among the traits, pod weight contributed the highest proportion to genetic divergence (30.30%). High heritability coupled with substantial genetic advance as a percentage of the mean was observed in most of the traits. This trend signifies predominant additive gene action, suggesting that direct phenotypic selection would be highly effective for trait improvement.

Key words: *Lablab purpureus*, genetic divergence, PCV, GCV, heritability, genetic advance

Introduction

Dolichos bean (*Lablab purpureus* L. var. *typicus* Prain), belonging to Fabaceae (sub family Faboideae, tribe Phaseoleae, sub tribe Phaseolinae; $2n=22$) is cultivated across Madhya Pradesh, Maharashtra, Andhra Pradesh, Telangana, Tamil Nadu, Karnataka and the North Eastern region of India. The crop thrives under cool conditions, with flowering during August-September and fruiting indeterminately from October to February (Savitha, 2008). Immature pods are nutritionally rich, containing 6.7 g carbohydrates, 3.8 g protein, 210 mg calcium, 1.7 mg iron, 312 IU vitamin A and 0.1 mg thiamine per 100 g (Gopalan *et al.*, 2004). Dolichos bean is

photoperiod sensitive, with short day and long day types and exhibits both determinate and indeterminate growth habits (Keerthi *et al.*, 2018). Breeding efficiency depends on genetic variability within germplasm (Parmar *et al.*, 2013), while heritability indicates trait transmission reliability (Singh *et al.*, 2019). Combined with genetic advance, it enables clearer separation of genetic variance, improving selection accuracy (Lahari *et al.*, 2022). The present study evaluates variability, heritability and genetic advance across 22 genotypes.

Material and Methods

The present investigation was carried out during the period from August, 2025 to March, 2026 at ICAR-

NBPGR Regional station, Rajendranagar, Hyderabad, Telangana. The experimental material for this study comprised of 22 different genotypes of dolichos bean provided by NBPGR *i.e.* KP/DRB/21-10, KP/DRB/21-116, NSJ-361, KP/DRB/21-20A, KP/PKM/59, IC-556813, KP/PR/21-67, KP/SC-1558, KP/18-161, KG/VK/SKT-239, KG/VK/SKT-245, KP/SC-1670, IC-526909, IC-383197, IC-384066, IC-427423, IC-398467, NSJ-356, IC-631536 including Arka Prasadhi, Pusa Garima and Kashi Haritima were used as standard checks in Randomized Block Design with three replications. The plants were trained to pandal at a spacing of 0.9 m between plants and 1.2 m between rows. Observations on 19 traits *viz.*, number of primary branches per plant, number of inflorescence per plant, number of days taken to first flowering, number of days taken to 50 percent flowering, number of days taken to first picking, number of days taken to last picking, pod length (cm), pod width (cm), pod weight (g), seed length (mm), seed breadth (mm), number of pods per plant, number of seeds per pod, pod yield per plant (g), pod yield per hectare (q/ha), hundred dry seeds weight (g), protein content (%), fibre content (%), reducing sugars (%) were recorded from five randomly selected, equally competitive plants of each genotype in every replication and their mean was obtained.

The data was analysed using Mahalanobis' (1936) D^2 statistics and genotypes were clustered following Tocher's method as outlined by Rao (1952). The genetic distance between all genotype pairs was computed using the squared Euclidean distance approach.

Assessing variability within a population provides breeders with a valuable framework for designing precise selection strategies to identify superior genotypes. Since variability reflects the degree of recombination, it aids in pinpointing promising genotypes for effective selection. To evaluate the true potential of the source material, both phenotypic and genotypic coefficients of variation were analysed.

The genotypic coefficient of variation serves as a valuable measure for assessing variability, as it reflects the heritable component of total variation (Allard, 1960). Estimates of heritability indicate the extent to which traits are transmitted across generations, thereby helping breeders isolate elite genotypes within a crop. Heritability quantifies the proportion of overall variance attributable to the average genetic effects, determining the degree of resemblance between parents and offspring. It also indicates how reliably phenotypic values can be used as predictors of breeding value.

Broad sense heritability represents the ratio of genotypic variance to phenotypic variance, serving as an

indicator of the effectiveness of selection. It is particularly valuable for identifying elite genotypes within diverse populations. High heritability estimates allow breeders to select superior genotypes based on quantitative trait performance. When combined with genetic advance, heritability becomes a more powerful selection criterion. Johnson *et al.*, (1955) emphasized that heritability together with genetic gain provides a better prediction of selection outcomes than heritability alone. They classified heritability values above 60% as high, 30-60% as moderate, and below 30% as low. Similarly, genetic advance exceeding 20% was considered high, 10-20% moderate and less than 10% low.

The simple measures of variability such as mean and range, along with major components including phenotypic and genotypic coefficients of variation (PCV and GCV), broad sense heritability (h^2b), genetic advance and genetic advance expressed as a percentage of the mean were presented in Table 5. All 19 traits examined showed considerable variability, as reflected in the estimates of mean, range, coefficients of variation, heritability and genetic advance.

Results and Discussion

Analysis of divergence characters for yield and yield characters

Based on genetic distances, the twenty-two dolichos bean genotypes were classified into five clusters, reflecting considerable variability. Cluster I comprised 12 genotypes, cluster II with 2 genotypes, cluster III with 6 genotypes, while cluster IV and cluster V was solitary with a single genotype, underscoring its distinct identity and importance due to unique traits. From the clustering pattern of the twenty-two genotypes (Table 1), it was evident that they were grouped into distinct clusters irrespective of geographical origin. Comparable results were reported by and Verma *et al.*, (2015) and Jyothireddy *et al.*, (2018). The cluster III ($D^2=91.03$) had maximum intra cluster distance followed by cluster I ($D^2=52.62$). The maximum inter cluster distance was recorded between clusters II and V ($D^2=958.39$), whereas the minimum was observed between clusters IV and V ($D^2=80.64$) (Table 2). The markedly lower intra cluster distance compared to inter cluster values indicated homogeneity within clusters and heterogeneity among clusters. The cluster V (Table 3) is most suitable to select the genotype for no. of inflorescence per plant, pod width, seed length, seed width, pod weight, no. of pods per plant, no. of seeds per pod and pod yield per plant followed by cluster IV. Cluster II exhibited the least mean values for most of the traits. Among the yield related

Table 1: Clustering pattern of 22 genotypes of dolichos bean by Tocher's method.

Cluster	NG	Genotypes
I	12	Arka Prasadhi, Kashi Haritima, KP/DRB/21-10, KP/PKM/59, KP/18-161, Pusa Garima, KP/SC-1558, NSJ-356, KP/DRB/21-116, IC-556878, IC-631536, IC-556813
II	2	NSJ-361 and KP/DRB/21-20A
III	6	KG/VK/SKT-239, IC-398467, KP/SC-1670, IC-427423, KG/VK/SKT-245, KP/PR/21-67
IV	1	IC-384066
V	1	IC-383197
NG: Number of genotypes		

traits (Table 4), the maximum contribution towards divergence was made by pod weight (30.30%) followed by days to first flowering (20.78 %), pod yield per plant (14.72 %), pod length (13.42 %), seed length (6.93 %), no. of inflorescences per plant (5.19 %), number of pods per plant (3.90%), pod width (1.73 %), seed width (1.30%), no. of primary branches per plant (0.43 %), Days to 50 % flowering and days to first flowering (0.43%).

Analysis of genetic parameters for yield and yield characters

Analysis of variance indicated significant differences among the genotypes for all traits studied. The highly significant variation observed confirms the presence of ample genetic diversity within the evaluated genotypes.

Number of primary branches per plant exhibited very low phenotypic (6.67) and genotypic (6.18) variances, yet showed high PCV (35.26%), high GCV (33.95%) and high heritability (92.72%). It was associated with low genetic advance (4.89) but a high genetic advance as a percentage of the mean (66.82%) (Table 5).

No. of inflorescence per plant exhibited very high phenotypic variance (123.54) and genotypic variance (118.33), accompanied by high PCV (32.46%) and GCV (31.77%). It also showed high heritability (95.78%), a moderate genetic advance (21.75) and a high genetic advance relative to the mean (63.53%).

Days to first flowering recorded very high phenotypic (361.52) and genotypic (357.08) variances, with correspondingly high PCV (30.09%) and GCV (29.90%) values, heritability was high (98.77%), genetic advance was moderately high (38.38) and genetic advance as a percentage of the mean was also high (60.74%).

For days to 50% flowering, the genotypes recorded high phenotypic variance (311.66) and genotypic variance (294.06), along with high PCV (23.47%) and GCV (22.80%). This trait also exhibited high heritability

Table 2: Average intra (bold) and inter-cluster D² values for five clusters in 22 genotypes of dolichos bean.

Cluster	I	II	III	IV	V
I	52.62	109.95	154.94	378.78	615.38
II		17.3	356.79	669.14	958.39
III			91.03	141.04	307.92
IV				0	80.64
V					0
Bold diagonal values indicate intra cluster distance, rest of the values show the inter cluster distances.					

(94.35%), high genetic advance (34.19) and a high genetic advance as a percentage of the mean (45.45%).

For days to first pod harvest, very high phenotypic variance (672.51) and genotypic variance (652.30) were observed, accompanied by high PCV (27.28%) and GCV (26.87%). The trait also exhibited high heritability (97.00%), high genetic advance (51.81) and a high genetic advance as a percentage of the mean (54.50%).

Days to last harvest recorded high phenotypic variance (891.15) and genotypic variance (855.97), along with elevated PCV (21.38%) and GCV (20.95%). It also exhibited high heritability (96.05%), substantial genetic advance (59.04) and a high genetic advance as a percentage of the mean (42.28%).

Pod length exhibited high phenotypic variance (21.53) and genotypic variance (21.08), with correspondingly high PCV (42.26%) and GCV (41.82%). The trait also showed high heritability (97.93%), low genetic advance (9.27) and a high genetic advance as a percentage of the mean (84.45%).

Pod width recorded low phenotypic variance (1.43) and genotypic variance (1.41), yet exhibited high PCV (64.83%) and GCV (64.31%). It also showed high heritability (98.41%), a low genetic advance (2.41) and an exceptionally high genetic advance as a percentage of the mean (130.88%).

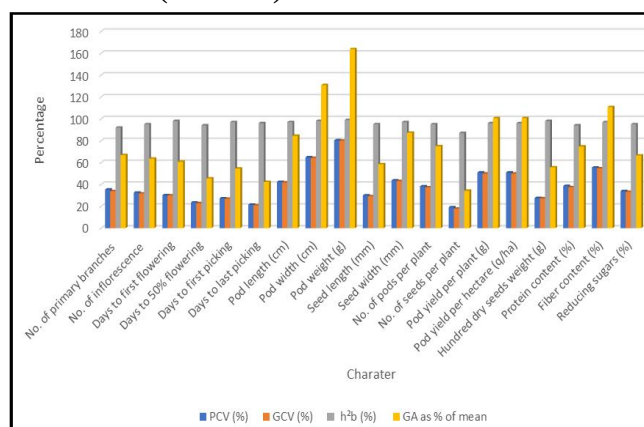
**Fig. 1:** Genetic parameters for 19 characters in dolichos bean genotypes.

Table 3: Mean values of clusters for fourteen characters in 22 genotypes of dolichos bean.

C	NBP	NIP	DF	DPF	DFP	DLP	PL	PW	PWG	SL	SW	NPP	NSP	PYP
I	7.59	32.24	60.14	72.41	88.07	130.48	9.72	1.52	61.58	13.51	7.30	155.53	4.95	881.04
II	5.07	26.17	43.70	56.90	75.40	122.61	8.33	1.48	41.62	12.63	6.00	102.04	4.84	568.50
III	7.64	39.19	72.47	84.37	107.87	152.91	13.14	2.10	99.18	15.94	9.96	138.27	5.65	1194.99
IV	7.22	36.73	75.20	84.87	121.6	179.24	14.95	2.70	163.45	18.45	11.99	102.53	5.49	1388.00
V	6.84	42.13	71.13	80.87	115	164.25	14.42	4.08	177.27	19.59	13.52	177.47	5.75	1692.54
C: Cluster; NBP: No. of primary branches per plant; NIP: No. of inflorescence per pod; DF: Days to 1 st flowering; DPF: Days to 50 percent flowering; DFP: Days to first picking; DLP: Days to last picking; PL: Pod length (cm); PW: Pod width (cm); PWG: Pod weight (g); SL: Seed length (mm); SW: Seed width (mm); NPP: No. of pods per plant; NSP: No. of seeds per plant; PYP: Pod yield per plant (g)														

Pod weight registered very high phenotypic variance (4116.73) and genotypic variance (4088.61), together with high PCV (80.29%) and GCV (80.02%). The trait also exhibited high heritability (99.32%), substantial genetic advance (130.85) and a very high genetic advance as a percentage of the mean (163.74%).

Seed length showed moderate phenotypic variance (19.07) and genotypic variance (18.20), accompanied by high PCV (29.23%) and GCV (29.23%). The trait also recorded high heritability (95.44%), low genetic advance (8.55) and a high genetic advance as a percentage of the mean (58.56%).

Seed breadth exhibited moderate phenotypic variance (13.44) and genotypic variance (13.17), along with high PCV (43.65%) and GCV (43.20%). The trait also showed high heritability (97.95%), low genetic advance (7.33) and a high genetic advance as a percentage of the mean (87.22%).

For number of pods per plant, very high phenotypic variance (3063.56) and genotypic variance (2912.54) were observed, accompanied by high PCV (38.29%) and GCV (37.34%). The trait also exhibited high heritability (95.07%), substantial genetic advance (108.32) and a high genetic advance as a percentage of the mean (74.94%).

For number of seeds per pod, very low phenotypic variance (0.98) and genotypic variance (0.86) were observed, with moderate PCV (19.10%) and GCV (17.88%). The trait also exhibited high heritability (87.67%), low genetic advance (1.78) and a high genetic advance as a percentage of the mean (34.23%).

Pod yield per plant exhibited very high phenotypic variance (257680.58) and genotypic variance (248363.62), together with high PCV (50.85%) and GCV (49.93%). The trait also recorded high heritability (96.38%), substantial genetic advance (1003.87) and a very high genetic advance as a percentage of the mean (100.57%).

Evaluation of pod yield per hectare revealed high phenotypic variance (2208.20) and genotypic variance (2128.44), along with high PCV (50.86%) and GCV

(49.93%). The trait also exhibited high heritability (96.39%), substantial genetic advance (92.93) and a very high genetic advance as a percentage of the mean (100.57%).

Assessment of 100 seed dry weight revealed high phenotypic variance (102.25) and genotypic variance (100.99), along with high PCV (27.53%) and GCV (27.36%). The trait also exhibited high heritability (98.77%), moderate genetic advance (20.41) and a high genetic advance as a percentage of the mean (55.57%).

Protein content analysis revealed high phenotypic variance (32.46) and genotypic variance (30.72), along with high PCV (38.57%) and GCV (37.52%). The trait also exhibited high heritability (94.61%), moderate genetic advance (11.03) and a high genetic advance as a percentage of the mean (74.70%).

Estimation of fibre content revealed low phenotypic variance (0.90) and genotypic variance (0.88), but recorded high PCV (55.41%) and GCV (54.73%). The trait also showed high heritability (97.56%), low genetic advance (1.89) and a very high genetic advance as a percentage of the mean (110.72%).

Table 4: Percent contribution of different characters towards genetic divergence in 22 genotypes of dolichos bean.

S.	Character	NTR	PC
1.	No. of primary branches per plant	1	0.43%
2.	No. of inflorescences per plant	12	5.19%
3.	Days to first flowering	48	20.78%
4.	Days to 50 % flowering	1	0.43%
5.	Days to first picking	1	0.43%
6.	Days to last picking	0	0.00%
7.	Pod length (cm)	31	13.42%
8.	Pod width (cm)	4	1.73%
9.	Pod weight (g)	70	30.30%
10.	Seed length (mm)	16	6.93%
11.	Seed width (mm)	3	1.30%
12.	Number of pods per plant	9	3.90%
13.	Number of seeds per pod	1	0.43%
14.	Pod yield per plant (g)	34	14.72%
NTR: Number of times ranked; PC: Percent contribution			

Table 5: Estimation of variability, heritability and genetic advance as percent of mean for 19 characters in twenty-two genotypes of dolichos bean.

S. No.	Character	Range		Mean	Variance			PCV (%)	GCV (%)	ECV (%)	h ² b (%)	GA	GPM
		Min.	Max.		PP	GP	EM						
1.	No. of primary branches per plant	4.54	10.05	7.33	6.67	6.18	0.49	35.26	33.95	9.52	92.72	4.89	66.82
2.	No. of inflorescence per plant	16.17	44.23	34.24	123.54	118.33	5.21	32.46	31.77	6.67	95.78	21.75	63.53
3.	Days to first flowering	43.27	83.80	63.13	361.52	357.08	4.44	30.09	29.90	3.33	98.77	38.38	60.74
4.	Days to 50% flowering	56.33	91.87	75.22	311.66	294.06	17.61	23.47	22.80	5.58	94.35	34.19	45.45
5.	Days to first picking	69.00	121.60	95.06	672.51	652.30	20.20	27.28	26.87	4.73	97.00	51.81	54.50
6.	Days to last picking	118.51	179.24	139.63	891.15	855.97	35.18	21.38	20.95	4.25	96.05	59.04	42.28
7.	Pod length (cm)	7.44	17.41	10.98	21.53	21.08	0.45	42.26	41.82	6.08	97.93	9.27	84.45
8.	Pod width (cm)	1.31	4.08	1.84	1.43	1.41	0.02	64.83	64.31	8.17	98.41	2.41	130.88
9.	Pod weight (g)	37.41	177.27	79.91	4116.73	4088.61	28.11	80.29	80.02	6.63	99.32	130.85	163.74
10.	Seed length (mm)	9.57	19.59	14.59	19.07	18.20	0.87	29.92	29.23	6.39	95.44	8.55	58.56
11.	Seed width (mm)	5.44	13.52	8.40	13.44	13.17	0.28	43.65	43.20	6.25	97.95	7.33	87.22
12.	No. of pods per plant	94.01	202.25	144.55	3063.56	2912.54	151.02	38.29	37.34	8.50	95.07	108.32	74.94
13.	No. of seeds per plant	4.25	5.89	5.19	0.98	0.86	0.12	19.10	17.88	6.71	87.67	1.78	34.23
14.	Pod yield per plant (g)	506.20	1692.54	998.18	257680.58	248363.62	9316.95	50.85	49.93	9.67	96.38	1003.87	100.57
15.	Pod yield per hectare (q/ha)	46.86	156.68	92.40	2208.20	2128.44	79.76	50.86	49.93	9.67	96.39	92.93	100.57
16.	Hundred dry seeds weight (g)	29.37	48.66	36.73	102.25	100.99	1.26	27.53	27.36	3.06	98.77	20.41	55.57
17.	Protein content (%)	9.22	23.44	14.77	32.46	30.72	1.75	38.57	37.52	8.95	94.61	11.03	74.70
18.	Fiber content (%)	1.18	2.76	1.71	0.90	0.88	0.02	55.41	54.73	8.66	97.56	1.89	110.72
19.	Reducing sugars (%)	4.09	8.11	5.61	3.63	3.48	0.15	33.96	33.23	6.97	95.78	3.73	66.45
PP: Phenotypic; GP: Genotypic; EM: Environmental; GA: Genetic advance; GPM: GA as per cent of mean													

Analysis of reducing sugars showed low phenotypic variance (3.63) and genotypic variance (3.48), but recorded high PCV (33.96%) and GCV (33.23%). The trait also exhibited high heritability (95.78%), low genetic advance (3.73) and a high genetic advance as a percentage of the mean (66.45%).

The present study revealed that cluster III exhibited the highest intra cluster distance (91.03). The greatest inter-cluster distance was noted between clusters II and V (958.39), followed by clusters II and IV (669.14). Hence, genotypes from cluster III along with those from clusters IV and V may be utilized to generate a broad spectrum of variability. The genotypes IC-383197, IC-384066, IC-398467, KP/PR/21-67, KG/VK/SKT-239 and IC-427423 were recognized as promising genotypes for yield exploitation. These genotypes, with superior mean performance and valuable genes across most traits, may be advanced through multilocation trials to exploit yield potential. They can further serve in breeding programs and, upon successful evaluation, be released as varieties.

In the present investigation growth, pod, seed and earliness traits that exhibited high PCV and GCV values

indicate considerable genetic variability, implying that these characters are only marginally affected by environmental factors and thus provide ample scope for effective selection. High heritability was recorded by all the characters except for no. of seeds per pod. These outputs indicate that these characters are under the influence of additive gene action. High heritability combined with high genetic advance as a percentage of the mean was noted for traits such as no. of primary branching, no. of inflorescence per plant, days to first flowering and days to first harvesting, pod and seed dimensions, yield components and quality attributes. This pattern reflects strong additive gene action, indicating that simple phenotypic selection would be highly effective for improving these traits. These findings are consistent with earlier reports by Afsan *et al.*, (2020), Chauhan *et al.*, (2021), Sahu *et al.*, (2018), Jyothireddy *et al.*, (2018), Raj *et al.*, (2021) and Thasneem *et al.*, (2022).

High variability coupled with considerable genetic advance as a percentage of the mean highlights the predominance of additive gene action. These traits may also be exploited through dominance and epistatic

interactions via heterosis breeding. Breeding strategies that combine additive and non additive gene actions are advisable, as both varietal and hybrid development can significantly enhance the success of dolichos bean improvement programs.

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References

- Allard, R.W. (1960). Principles of plant breeding. John Willey and sons inc, London. 83-108.
- Afsan, N. and Roy A.K. (2020). Genetic variability, heritability and genetic advance of some yield contributing characters in lablab bean (*Lablab purpureus* L. Sweet). *Journal of Biological Science*. **28**, 13-20.
- Chauhan, S. and Kundu S. (2021). 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*. **6**, 4.
- Gopalan, C., Rama-Sastri B.V. and Balasubramanian, S. C. 2004. *Nutritive Value of Indian Foods*, National Institute of Nutrition, ICMR, Hyderabad, India.
- Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy journal*. **47**(7), 314-318.
- Jyothireddy, K., Prabhakar B.N., Saidaiah P. and Pandravada S.R. (2018). Genetic divergence, variability, heritability and genetic advance for growth, pod quality and yield characters in dolichos bean (*Dolichos lablab* L. var. *typicus* Prain) germplasm. *Legume Research - An International Journal*. **41**(6), 804-9.
- Keerthi, C.M., Ramesh S., Byregowda M., Rao A.M and Reena G.M. (2018). Photo-thermal effects on time to flowering in dolichos bean (*Lablab purpureus* L. sweet) var. *lignosus*. *Current Science*. **115**(7), 1320-1327.
- Lahari, V., Ashok P., Babu B.R. and Sasikala K. (2022). Genetic variability, heritability and genetic advance of yield and yield attributing characters of Dolichos bean (*Lablab purpureus* L.). *The Pharma Innovation Journal*. **11**(8), 1205-1208.
- Parmar, A.M., Singh A.P., Dhillon N.P.S. and Jamwal M. (2013). Genetic variability of morphological and yield traits in Dolichos bean (*Lablab purpureus* L.). *African Journal of Agricultural Research*. **8**(12), 1022-1027.
- Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Wiley and Sons Inc. New York. 357-363.
- Raj, N., Anitha P., Pradeepkumar T., Jose D., Beena V. and Laly C. (2021). Genetic Divergence Analysis in Dolichos Bean (*Lablab purpureus* var. *typicus*). *Research Journal of Agricultural Sciences*. **12**, 195-199.
- Sahu, S. and Bahadur V. (2018). Genetic analysis of dolichos bean (*Lablab purpureus* L.) genotypes for horticultural traits. *Journal of Pharmacognosy phytochemistry*, **7**(4), 3112-3116.
- Savitha, B.N. (2008). Characterization of Avare (*Lablab purpureus* L. Sweet) local collections for genetic variability. *Unpublished MSc thesis. Dharwad, UAS*.
- Singh, S., Dey S.S., Bhatia R., Kumar R., Sharma K. and Behera T.K. (2019). Heterosis and combining ability in cytoplasmic male sterile and doubled haploid based *Brassica oleracea* progenies and prediction of heterosis using microsatellites. *PLoS One*. **14**(8), e0210772.
- Thasneem, S.N., Sreenivas M., Nagaraju K., Saidaiah P. and Pandravada S.R. (2022). Variability, heritability (h^2_b) and genetic advance studies in dolichos bean (*Lablab purpureus* L.) genotypes. *The Pharma Innovation*. **11**, 6005-6008.
- Verma, A.K., Jyothi K.U. and Rao A.D. (2015). Variability and character association studies in dolichos bean (*Lablab purpureus* L.) genotypes.