The Andhra Agric. J 72 (4): 442-445, 2025
doi :10.61657/aaj.2025.234

Genetic parameters for yield attributes and physiological traits in greengram [*Vigna radiata* (L.) Wilczek]

A Chaithenyaa, N Hari Satyanarayana, T Haritha and K Jayalalitha
Department of Genetics and Plant Breeding, Acharya N G Ranga Agricultural University,
Agricultural College, Bapatla-522101, Andhra Pradesh, India

ABSTRACT

Greengram [*Vigna radiata*(L.) Wilczek] belongs to the family Leguminosae (Fabaceae) and is an important annual legume crop widely cultivated in semi-arid tropics. In the present investigation, a total of 30 genotypes of greengram including three check varieties were evaluated during *rabi,* 2024-25 in Randomized Block Design with three replications to study genetic variability, heritability, and genetic advance by using 10 quantitative traits and six physiological traits. Analysis of variance for various quantitative and physiological characters revealed that the mean sum of squares due to genotypes showed high significant differences for all characters under study. High GCV, PCV, heritability, and genetic advance were recorded by proline content and seed yield per plant.

Keywords: *Genetic Advance, GCV, Greengram, Heritability and PCV*

Greengram [*Vigna radiata* (L.) Wilczek], commonly called mung bean, is also known as "Golden gram", is one of the most ancient and extensively grown leguminous crops of India (2n=22 and genome size of 494 to 579 Mb). It is the third most important pulse crop after chickpea and pigeon pea, cultivated throughout India for its multipurpose uses as a vegetable, pulse, fodder, and green manure crop. Its seed is more palatable, nutritive, digestible, and nonflatulent than other pulses grown in the world. Greengram is primarily a native of India and Central Asia may be a secondary center. There are around 7.3 million hectares of mungbean cultivated worldwide, with an average production of 721 kg/ha and. 30% of the 5.3 million tonnes of production produced globally is split between India and Myanmar. China, Indonesia, Thailand, Kenya, Tanzania, Nepal, Sri Lanka, Korea, and Pakistan are other significant producers (Nair *et al*., 2024). In India, the dominant contributors to mungbean cultivation in terms of area and production are Rajasthan, Madhya Pradesh, Maharashtra, Karnataka, Odisha, Bihar, Tamil Nadu, Gujarat, Andhra Pradesh, and Telangana as stated in the Annual Report (2022-23) by AICRPR on *Kharif* pulses. Despite its importance, the productivity of greengram remains low due to various biotic and abiotic stresses, limited genetic variability, and low harvest index. Hence, there is a growing need to explore and utilize genetic diversity, improve agronomic practices, and adopt advanced breeding approaches to enhance yield potential and resilience of this vital legume. The crop is well-adapted to arid and semi-arid regions and is often included in crop rotations due to its quick maturity and low input requirement. For the success of any breeding programme, understanding the nature and magnitude of genetic variability, heritability, and genetic advance is critical. High heritability along with high genetic advance suggests the prevalence of additive gene action, which can be exploited through selection. Hence, the present study aims to estimate these parameters in a set of diverse greengram genotypes.

MATERIAL AND METHODS

The experiment was laid out in a randomized block design with 30 genotypes including 3 checks *viz,* LGG 607, LGG 630 and VBN–2 in three replications with 2rows each at the spacing of 30x10 cm. at Agricultural College Farm, Bapatla during *rabi*, 2024-25 and the genotypes were evaluated for different yield attributing characters and physiological traits. Observations were recorded on 16 quantitative and physiological traits. Days to 50% flowering, days to maturity are recorded on plot basis and data on remaining all the traits are recorded on five plant basis. Physiological traits *viz*., relative water content (Barr's and Weatherly's, 1962), specific leaf weight and specific leaf area (Kvet *et al*., 1971), proline content (Bates *et al*., 1973) and chlorophyll stability index (Koleyoreas., 1958) were estimated as per the standard procedures. SPAD (Soil Plant Analytical Development) Chlorophyll Meter Readings were recorded with Minolta chlorophyll meter (Model SPAD 502). The analysis of variance for each character was calculated as per the standard statistical procedure given by Panse and Sukhatme (1978). The phenotypic and genotypic coefficients of variation were calculated by using the formula given by Burton (1952). Standard statistical procedures were used to compute the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2), and genetic advance as percent of mean.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of sufficient variation among the genotypes studied Table 1. The estimates of variability, heritability and genetic advance as per cent of mean were detailed in the Table 2.

High genotypic co-efficient of variation and high phenotypic coefficient of variation was recorded for proline content (29.11and 30.17) and seed yield (29.11and 26.14) per plant. These results were in conformity with the Kumawat *et al*., 2022 and Jain *et al.,*2024 for seed yield per plant. Moderate genotypic and phenotypic coefficient of variation were recorded for clusters per plant, pods per plant, specific leaf weight and specific leaf area and these findings were in conformity with. Low genotypic and phenotypic coefficients of variation were recorded for days to 50% flowering (2.39 and 3.21), days to maturity (2.10 and 2.77), plant height (4.33 and 8.277), branches per plant (6.09 and 9.24), SPAD (3.08 and 5.96) and RWC (5.69 and 9.62). These results were in conformity with Muthuswamy *et al*. (2022) and Varma *et al*. (2022) for plant height, Harsh and Priyal (2023), Priyanka *et al*. (2023) and for clusters per plant. High heritability along with moderate genetic advance was observed for test weight and the results are in accordance with the findings of Anuradha *et al*. (2022) and Priyanka *et al*. (2023). High heritability accompanied with high genetic advance as per cent of mean was observed for the characters *viz*., proline content and seed yield per plant. Moderate heritability accompanied with low genetic advance as percent of mean was observed for clusters per plant, pods per plant and pod length. Low heritability along with low genetic advance was observed for days to 50% flowering, days to maturity, branches per plant, seeds per pod, relative water content and chlorophyll stability index. Low heritability accompanied with low genetic advance as percent of mean was observed for plant height and SPAD chlorophyll meter reading and the similar findings were observed by Sabatina *et al*. (2021) and Prajapati *et al*. (2022) for plant height. Low phenotypic and genotypic coefficients of variation were recorded for days to 50% flowering and days to maturity and these results are in accordance with Priyanka *et al*., 2023 for days to 50% flowering (Thonta, 2023) and for

Table 1. Analysis of variance for seed yield and other characters in greengram (*Vigna radiata*(L.))

Source of variations	D.F	Days to 50% Units	Days to maturity	Plant height	Branches per plant	Clusters per plant	Pods per plant	Pod length	Seeds per pod
		Mean sum of squares							
Replications	2	1.54	0.95	11.78	0.11	0.251	2.58	0.48	2.07
Treatments	29	3.72**	8.49**	12.59**	0.17**	0.46**	3.65**	1.08**	2.36**
Error	58	0.78	1.66	5.91	0.05	0.09	1.29	0.23	0.95

Source of variations	D.F	Test weight Units	SPAD	RWC	CSI	PROLINE	SLW	SLA	Seed yield per plant
		Mean sum of squares							
Replications	2	0.08	13.88	65.68	14.81	449.936	1.323	841.23	0.16
Treatments	29	0.225**	13.27**	86.21**	20.75**	8459.07**	1.35**	2188.96**	0.54**
Error	58	0.04	6.33	32.96	7.08	203.79	0.63	418.97	0.07

**Significant at 1% level

Table 2. Estimates of variability, heritability and genetic advance as per cent of mean for seed yield and other traits in greengram (*Vigna radiata* L.)

S. No.	Character	Mean	Range		Coefficient of		Heritability (broad sense) (%)	Genetic advance as % of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	41.33	39.33	43.68	3.21	2.39	55.79	3.69
2	Days to maturity	71.74	68.62	75.63	2.77	2.1	57.79	3.29
3	Plant height (cm)	34.49	31.33	38.93	8.27	4.33	27.42	4.67
4	Branches per plant	3.22	2.8	3.6	9.24	6.09	43.42	8.27
5	Clusters per plant	3.49	2.8	4.14	13.29	10.05	57.13	15.65
6	Pods per plant	8.8	7.07	11.26	16.39	10.07	37.69	12.73
7	Pod length (cm)	6.73	5.63	7.96	10.64	7.86	54.63	11.97
8	Seeds per pod	9.74	7.73	11.2	12.22	7.06	33.32	8.39
9	Test weight (g)	3.06	2.79	3.83	10.45	8.12	60.29	12.99
10	SPAD chlorophyll meter reading	49.36	46.28	54.36	5.96	3.08	26.8	3.29
11	Relative Water Content (%)	74.03	51.55	80.91	9.62	5.69	35	6.94
12	Chlorophyll Stability Index	87.37	82.11	93.5	3.9	2.44	39.17	3.15
13	Proline content (µ g/g Fw)	180.21	111.25	360.13	30.17	29.11	93.11	57.86
14	Specific Leaf Weight (mg/cm^2)	4.79	3.31	6.2	19.51	10.22	27.42	11.02
15	Specific Leaf Area (cm^2/g)	218.53	181.1	321.09	14.54	11.12	58.48	17.51
16	Seed yield (g/plant)	1.84	0.89	2.47	26.14	21.54	67.94	36.58

PCV= Phenotypic Coefficient of Variation GCV=Genotypic Coefficient of Variation

days to maturity (Jain *et al*. 2024). The narrow difference between PCV and GCV for most of the traits indicated that environmental influence was minimal.

CONCLUSION

The study revealed that high genotypic and phenotypic coefficients of variation (GCV and PCV) were recorded for proline content and seed yield per plant, while moderate estimates were observed for clusters per plant, pods per plant, specific leaf weight, and specific leaf area. High heritability coupled with high genetic advance as percent of mean for proline content and seed yield per plant suggested the predominance of additive gene action.

Traits with moderate to low genetic advance despite high heritability may require different breeding strategies such as hybridization followed by selection. Seed yield per plant showed highest heritability and a very high genetic advance, suggesting it is a reliable selection index. Yield Components such as branches per plant and pods per plant also showed promising genetic parameters suitable for improvement. These findings provide valuable insights for greengram improvement programs aiming for higher productivity and nutritional quality.

LITERATURE CITED

Anuradha C, Patta S, Malothu R and Perala A 2022. Genetic variability and vergence of morphological and seed quality traits of greengram (*Vigna radiata* L.) genotypes. International Journal of *Plant and Soil Science*. 34 (23): 1002-1011.

Barrs H D and Weatherly P E 1962. A re-examination of relative turgidity techniques for estimating water deficits in leaves. *Australian Journal of Biological Sciences*. 15: 413-428.

Bates L S, Waldren R P and Teare I D 1973. Rapid determination of proline for water stress studies. *Plant and soil.* 39: 205-207.

Burton G W 1952. Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*. 277-283.

Harsh P and Priyal P 2023. Genetic variability and correlation in greengram [*Vigna radiata* (L.) R. Wilczek]. *Plant Archives*. 23 (2): 144-148.

Jain N, Sikarwar R S, Tripathi M K and Tiwari S 2024. Evaluation of genetic parameters for yield and its attributing traits in green gram [*Vigna radiata* (L.) Wilczek]. *International*

Journal of Environment and Climate Change. 14 (2): 482-487.

Koleyoreas S A 1958. A new method for determining drought resistance. *Plant physiology*. 33:22

Kvet J, Ondok J P, Necas J and Jarvis P G 1971. Methods of growth analysis. In: *Plant photosynthetic production, A manual of methods* (Ed. by . Sestak, J. Catsky and P.G. Jarvis): 349-391

Kumawat S, Nitharwal M, Jatav H S, Attar S K, Khan M A, Chandra K, Uddin A, Dhaka S R and Khatik C L 2022. Estimates of genetic variability for seed yield and its component characters in greengram (*Vigna radiata*, Fabaceae). *Asian Journal of Agricultural Extension, Economics and Sociology*. 40 (10): 992-997.

Muthuswamy A, Jayamani P and Kumaresan D 2022. Genetic variability studies for yield related traits in greengram [*Vigna radiata* (L.) Wilczek]. *The Pharma Innovation Journal*. 11 (5): 1310-1313.

Nair R M, Chaudhari S, Devi N, Shivanna A, Gowda A, Boddapalli V N and Somta P 2024. Genetics, genomics and breeding of blackgram (*Vigna mungo* L.). *Frontiers in Plant Science* 14: 1273363

Panse V G and Sukhatme P V 1978. *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Reasearch, 347.

Prajapati S S, Singh S K, Shrivastava M K, Singh Y, Kumar P, Rahangdale S and ehera K 2022. Assessment of genetic parameters for yield and its associated traits in greengram [*Vigna radiata* (L.) Wilczek]. International Journal of Environment and Climate Change. 12 (12): 840-848.

Priyanka S L, Satyanarayana N H, Babu J S and Ramesh D 2023. Genetic variability Studies for yield and nutritional quality traits in greengram [*Vigna radiata* (L.) Wilczek]. The Andhra Agricultural Journal. 70 (1): 062-065.

Sabatina A S, Lal Ahamed M, Ramana J V and Harisatyanarayana N 2021. Genetic variability studies in mungbean (*Vigna radiata* L.). *The Pharma Innovation Journal*. 10 (6): 906-909.

Thonta R 2023. Analysis of genetic variability, heritability and genetic advance for growth and yield attributes in green gram (*Vigna radiata* L. Wilczek). *International Journal of Statistics and Applied Mathematics*. 8 (3): 43-47.

Varma V C, Lal G M, Kumar D M and Shakeer S 2022. Study of genetic diversity in greengram (*Vigna radiata* (L.) Wilczek) germplasm in prayagraj region. *International Journal of Environment and Climate Change*. 12 (11): 2499-2506.

Received on 02.09.2025 and Accepted on 04.11.2025