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INVESTIGATION ON HERITABILITY AND GENETIC ADVANCE FOR YIELD AND ITS CONTRIBUTING TRAITS IN GREENGRAM (VIGNA RADIATA L. WILCZEK)

Mitali Srivastava*, H.G. Manojkumar and Atar Singh

Department of Genetics & Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, U.P., India. *Corresponding author E-mail : srivastavamitali04@gmail.com

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ABSTRACT
 This study, entitled Investigation into Heritability and Genetic Advance for Yield and its Contributing Traits in Greengram (*Vigna radiata* L. Wilczek) was conducted in the Kharif season of 2021 at the Crop Research Center (C.R.C.), Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. Twelve yield and yield-related characteristics have been examined in 25 distinct genotypes of greengram. For every variable, the mean sum of squares for genotypes were extremely significant. For all trait under investigation, the GCV was found to be lower than the PCV, implying that these genotypes were interacting with their environment to some degree. The number of branches/ plant, number of pods/plant, and seed yield/plant showed the highest percentage of genotypic coefficient of variation (>25%). The number of branches/ plant, number of pods/plant and seed yield/plant all showed a significant phenotypic coefficient of variation (>25%). The high broad sense heritability was obtained (>60%) in case of plant height, number of pods/cluster, seed yield/ plant followed by biological yield per plant harvest index, days to maturity and days to 50% flowering. High genetic advance (>20%) was observed for plant height, number of branches/ plant, number of pods/plant, number of pods/plant.

Key words : Greengram, Genetic variability, Genetic advance, Heritability.

Introduction

Arising as the third-most important type of pulse in India after chickpea and pigeon pea, mungbean [*Vigna radiata* (L.) Wilczek], 2n=22, is a widely dispersing, annual and self-pollinating herbaceous crop. The potential ancestor of greengram is *Vigna radiata* var. *sublobata*, which originates from South Asia. Also referred to as moong or mungbean, it is a significant pulse crop that is widely cultivated in tropical and subtropical climates worldwide. Food grains make up 65% of the gross agricultural area in India, with cereals making up 50% and pulses making up roughly 15% (Tiwari and Shivhare, 2016). Greengram makes up only 2% of the total cultivated area in pulses. The leading global grower as well as consumer of greengram is India, representing approximately sixty-five percent of the world's cultivated area and fifty-four percent of total global output (Anonymous, 2022). Mungbean is cultivated on 5.5 mha of land in India, with 3.17 mt of yield and 570 kg/ha of productivity (Khatik *et al.*, 2023). Of all the pulses produced in India, greengram accounts for 11.48 percent and 18.07 percent of the total area. India's top growing states for greengram include Maharashtra, Andhra Pradesh, Rajasthan, Orissa, Karnataka and Uttar Pradesh (Anonymous, 2021).

Mungbean is a highly valuable legume crop among the many pulses that are grown in India because of its rich protein content and strong adaptability, minimal water requirement, capacity to increase soil fertility and digestibility. They have a specific role in agricultural intensification, diversity and sustainable production systems because of their short lifespan, photoinsensitivity and dense canopy. As greengram reaches maturity within 60 to 70 days following seeding, it makes a great crop to rotate across various cropping systems.

Protein from greengram is generally free from antinutritional factors, digests quickly and doesn't cause flatulence. It also contains a relatively high amount of lysine, an amino acid that is lacking in cereal grains. The nutritious value of greengram makes them stand out. It is an inexpensive and abundant source of 24.5% protein and 59.9% carbohydrates. For every 100 grams of split dual, it also has 75 mg of calcium, 8.5 mg of iron and 49 mg of beta-carotene. Green grams have two to three times the protein content of grains. In addition, it contains elevated amounts of calcium, phosphorus, iron, β -carotene, vitamin B_1 , vitamin B_2 and folic acid (Khan *et al.*, 2022). Since sprouted green gram seed is an invaluable source of ascorbic acid (Vitamin C) and include elevated levels of niacin, riboflavin, and thiamine, most people who eat salads find them to be their favorite. Greengram is consumed in various forms like daal, sprouts, sundal and snacks.

The absence of varieties with a high yield capacity and resilience to biotic and abiotic stressors is the main reason for the low productivity of greengram. Any crop needs genetic variability to be further improved upon because it gives breeders a method for generating novel kinds. Superior parents with high genetic advancement and heritability for the important characters are necessary for any effective yield improvement programme. The degree of genetic variation and the heritability of favorable traits are key factors in crop genetic improvement.

Selecting the optimal yield traits for hybridization or selection is aided by genetic variability. It is crucial since it serves as the foundation for prudent selection. Understanding the genetic variability found in the wild relatives for productivity and the characteristics that go along with it is crucial for creating an effective selection strategy. In greengram, yield is a multifaceted characteristic composed of multiple interconnected contributing factors. The principal aim of this research is to determine the relationships and differences between the quantitative traits that affect yield. Therefore, by investigating the genetic potential that exists among the genotypes of greengram, crop yield can be improved.

Like other crops, greengrams have a complicated grain yield that is controlled by both environmental and genetic influences. Since polygenes rule it and constant variation contributes to its characteristics, it is regarded as quantitative in nature. Thus, Phenotypic variance in yield or a yield-related trait arises from genetic and environmental elements and how they interact. Heritability of a trait is measured by the part of its phenotypic variance that is because of genetic factors. Heritability of a character measures the degree of similarity between a genotype and its offspring, which is particularly important to breeders because it shows how well a material can be recognised through its phenotypic expression. Genetic advancement also helps to exert the necessary selection pressure (Desai *et al.*, 2020).

Materials and Methods

At the Center for Crop Research (C.R.C.) of the Sardar Vallabhbhai Patel University of Agriculture & Technology in Meerut. The field investigation was conducted in the Kharif season of 2021. From a geographic perspective, Meerut is situated in the North Western Plain Zone at 29.010 latitude north and 77.450 longitude, or 217 meters above sea level. This environment is characterized by cold, dry winters and hot, muggy

Name of the Genotype	Source	Name of the Genotype	Source
1.Pusa-16	IARI, New Delhi	14.Asha Mung	IIPR, Kanpur
2.Pusa Vaishali	IARI, New Delhi	15.MH-521	IIPR, Kanpur
3.IPM-02-19	IIPR, Kanpur	16.Pusa 9531	IARI, New Delhi
4.OMG-1045	IIPR, Kanpur	17.PDM-191	PAU, Ludhiana
5.Pusa-371	IARI, New Delhi	18.ML-141	PAU, Ludhiana
6.Hum-12	IIPR, Kanpur	19. MH-21	IIPR, Kanpur
7.VBG-04-008	IIPR, Kanpur	20.IPM-05-2-8	IARI, New Delhi
8. Kaporgaon	GBPUAT, Pantnagar	21.Pusa -0891	IARI, New Delhi
9.WGG-37	GBPUAT, Pantnagar	22.SMM-15-72	PAU, Ludhiana
10.Indore Mung	GBPUAT, Pantnagar	23.PDM-262	PAU, Ludhiana
11.Pant Mung-7	GBPUAT, Pantnagar	24.Pusa Vishal	IARI, New Delhi
12.Pusa-0871	IARI, New Delhi	25.WNM-16	IIPR, Kanpur
13.Tarun-18	PAU, Ludhiana		

Table 1 : Detail of the Mungbean genotypes used in investigation.

summers. The sandy-loam soil in the trial field possessed a consistent texture, good drainage and a slightly alkaline (pH 7.68) reactivity. The materials utilized for the experiment in the inquiry comprised 25 genotypes (Table 1). The assessment procedure was carried out employing three replications, following a Randomized Block Design (RBD), during the Kharif season of 2021. Each plot consisted of two rows, each 4 meters in length, with a row spacing of 30 cm and plant spacing maintained at 20 cm through appropriate thinning. To maintain a good crop stand, all the suggested collection of standard procedures was followed. To record notes on days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, pod length, number of seeds per pod, biological yield per plant, test weight and harvest index, five randomly selected competitive plants from each replication were tagged. The statistical and biometrical analysis for the parameters was conducted using the mean data from twelve traits across twenty-five genotypes, with replication: variation analysis using methods from Panse and Sukhatme (1969), genotypic and phenotypic coefficient of variability using methods from Burton (1952), estimation of heritability (broad sense) using methods from Lush (1940) and Burton and De vane (1953) and genetic advancement using methods from Johnson et al. (1955).

Results and Discussion

The twenty-five mungbean genotypes were significant differences among the them, according to the statistical analysis (Table 2). Each of the twelve characteristics being examined demonstrated a great deal of variation in the current study. Vadivel *et al.* (2020), Nayak *et al.* (2022) and Varma *et al.* (2022) achieved comparable results.

Based on mean performance, cultivar ML-141 displayed the highest number of days to 50% flowering, whereas OMG-1045 showed the lowest number of days to 50% flowering. The genotype VBG-04-008 recorded the maximum days to maturity and minimum days to maturity was recorded for Tarun-18 and PDM-191. The cultivars HUM-12 and IPM-02-19 demonstrated the largest and smallest plant heights, respectively. The genotype WNM-16 had minimum number of branches per plant, while the genotype MH-21 had the greatest number of branches per plant. The genotype Tarun-18 indicated the lowest number of pods per plant. The MH-521 genotype showed the highest number of pods/clusters, whereas the OMG-1045

genotype showed the lowest number of pods/clusters. The cultivar Pusa-371 showed the highest number of seeds/pod, whereas Pusa-0871 showed the lowest number of seeds/pod. The genotypes WNM-16 and WGG-37, respectively, displayed the largest and smallest pod lengths. The cultivar IPM-02-19 displayed the minimum 1000 seed weight, and the genotype Kaporgaon showed the greatest 1000 seed weight. The cultivar Pant Mung-7 had the lowest biological yield per plant, whereas the genotype Pusa-371 had the largest biological yield/plant. The harvest index was highest for the genotype Pusa-16 and lowest for the genotype PDM-262. Cultivar Pant Mung-7 showed the lowest seed yield/plant whereas cultivar Pusa-371 showed the highest seed yield/plant (Fig. 1). These results align with the studies conducted by Mariyammal et al. (2019), Wesly et al. (2020) and Mohammed et al. (2020).

For all trait under investigation, the GCV was found to be lower than the PCV, indicating that these were interacting with their environment to some degree. The number of branches/plant, number of pods/plant, and seed yield/plant showed the highest percentage of genotypic coefficient of variation (>25%). Plant height, number of pods/cluster, and pod length all showed a moderate genotypic coefficient of variation (10–25%). Conversely, days to 50% flowering, days to maturity, number of seeds/ pod, 1000 seed weight, biological yield and harvest index showed modest genotypic coefficient of variation (<10%).

 Table 2: Analysis of variance for seed yield and its component characters.

Source of variation	Replication	Treatment	Error
DF	2	24	48
Days to 50% flowering	0.36	29.54**	1.05
Days to Maturity	1.96	88.65**	1.42
Plant Height (cm)	0.03	385.98**	0.01
Number of Branches per plant	0.06	42.11**	0.02
Number of Pods per plant	0.03	184.56**	0.06
Number of Pods per cluster	0.01	1.42**	0.03
Number of Seeds per pod	0.08	1.83**	0.16
Pod Length (cm)	0.03	2.16**	0.01
1000 Seed weight	0.03	21.39**	0.01
Biological Yield (g/plant)	0.02	22.56**	0.37
Harvest Index (%)	1.61	69.02**	2.21
Seed yield (g/plant)	0.01	5.40**	0.06





Table 3 : Genetic variability parameters for yield and its const	ituent
traits.	

Genotypes	Heritability (%)	GA as % mean	GCV (%)	PCV (%)
Days to 50% flowering	90.01	18.07	9.25	9.75
Days to Maturity	95.35	15.67	7.79	7.98
Plant Height (cm)	99.99	42.18	20.47	20.48
No of Branches/Plant	99.85	53.02	25.76	25.78
Number of pods/plant	99.90	65.19	31.66	31.68
Number of pods/Cluster	94.59	34.26	17.10	17.58
Number of seeds/Pod	77.97	11.98	6.59	7.46
Pod length	98.00	22.11	10.84	10.95
1000 Seed weight	99.84	14.01	6.81	6.81
Biological yield (g/plant)	95.21	36.80	18.31	18.76
Harvest Index (%)	90.96	25.92	13.19	13.83
Seed yield (g/plant)	96.85	50.79	25.06	25.46

The number of branches/plant, number of pods/plant, and seed yield/plant all showed a significant phenotypic coefficient of variation (>25%). Plant height, number of pods/cluster and pod length showed a moderate phenotypic coefficient of variation (10-25%). Conversely, days to 50% flowering, days to maturity, number of seeds/pod, 1000 seed weight, biological yield and harvest index showed low Phenotypic Coefficient Variation (<10%). Furthermore, for every character under study, the current findings demonstrated that estimates of PCV were typically greater than corresponding GCV (Table 3). These findings are consistent with those of John Kingsly and Aravinth (2024), Saikumar et al. (2023) and Salman et al. (2023).

The high broad sense heritability was obtained (>60%) in case of plant height, number of pods/plant, number of branches/ plant,1000 seed weight, pod length, number of seeds/pod, number of pods/cluster, seed yield/plant followed by biological yield per plant harvest index, days to maturity and days to 50% flowering. The high heritability may be utilized to increase seed output because it indicates a significant proportion of genetic factors in the determination of these characters (Table 3). These results align with the studies conducted by Asari *et al.* (2019), Hema *et al.* (2023) and Jain *et al.* (2024).

In the current study, high genetic advance (>20%) was obtained for plant height, number of branches/plant, number of pods/plant, number of pods/cluster, pod length, biological yield, harvest index and seed yield/plant.

While the moderate genetic advance (10-20%) was obtained for days to 50% flowering, days to maturity and 1000 seed weight (Fig. 2). This was in consonance with the findings of Joshi *et al.* (2022), Nirmala *et al.* (2023), Thonta *et al.* (2023) and Nalajala *et al.* (2023).

Conclusion

The statistical study demonstrated substantial variations between the twenty-five mungbean genotypes. In the present study, there was a significant amount of variation observed in all twelve of the qualities under evaluation. For all trait under investigation, the GCV was observed to be lower than the PCV, indicating that these were interacting with their environment to some degree. The number of branches/plant, number of pods/plant, and seed yield/plant showed the highest percentage of genotypic coefficient of variation. The number of branches/plant, number of pods/plant and seed yield/plant all showed a significant phenotypic coefficient of variation. The high broad sense heritability was obtained in case of plant height, number of pods/plant, number of branches/plant,1000 seed weight, pod length, number of seeds/pod, number of pods/cluster, seed yield/plant followed by biological yield per plant harvest index, days to maturity and days to 50% flowering. High genetic advance (>20%) was observed for plant height, number of pods/cluster, pod length, biological yield, harvest index and seed yield/plant.

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Competing interests

The authors have stated that there are no conflicting interests.

Authors' contributions

All authors worked together to complete this work. The final manuscript was read and approved by all writers.

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