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Character association studies for grain yield and its components in Greengram (*Vigna radiata* (L.) Wilczek) germplasm

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Abstract

This investigation, titled "Genetic Divergence, Correlation, and Path Analysis in Greengram (*Vigna radiata* (L.) Wilczek)," focused on assessing genetic diversity and correlations among 42 Greengram genotypes during the kharif 2023-24 at the Agricultural Research Station Badnapur. Utilizing a Randomized Block Design with three replications, nine traits were evaluated, including days to flowering, maturity, plant height, and seed yield. The genotypes were categorized into six clusters using Tocher's method, with Cluster II comprising the most genotypes (15). The highest genetic divergence was observed between Clusters V and VI (287.10), while the smallest was between Clusters I and III (67.18). These findings contribute to a better understanding of genetic variation and inform breeding strategies for Greengram.

Keywords: Greengram, genetic diversity, clustering pattern, D² statistics

Introduction

Mungbean, commonly referred to as greengram (*Vigna radiata* (L.) Wilczek), is an essential legume known for its nutritional value and adaptability. With a diploid chromosome number of $2n = 22$, it belongs to the Fabaceae family and the Papilionoideae subfamily. The species is native to India and Central Asia and is categorized into three subgroups: one cultivated (*V. radiata* subsp. *radiata*) and two wild varieties (*V. radiata* subsp. *sublobata* and *V. radiata* subsp. *glabara*) (Asari *et al.* 2019) [2]. The belief that greengram originated in the Indian subcontinent is supported by historical sources (DeCandolle, 1884; Vavilov, 1926; Zukovskij, 1962) [4, 6, 7] reflecting its rich genetic diversity among both cultivated and wild types.

Greengram's significance as a pulse crop is attributed to its short growth cycle, high nutritional content, and ability to thrive in low-water conditions. It is widely cultivated and consumed across India, making it a vital food source. India stands as the leading global producer of mungbean, with cultivation extending to nearly all states. As of the 2021-22 season, mungbean was grown over 40.38 lakh hectares, yielding a total production of 31.5 lakh tonnes and a productivity rate of 783 kg/ha, which accounts for 11% of the nation's total pulse production.

In the 2022-23 kharif season, mungbean cultivation decreased to 33.37 lakh hectares, resulting in a production of 17.5 lakh tonnes (agricoop.nic). Within Maharashtra, it occupied 3.78 lakh hectares, yielding 1.47 lakh tonnes with a productivity of 390 kg/ha. Notably, approximately 82% of the total kharif production comes from six major states: Rajasthan, Karnataka, Maharashtra, Madhya Pradesh, Bihar, and Andhra Pradesh. Overall, mungbean contributes 16% of the area and 10% of the production within India's total pulse crop sector, highlighting its importance in the agricultural landscape (Annual report (2021-22): DES, Ministry of Agri. & FW (DA&FW), Govt. of India).

Materials and Methods

The study titled "Genetic Divergence, Correlation, and Path Analysis in Greengram (*Vigna radiata* (L.) Wilczek)" involved 42 greengram germplasm lines, including two checks, and

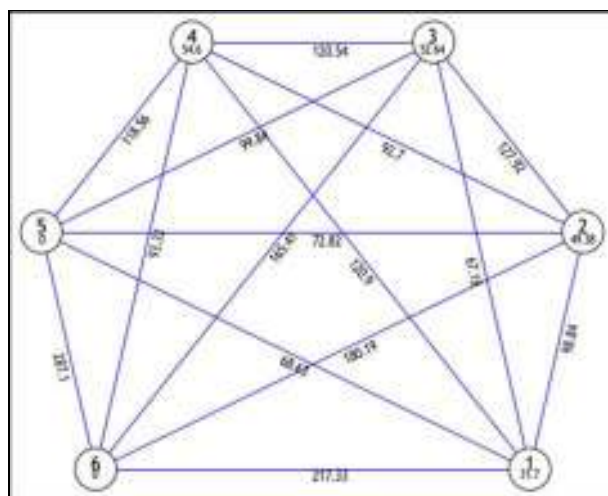
was conducted at the Agricultural Research Station Badnapur during the kharif season of 2023-2024. The genotypes were arranged in a randomized block design with two replications, each genotype planted in two rows of 4 meters, spaced 45 cm apart with 10 cm between plants. Data were collected from five randomly selected plants per replication on various traits, including days to 50% flowering, days to maturity, plant height, number of primary and secondary branches, number of pods and seeds per pod, 100-seed weight, and seed yield per plant.

Results and Discussion

D^2 values were computed for all pairwise comparisons among the genotypes, which led to the classification of the 42 genotypes into eleven distinct clusters, highlighting significant diversity in most traits (Table 1). The squared Euclidean distance method was utilized to measure distances between genotype pairs, and clustering was achieved using Tocher's method (Figure 1). The mean values for nine yield-related traits in pigeonpea were estimated for each cluster, demonstrating a wide range of variation (Table 2). The cluster mean for days to 50 percent flowering ranged from 32.00 days in cluster VI to 38.72 days in cluster III. For days to maturity, the mean varied between 62.50 days in cluster VI and 68.67 days in cluster I. The highest plant height mean was observed in cluster III at 63.63 cm, while cluster II had the lowest at 44.91 cm. The number of primary branches per plant ranged from 3.91 in cluster II to 6.10 in cluster III. For secondary branches, the means varied from 4.80 in cluster II to 7.66 in cluster I. Cluster I had the highest mean number of pods per plant at 22.92, while cluster VI had the lowest at 15.40. The maximum number of seeds per pod was found in cluster V (13.75), and the minimum was in cluster IV (11.96). The mean for 100-seed weight ranged from 2.50 in cluster VI to 6.00 in cluster V. Finally, seed yield per plant varied from 11.45 grams in cluster VI to 16.00 grams in cluster V. The clustering pattern of genotypes confirmed significant diversity. Cluster II contained the largest group with 15 genotypes, while Cluster I and Cluster III each had 9 genotypes, and Cluster IV had 7 genotypes. Clusters V and VI each had a single genotype. These findings align with those of Bhareti *et al.* (2019) [3], who also reported six clusters. Similarly found 15 genotypes, identifying Cluster II as the largest polygenotypic cluster. The observed divergence within clusters indicates variability among genotypes in the same cluster, while inter-cluster divergence reflects genetic distances between different clusters. Both inter- and intra-cluster D^2 values were calculated during the divergence analysis. A detailed assessment of the clusters showed heterogeneity within and between them based on key traits. The composition of each cluster, along with inter- and intra-cluster distances, is presented in Table 3, and a cluster diagram illustrating the relationships among different populations was created. The greatest distance between clusters was observed between Cluster V and Cluster VI (287.10), indicating the highest divergence, followed by distances between Cluster I and VI (217.33), VI and II (180.19), III and VI (165.41), II and III (127.92), I and IV (120.90), IV and III (120.54), and IV and V (118.56). The smallest distance was recorded between Cluster I and III

(67.18), followed by Cluster II and V (68.63), II and IV (72.82), IV and VI (93.32), I and II (98.84), and III and V (99.84), indicating minimal genetic divergence among those genotypes. The high inter-cluster distance between Cluster V and VI suggests a wide range of variation among the clusters, consistent with the findings of Bhareti *et al.* (2019) [3].

The intra-cluster values ranged from 0.00 to 54.60, with the highest intra-cluster distance of 54.60 observed in Cluster IV, followed by 52.64 in Cluster III and 49.38 in Cluster II. The genotypes in these clusters can be considered suitable parents for hybridization programs, as the high degree of divergence among them is likely to yield more desirable breeding material for maximizing genetic advancement. This finding aligns with, who reported intra-cluster values ranging from 0.00 to 24.47, also noting that Cluster IV exhibited the maximum intra-cluster distance. Genotypes within these clusters, showing significant divergence, are ideal candidates for hybridization programs, as they are likely to produce desirable breeding material and enhance genetic advancement for specific traits. This implies that genotypes from these clusters can effectively serve as parents in hybridization efforts, given that crosses between genetically diverse parents can result in transgressive segregants. Greater emphasis should be placed on the traits contributing most to genetic divergence when selecting parents within their respective clusters for hybridization. The frequency of each yield component character ranked first and its corresponding contribution percentage toward genetic divergence is presented in Table 4. It was observed that 100-seed weight contributed the most to divergence at 25.67%, followed by the number of secondary branches per plant (24.39%), plant height (15.08%), number of primary branches per plant (13.01%), number of pods per plant (9.87%), number of seeds per pod (6.39%), days to 50 percent flowering (3.72%), seed yield per plant (0.81%), and days to maturity (0.35%). Similar findings were reported by Bhareti *et al.* (2019) [3], who noted that 100-seed weight accounted for the highest percentage of divergence at 59.00%. Comparable results were also observed.



Mahalanobis Euclidean Distance (Not to the Scale)

Fig 1: Distances among cluster by Touchers method

Table 1: Composition of forty-two greengram genotypes into different clusters by Tocher's method.

Cluster Number	No. of genotypes	Germplasm included in the cluster
I	9	AKM-12-14, PM-504-20-27, PM-809-12, PM-818-08, TARM 01, PM-402-2-1, TAM 141, AKM 1608, PM-809-10.
II	15	BM-2021-5, BM-2021-40, BM-2021-7, BM-2021-43, BM-2021-20, BM-2021-36, BM-2021-35, IPM-410-3, BM-2021-21, BWMC 25, BM-2021-01, BM-2021-12, BM-2021-10, ML 2479, MML 2570.
III	9	PM-811-04, BM-2003-02, Phule Chetak, PM-811-17, BWMC 10, PM-702-1, TAM 127, BWMC 31, BWMC 05.
IV	7	IPM-512-1, RMG 1028, BM-2021-4, MH 1468, BWMC 20, ML 1808, IPM-404-4.
V	1	BM-2021-02
VI	1	LGG-460

Table 2: Cluster means for seed yield and its components in Greengram.

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plants.	Number of secondary branches/plants.	Number of pods/plants.	Number of seeds/pods	100 Seed weight (g)	Seed yield/Plant
Cluster I	37.94	68.67	53.78	4.75	7.66	22.92	12.49	4.74	15.13
Cluster II	35.30	66.27	44.91	3.91	4.80	16.56	13.08	4.72	13.22
Cluster III	38.72	68.33	63.63	6.10	7.01	20.62	13.38	4.60	15.67
Cluster IV	33.14	63.50	45.76	5.44	6.11	13.89	11.96	3.95	12.39
Cluster V	35.50	66.50	47.50	5.55	6.00	16.90	13.75	6.00	16.00
Cluster VI	32.00	62.50	58.50	5.40	5.95	15.40	12.60	2.50	11.45

Table 3: Average intra and inter cluster distance (D) values from 42 genotypes in greengram.

Cluster No.	I	II	III	IV	V	VI
I	31.70	98.84	67.18	120.90	68.63	217.33
II		49.38	127.92	92.70	72.82	180.19
III			52.64	120.54	99.84	165.41
IV				54.60	118.56	93.32
V					0.00	287.10
VI						0.00

Table 4: Percent contribution of different characters to genetic diversity.

Sr. No	Characters	No. of times appearing I in ranking	% Contribution
1.	Days to 50 % flowering	32	3.72%
2.	Days to maturity	3	0.35%
3.	Plant height (cm)	136	15.8%
4.	Number of primary branches/plant	115	13.01%
5.	Number of secondary branches/plant	210	24.39%
6.	Number of pods/plant	85	9.87%
7.	Number of seeds/pod	55	6.39%
8.	100 seed weight (g)	221	25.67%
9.	Seed yield/plant	7	0.81%
10.	Total	861	100 %

Conclusion

The clustering analysis of 42 pigeonpea genotypes revealed significant genetic diversity, with eleven distinct clusters identified. Key yield-related traits exhibited notable variation, highlighting the potential for selective breeding. Clusters II and IV showed the highest intra-cluster distances, indicating suitable candidates for hybridization to enhance genetic advancement. The 100-seed weight emerged as the primary contributor to genetic divergence, followed by the number of secondary branches and plant height. These findings underscore the importance of genetic diversity in breeding programs, emphasizing the selection of diverse parent genotypes to maximize trait improvement and achieve desirable breeding outcomes.

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