Original Research Article

Analysis of Genetic Diversity in Greengram(*Vigna radiata* L. Wilczek)

ABSTRACT

The current study titled “Analysis of genetic diversity in green gram [*Vigna radiata* (L.) Wilczek]” was carried out at Center for Crop Research(C.R.C.), Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. A set of twenty five mungbean genotypes were examined to investigate the essence and extend of divergence of genes using Mahalanobis'sD^2 Statistics on twelve critical quantitative attributes. The study material was assessed using Randomized Block Design (RBD) with three replication plots of two rows of 4 meter length. Out of every replication, five plants were selected at random, marked, and observations were recorded for twelve quantitative attributes. Analysis of variance showed that there was significant variation among all characters examined. The twenty-five genotypes of mungbean have been split into seven distinct clusters.With seven genotypes apiece, Cluster I and Cluster IV were determined to be the largest. The intra cluster distance was maximum for Cluster IV. The maximum inter cluster distance between cluster V and cluster II suggests that the genotypes in these clusters doesn't correlate with one another and the minimal inter-cluster distance between cluster V and cluster IV demonstrates a high degree of connection between the genotypes in these clusters. Plant height, number of branches/plants, number of pods/plant, number of pods/clusters, pod length, biological yield, harvest indexand seed yield per plant are vital for genetic diversity and were recognized as significant contributors to genetic divergence.

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Keywords: Greengram, genetic diversity, cluster analysis,D^2 statistics

1. INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek] also known as mungbean, mash or simply moong ranks as the third most crucial pulse crop and is much esteemed as a grain legume. Mungbean is cultivated worldwide mainly in Asian countries such as China, India, Bangladesh, Indonesia and Myanmar. Globally, India holds the position of the largest producer and consumer of mungbean accounting for about 65% of the world acreage and 54% of the world production of this crop [1].In India Mungbean is cultivated over an area of 5.5 million hectares with a production of 3.17 million tonnes and productivity of about 570 kg/ha (2022-23, IIPR, Kanpur). The largest share of mung bean cultivation in the context of both land coverage and output is in Rajasthan (46% and 45% respectively), with Madhya Pradesh (9% and 14%), Maharashtra (9% and 8%), Karnataka (9% and 6%), Odisha (5% and4%) and Bihar (4% and 5%) [2].

In India greengram is sown in three different seasons, viz., kharif, rabi and summer. About 70 percent of mungbean is grown during Kharif season while the remaining 30 percent is sown in summer season. Cultivation of Zaid Moong is important to increase soil fertility in the areas where rice–wheat crop rotation is practiced. Mungbean being a low-

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input, short-duration, high-value crop,is very much compatible with rice-wheat cropping systems and other crop rotation systems. Greengramis an indispensable component in cropping system of India owing to their capacity offixingthe nitrogen from the atmosphere into the soil through rhizobium nodules, extracting water from lower layers of soil due to tap root system, fallen leaves serves as organic matter to soil, crop residue serves as an excellent source of feed for livestock. Mungbean requires a favorable warm climate during vegetative growth and cool climatic conditions at the time of ripening. The crop species have evolved under a broad spectrum of agroclimatic conditions. It grows mainly in sub-humid and sub-tropical regions with a mean temperature of of 22°C to 35 °C and an annual precipitation of 60 to 100 cm. Mungbean is a warm season, annual, short duration (65-90 days), autogamous, diploid species with a chromosome number of 2n =22. Mungbean has become extremely valuable short-lived grain legume crop with many desirable characteristics, such as wide adaptability, low input requirements and the ability to improve soil fertility [3].

In places where meat is scarce or people are primarily vegetarians, ripe mungbean seeds are a valuable reservoir of easily digestible protein. Mung beans can be freshly cooked or sun-dried. It can be eaten whole or in flour, soups, porridge, sandwiches, bread, pasta, and ice cream. Split seeds can be turned into pigeon peas such as black beans and lentils. Sprouted seeds are consumed raw or cooked all over the world. The immature pods and young leaves can be eaten as vegetables. The consumption of greengram and its value-added products improves the nutritional status of individuals; therefore, it serves a significant provider of nutrients and helps to eliminate malnutrition in theworld. The nutritional value of mung bean lies in their rich and easily digestible protein. Based on dry weight, it contains approximately 25-28% protein, 1.0% oil, 3.5-4.5% fiber, 4.5-5.5% ash and 62-65% carbohydrates. It also contains vitamin A (94 mg), iron (7.3 mg), calcium (124 mg), zinc (3 mg) and folic acid (549 mg) per 100 g dry seed [5].

Although this cropholds great significance in our day-to-day diet and agricultural production, the productivity of this crop in India is very low. Since the beginning of systematic crop improvement, natural variation and divergence between crops have been widely identified and exploited to improve crop species. Diversity is the essence of living world. Assessment of phenotypic or genotypic diversity offers valuable insights for efficient utilization of germplasm collections, which is thefundamental material for enhancing genetic traits and in breeding. Genetic diversity serves as a way for population to adapt to changes in the environment that involves greater variation. Furthermore, in the context of climatic changes and associated unforeseen events, genetic diversity may serve as the reservoir for many novel characteristics that confers resistance to different biotic and abiotic stresses [7].

The diversity in plant genetic resource provides plant breeders with the ability to select desirable traits that consist of both farmer- preferred characteristics (significant yield potential and substantial seed size etc.) and breeder-preferred characteristics (pest and disease resistance and photosensitivity and thermosensitivity etc.). Genetic variability between two parents is essential to detect heterosis and to obtain transgressive segregants. Genetic diversity enables breeders to develop varieties for precise attributes likeyield potential, early maturity, quality improvement and tolerance to biotic and abiotic stresses. Amount of variability is high in mungbean for different traits like days to flowering, days to maturity, plant height, harvest index, number of pods per plant, number of clusters per plant, etc. All these traits are used in breeding programs to release good number of varieties in greengram. Considering all these aspects, a researchinvestigation was performedto analyze genetic diversity of greengram.

2. MATERIAL AND METHODS

The field investigation was carried out at Center for Crop Research (C.R.C), Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut during Kharif season 2021.

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Geographically Meerut is located at 29.010 latitude in the North and at 77.450 longitude and at an altitude of 217 meters elevated above the sea level, signifying the North Western Plain Zone. The climate here is bestowed with hot and humid summers followed by cold and dry winters. The experimental field had soil with a sandy-loam consistency, with decent drainage and uniform texture, slightly alkaline (pH 7.68) in reaction. The investigation's experimental materials included of 25 genotypes (Table 1) gathered from all over India and the evaluation was conducted employing three replications of a Randomized Block Design (RBD) during the Kharif season 2021 in the plot of 2 rows of 4m length. Spacing between the rows was 30cm and the gap between plant was maintained at 20cm by proper thinning.The entire recommended collection of standard approaches were adheredto retain a good crop stand. The details of experimental materialispresented in Table 2. Five randomized competitive plants from each replications were tagged for recording observations 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, harvest index. Statistical analysis was employed in this experimentand replication wise mean data for twelve traitsof twenty five genotypes wereutilized for the statistical and biometrical analysis for the parameters- Analysis of variance as per the methods given by Panse and Sukhatme[8] and the assessment of genetic divergence was conducted as per the MahalanobisD^2 [9] statistics followed by the Rao [10].The determination of cluster means, average distances within and between clusters, and the contribution of various traits totaldivergence was carried out as per the Singh and Choudhary [11].

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Table 1: Detailof theMungbeangenotypesusedininvestigation

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Genotype	Source	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		

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3. RESULTS AND DISCUSSION

The statistical evaluation showed notable differences between the twenty five genotypes of mungbean.In this particular investigation, noteworthy variation was observed in all twelve characters under investigation. Similar findings were obtained byChandra *et al.* (2017)**,**Susmitha and Jayamani(2018), Kate *et al*. (2018),Mariyammal*et al.* (2019), Charles *et al.* (2020), Singh*et al.* (2021) and Kingsly *et al.*(2023).

Based on D^2 values twenty five genotypes of mungbean were split into five distinct clusters. (**Table 2**) using twelve component characters. Out of five clusters, Cluster I (Pusa-16, Pusa-371, MH-521, Pusa-9531, ML-141, IPM-05-2-8 and WNM-16) and Cluster IV (WGG-37, Indore Mung, Pant Mung-7, Tarun-18, Asha Mung, PDM-191 and MH-21) was identified as the largest one with 7 genotypes each, followed by Cluster II (Pusa Vaishali, IPM-02-19, IPM-02-19, OMG-1045 and VBG-04-008) and Cluster V (Pusa-0871, Pusa-0891, SMM-15-72 and PDM-262) with 4 genotypes each and least count of genotypes 3 are present in Cluster III (HUM-12, Kaporgaon and Pusa Vishal).Comparable results were obtained by Chandra *et al.* [12]**,**Jeeva*et al*. [13] andMathankumar*et al.*[14].

Table 2: Distribution of Greengram genotypes within each cluster

Clusters	No. of genotypes	Genotypes
I	7	Pusa-16, Pusa-371, MH-521, Pusa-9531, ML-141, IPM-05-2-8, WNM-16
II	4	Pusa Vaishali, IPM-02-19, IPM-02-19, OMG-1045,VBG-04-008
III	3	HUM-12, Kaporgaon, Pusa Vishal
IV	7	WGG-37, Indore Mung, Pant Mung-7, Tarun-18, Asha Mung, PDM-191, MH-21
V	4	Pusa-0871, Pusa-0891, SMM-15-72, PDM-262

The intra cluster distance was maximum for Cluster IV (2.607) followed by Cluster I (2.599), Cluster III (2.343), Cluster V (2.316) and minimum for Cluster II (2.106) suggesting that the genotypes of Cluster II have similar genetic constitution i.e., homogeneous and less divergent (**Table 3**). The maximum inter cluster distance was observed between Cluster V and Cluster II (4.410), followed by Cluster V and Cluster I (4.369), Cluster III and Cluster I (4.204), Cluster III and Cluster II (3.873), Cluster IV and Cluster I (3.746), Cluster IV and Cluster II (3.655), Cluster IV and Cluster III (3.594), Cluster V and Cluster III (3.559), Cluster II and Cluster I (3.324). hence, hybridization can be taken up between these genotypes for obtaining desirable segregants for the Seed yield and other yield contributing characters. The minimum inter cluster distance between the Cluster V and Cluster IV (2.961) indicating close association between genotypes of these clusters, which is not recommended for hybridization programme. The maximum inter cluster distance showed that genotypes of Cluster V and Cluster II areuncorrelated while minimum inter cluster distance between Cluster V and Cluster IV revealedthat the genotypes of these cluster are strongly correlated.Similar findings were obtained byCharles *et al.*[15], and Kingsly *et al.* [16].

Table 3: Average intra and inter cluster D2 values of 25 genotypes of Greengram

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Clusters	I	II	III	IV	V
I	**2.599**				
II	3.324	**2.106**			
III	4.204	3.873	**2.343**		
IV	3.746	3.655	3.594	**2.607**	
V	4.369	4.410	3.559	2.961	**2.316**

The cluster mean values for twelve characters are presented in **table 4**. The data indicated a wide range of mean values between the characters under study. Days to 50 % flowering showed highest mean for Cluster II (36.83) and least mean for Cluster III (30.33), Days to maturity showed highest mean for Cluster IV (16.37) and least mean for Cluster II (66.33), Plant height showed highest mean for Cluster III (60.20) and lowest mean for Cluster II (48.29), Number of branches/plant showed highest mean for Cluster IV (16.37) and least mean for Cluster III (12.27), Number of pod/plant showed highest mean for Cluster I (33.18) and least mean for Cluster III (18.79), Number of pods/cluster showed highest mean for Cluster I (4.60) and lowest mean for Cluster III (2.97), Number of seeds/pod showed highest mean for Cluster I (11.94) and least mean for Cluster V (10.56), Pod length showed highest mean for Cluster II (8.37) and least mean for Cluster III (7.09), 1000 seed weight showed highest mean for Cluster III (43.10) and lowest mean for Cluster I (37.87), Biological yield showed highest mean for Cluster I (17.06) and lowest mean for Cluster IV (11.26), Harvest index showed highest mean for Cluster I (39.20) and least mean for Cluster IV (26.16) and Seed yield/plant showed highest mean for Cluster I (6.70) and lowest mean for Cluster V (3.96).Similar results were obtained by Sen *et al.* [17], Mahalingam *et al.* [18] andSharma *et al.* [19].

Table 4: Cluster mean for twelve characters in Greengram (*Vigna radiate* L. Wilczek)

Characters	Days to 50% flowering	Days to Maturity	Plant Height (cm)	No of Branches / Plant	No. of Pods / Plant	No. of Pods /Cluster
I	32.43	66.90	58.33	14.13	33.18	4.60
II	36.83	66.33	48.29	12.57	20.55	3.25
III	30.33	70.67	60.20	12.27	18.79	2.97
IV	34.33	72.14	52.17	16.37	22.61	4.16
V	31.83	70.08	59.43	15.75	22.51	4.05

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Characters	No. of Seeds / Pod	Pod Length(cm)	1000 Seed Weight(g)	Biological Yield (g/plant)	Harvest Index (%)	Seed yield (g/plant)
I	11.94	7.90	37.87	17.06	39.20	6.70
II	11.06	8.37	38.35	17.01	38.83	6.61
III	11.82	7.09	43.10	14.81	35.36	5.15
IV	11.16	7.91	39.09	11.26	36.25	4.08
V	10.56	7.38	39.69	15.19	26.16	3.96

Out of twelve characters studied the maximum contribution (79.57%) towards total divergence (**Fig.1**) is by seven characters only *i.e.,* Days to 50% flowering(13.92), Days to maturity (13.02), Pod length (11.79), Number of seeds/pod (9.91), Seed yield/plant (8.85), Harvest index (7.65), Biological yield (7.43) and Number of branches/plant (7.00).Jadhav *et al.* [20], Sridhar *et al.* [21] and Aijaz *et al*. [22] reported similar results.

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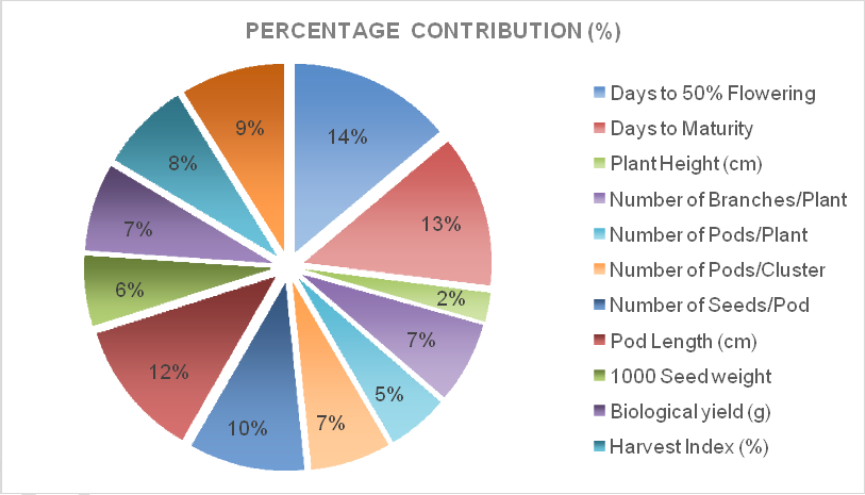
Fig. 1: Percentage contribution of characters



4. CONCLUSION

Plant height, number of branches/plant, number of pods/plant, number of pods/cluster, pod length, biological yield, harvest index and seed yield/plant were recognized as significant contributors to genetic diversity, which may be utilized as a guide when choosing parents from a variety of backgrounds for hybridization in breeding programs to increase yield substantially. Also, these attributes can be employed for direct selection of mungbean genotypes for future utilization in various breeding practices of crop improvement. Basedon high inter cluster distances, hybridization programme could be taken up between the

varieties of cluster II (Pusa Vaishali, IPM-02-19, IPM 02-19, OMG-1045, VBG-04-008) and cluster V (Pusa-0871, Pusa-0891, SMM-15-72, PDM-262).Hence, these nine genotypes are recognized as promising progenitors and can be employed in further breeding programme in which the above mentioned attributes will be considered for selection to achieve the best outcome of the breeding programme.

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