



E-ISSN: 2278-4136

P-ISSN: 2349-8234

www.phytojournal.com

JPP 2020; 9(2): 1890-1893

Received: 20-01-2020

Accepted: 24-02-2020

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Estimation of genetic variability and divergence in Greengram *Vigna radiata* (L.) germplasm

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Abstract

100 greengram genotypes were evaluated to estimate genetic variability and divergence among genotypes for future breeding studies during *Kharif*, 2018 in RBD with three replications. Genetic analysis revealed that number of primary branches per plant showed high GCV and PCV followed by number of clusters per plant. High heritability was recorded for protein content. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering and number of clusters per plant. The germplasm was further subjected to Mahalanobis D^2 statistics and grouped into ten clusters. Cluster II was largest with 18 genotypes followed by cluster IV and VI. The maximum inter cluster distance was observed between cluster III and IV (1128.22) followed by cluster I and IV (1106.89), while minimum inter cluster distance was observed between cluster III and X (39). Cluster IV showed highest mean value for seed yield per plant.

Keywords: Greengram, diversity, D^2 analysis, Mahalanobis

Introduction

Greengram [*Vigna radiata* (L.) Wilczek] is one of the important grain-legume crop ranks third among the pulses that grown in India after chickpea and pigeon pea. It is one of the important pulse crops because of its adaptation to short growth duration, low water requirement, soil fertility and is favored for consumption due to its easy digestibility and low production of flatulence. Greengram is a major source of protein and minerals for the predominantly vegetarian population of India. The sprouted seeds contain an increased amount of thiamine, niacin and ascorbic acid, thus greengram sprouts are increasingly becoming popular in certain vegetarian diets. Greengram contains per 100g vitamin A (94 mg), vitamin C (8 mg), iron (7.3 mg), calcium (124 mg), magnesium (189 mg), phosphorus (367 mg), potassium (1246 mg), zinc (3 mg) and foliate (549 mg).

Unlike other pulses, it is free from flatulent effects in stomach. It fits well in various multiple and intercropping systems. The total world acreage under pulses is about 85.40 (Mha) with production of 87.40 (Mt) at 1023kg/ha productivity. In India, greengram is grown over an area about 42 Lha with an area production of 20 Lt having an average grain yield of 476 kg/ha (Annual report, Directorate of Pulses Development 2017-18).

Selection of superior parents exhibiting better heritability and genetic advance for various characters is an essential prerequisite for any yield improvement programme. Genetic variability with the help of suitable parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding program. Studies on genetic diversity are of considerable importance to classify the available genotypes into discrete classes, so that the parents belonging to diverse groups could be selected. In addition to aiding in the selection of divergent parents for hybridization, multivariate analysis by means of Mahalanobis D^2 statistics is a powerful tool that measures the degree of divergence at genotypic level and determines the relative contribution of each component character to the total divergence.

Materials and Methods

The present experiment was carried out during *Kharif* –2018, at the Field Experimentation Centre, department of Genetics and Plant Breeding, SHUATS, Prayagraj (Allahabad) Uttar Pradesh in Randomized Block Design with 100 Greengram germplasm. The treatments were replicated three times. Treatments were randomly arranged in each replication divided into 300 plots. The gross area of experiment was 456.05 m² and plot size was 1 X 1 m, the row to row spacing was 30 cm and plant to plant distance was 10 cm. Soil in this region is sandy loam and slightly alkaline. The experimental material for the present study was obtained from Indian Institute of Pulses Research, Kanpur, Rajasthan Agriculture Research Institute, Durgapura

(Rajasthan) and Agriculture Research Station, Badnapur (Maharashtra). The technique of random sampling was adopted for recording the observations of 12 quantitative characters namely days to 50 percent flowering, days to maturity, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, seed index, biological yield per plant, harvest index and seed yield per plant. Recommended package of practices were applied to raise a healthy crop. Metric data on 12 characters were recorded at different stages of growth.

The data collected on different characters were analyzed through the method of analysis of variance for single factor (Gomez and Gomez, 1984) [8] and different genetic parameters were estimated. Mahalanobis's generalized distance (D^2) for genetic diversity. Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao (1952) [14]. The criterion used in clustering by this method is that any two varieties belonging to the same cluster should at least, on an average show a smaller D^2 values of the combinations of each genotype arranged in increasing (ascending) order of their magnitudes in a tabular form as described by Singh and Choudhary (1985) [15].

Results and Discussion

Hundred genotypes taken for analysis of variance showed significant difference for all the characters studied (Table 1) indicates that there is ample scope for selection of promising genotypes from present germplasm for yield improvement. Maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for number of primary branches per plant and number of clusters per plant, while minimum genotypic variation was observed for days to 50% flowering and days to maturity table 2. Similar results were obtained by Lavanya (2006) [10], Kumhar and Chaudhary (2007) [9], and Sreethy (2017) [16]. The studies on GCV and PCV indicated that the presence of high amount of variation and role of the environment on the expression of these traits. The magnitude of PCV was higher than GCV for all the characters which may be due to high degree of interaction of genotypes with the environment.

All the characters showed high heritability percent in broad sense. Highest value of heritability was observed for protein content (98.80) followed by number of pods per plant (98.70) and seed index (98.40) table 2. Similar results were reported by Pandiyan *et al.* (2006) [12] and Makeen *et al.* (2007) [11]. The high heritability of these traits indicates that there is a close correspondence between the genotype and phenotype and selection can be done. High estimates of genetic advance were noticed in character, plant height (22.20) followed by harvest index (19.80) and number of pods per plant (12.40) whereas low estimates of genetic advance were observed for seed index (2.30) and pod length (2.60) table 2. The results are in consonance with Makeen *et al.* (2007) [11], Yimram *et*

al. (2009) [17] and Garje *et al.* (2014) [6]. The estimates of genetic advance as percent of mean was high for number of primary branches per plant (75.90) followed by number of clusters per plant (73.20) and pod length (69.30) Azam *et al.* (2018) [3]. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering and number of clusters per plant. The high heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such traits may not be useful.

Genetic divergence analysis are differed significantly with regard to characters studied and displayed marked divergence when subjected to Wilk's criteria taking all the 12 quantitative characters together. On the basis of magnitude of D^2 values, hundred genotypes were grouped in 10 clusters (Table 3). Cluster II with 18 genotypes emerged as the largest cluster followed by cluster IV includes 17 genotypes, cluster VI comprised 15 genotypes, and cluster X includes 1 genotype (Fig. 1). The pattern of group constellation proved the existence of significant amount of variability. Wide diversity was also reported by Prasanna *et al.* (2013) [13] for 50 greengram genotypes into eight clusters, Garje *et al.* (2013) [5] for 40 genotypes into 13 clusters, Ahmad *et al.* (2016) [1] for 35 genotypes into seven clusters, Chandra *et al.* (2017) [4] grouped 40 genotypes into seven clusters.

Average intra cluster distance was ranged from 0.00 to 34.692 maximum intra cluster distances were recorded for cluster VI (34.692) followed by cluster IV (13), cluster IX (11.155) whereas minimum intra cluster distance recorded for cluster II (7.518) followed by cluster I (7.524) (Table 4). The inter cluster D^2 value was maximum between cluster III and IV (1128.22) followed by cluster I and IV (1106.89), cluster II and IV (1102.97), cluster I and II (721.94) and cluster I and VI (626) while minimum inter cluster distance recorded for cluster III and X (39). Suggesting that the genotypes present in these clusters may be used as parents for hybridization programme to develop desirable lines as heterosis can be best exploited and chance of getting transgressive segregants are maximum when diverse genotypes are crossed.

Cluster IV mean values showed maximum for the characters days to 50% flowering, days to maturity, plant height, number of pods per plant and seed yield per plant (Table 5). Similar findings were reported by Gokulkrishnan *et al.* (2012). On basis of seed yield performance and other specialized characters genotypes KMII-584, KM-1413, COGG-10-10 and BM-4 are identified that can be used for future breeding programmes.

The present investigation results indicate that considerable variability and diversity present in the experimental material as hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives probably due to complementary interaction of different genes in parents.

Table 1: Analysis of variance for different Characters in Greengram (kharif, 2018)

| Sl. No | Characters | Mean Sum of Squares | | |
|--------|--------------------------------------|---------------------|--------------------|-----------------|
| | | Replication (d.f=2) | Treatment (d.f=99) | Error (d.f=198) |
| 1 | Days to 50% Flowering | 17.52 | 18.74** | 2.87 |
| 2 | Days to Maturity | 3.79 | 44.76** | 4.47 |
| 3 | Plant Height | 10.2 | 256.87** | 15.85 |
| 4 | Number of Primary Branches per Plant | 0.03 | 2.04** | 0.12 |
| 5 | Number of Clusters per Plant | 0.56 | 8.43** | 0.24 |
| 6 | Number of Pods per Plant | 2.3 | 73.12** | 1.49 |
| 7 | Number of Seeds per pod | 2.21 | 11.89** | 0.62 |

| | | | | |
|----|----------------------|-------|----------|-------|
| 8 | Pod length | 0.09 | 1.43** | 0.18 |
| 9 | Seed Index | 0.1 | 0.49** | 0.06 |
| 10 | Biological yield | 0.31 | 49.15** | 2.12 |
| 11 | Protein Content | 7.58 | 14.18** | 0.28 |
| 12 | Harvest index | 24.41 | 200.82** | 10.98 |
| 13 | Seed yield per plant | 0.87 | 3.77** | 0.15 |

** Significant at 1% level of significance

Table 2: Genetic parameters for 13 different characters of 100 greengram genotypes

| Sl. No. | Characters | Coefficient of variation | | Heritability (%) (bs) | Genetic Advance | Genetic advance % of mean |
|---------|-----------------------------------|--------------------------|------------|-----------------------|-----------------|---------------------------|
| | | Genotypic | Phenotypic | | | |
| 1 | Days to 50% Flowering | 7.23 | 7.61 | 90.30 | 5.90 | 14.20 |
| 2 | Days to Maturity | 7.30 | 7.55 | 93.40 | 9.20 | 14.50 |
| 3 | Plant Height | 17.38 | 17.75 | 95.80 | 22.20 | 35.00 |
| 4 | No. of Primary Branches per Plant | 37.19 | 37.55 | 98.10 | 2.90 | 75.90 |
| 5 | No. of Clusters per Plant | 35.80 | 36.08 | 98.40 | 4.60 | 73.20 |
| 6 | No. of Pods per Plant | 33.32 | 33.54 | 98.70 | 12.40 | 68.20 |
| 7 | No. of Seeds per pod | 23.60 | 23.97 | 97.00 | 5.20 | 47.90 |
| 8 | Pod length | 17.74 | 18.06 | 96.50 | 2.60 | 35.90 |
| 9 | Seed Index | 33.91 | 34.19 | 98.40 | 2.30 | 69.30 |
| 10 | Biological yield per plant | 25.17 | 25.53 | 97.20 | 10.10 | 51.10 |
| 11 | Protein content | 13.63 | 13.71 | 98.80 | 5.80 | 27.90 |
| 12 | Harvest Index | 31.37 | 31.96 | 96.30 | 19.80 | 63.40 |
| 13 | Seed yield per plant | 28.38 | 28.64 | 98.20 | 3.40 | 58.00 |

Table 3: Distribution of the 100 greengram genotypes into different clusters

| S. No. | Cluster No. | No. of genotypes | Name of Genotypes |
|--------|-------------|------------------|--|
| 1 | I | 8 | RMG – 62, RMG – 1027, PUSA – 672, KM – 1405, KM – 1409, KM – 1410, KM – 2342, JYOTHI |
| 2 | II | 18 | RMG – 268, RMG – 344, RMG – 492, RMG – 1014, RMG – 1015, RMG – 1041, RMG – 1042, RMG – 1045, RMG – 1083, RMG – 1091, RMG – 1092, COGG – 12-16, IPM – 02-03, PUSA – 871, JLM – 1702, ML – 1299, MH – 934, G – 4 |
| 3 | III | 12 | RMG – 871, RMG – 1030, JLM – 1748, T – 44, KM – 1415, VGG-05-26-3, RMG-1039, RMG - 2029, DGG - 3, RMG - 118, RMG - 1028, DGG – 6 |
| 4 | IV | 17 | RMG – 975, BM – 4, IPM – 5-07, IPM – 1-9901-08, PM – 9-11, PUSA – 1471, PUSA – 1472, HUM – 27, KMII – 551, KMII – 564, KMII – 583, ML – 2333, SGC – 20, IGKM – 05-26-3, NDMK – 13-1, KM – 1406, KM – 2346 |
| 5 | V | 9 | RMG – 1004, RMG – 1-1083, KMII – 582, KMII – 584, KMII – 585, KMII – 587, SHARIF – 1, NAVYA, SAMRAT – CHECK |
| 6 | VI | 15 | RMG – 1040, RMG – 1093, MSJ – 118, BM – 2002-1, BGS – 9, BGS – 11, NVL – 641, IPM – 02-14, IPM – 9901-8, SML – 668, BPMR – 145, ML – 2024, KM – 1422, KM – 1423, KM – 2241 |
| 7 | VII | 4 | BM – 2003-2, JLM – 1754, JLM – 1764, ML – 2056 |
| 8 | VIII | 10 | COGG – 10-10, COGG – 12-10, KMII – 563, KMII – 575, KM II – 586, KM – 1401, KM – 1404, KM – 1408, KM – 1413, KM – 1414 |
| 9 | IX | 6 | JLM – 1751, JLM – 1752, JLM – 1757, JLM – 1758, JLM – 1763, JLM – 1773 |
| 10 | X | 1 | KM – 2195 |

Table 4: Intra (diagonal) and inter cluster average distances (D^2) for 12 different quantitative characters in greengram

| | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X |
|-------------|---------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|----------------|
| Cluster I | 7.524 (2.743) | 721.943 (26.869) | 493.728 (22.223) | 1,106.89 (33.278) | 276.257 (16.621) | 626 (25.026) | 408.444 (20.21) | 292.41 (17.108) | 221.087 (14.869) | 54.066 (7.353) |
| Cluster II | | 7.518 (2.742) | 455.95 (21.353) | 1102.97 (33.211) | 293.88 (17.143) | 603.291 (24.562) | 205.176 (14.324) | 311.381 (17.646) | 198.61 (14.077) | 41.770 (6.463) |
| Cluster III | | | 10.048 (3.17) | 1128.220 (33.589) | 295.324 (17.185) | 595.848 (24.41) | 204.461 (14.299) | 332.88 (18.245) | 181.683 (13.479) | 39 (6.245) |
| Cluster IV | | | | 13 (3.606) | 294.465 (17.162) | 616.975 (24.839) | 105.616 (10.277) | 296.287 (17.213) | 216.972 (14.731) | 49.984 (7.074) |
| Cluster V | | | | | 9.734 (3.122) | 606.242 (24.622) | 252.778 (15.899) | 320.052 (17.893) | 229.825 (15.165) | 43.56 (6.6) |
| Cluster VI | | | | | | 8.236 (2.878) | 242.736 (15.584) | 355.322 (18.851) | 207.072 (14.391) | 41.107 (6.413) |
| Cluster VII | | | | | | | 34.692 (5.891) | 367.105 (19.169) | 215.208 (14.677) | 58.064 (7.623) |

| | | | | | | | | | | | |
|--------------|--|--|--|--|--|--|--|--|---------------|------------------|----------------|
| Cluster VIII | | | | | | | | | 8.352 (2.891) | 208.802 (14.455) | 52.417 (7.248) |
| Cluster IX | | | | | | | | | | 11.155 (3.345) | 79.21 (8.905) |
| Cluster X | | | | | | | | | | | 0.000 |

Table 5: Clusters mean for 12 quantitative characters of 100 greengram genotypes.

| S. No. | Characters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X |
|--------|-----------------------------------|-----------|------------|-------------|------------|-----------|------------|-------------|--------------|------------|-----------|
| 1 | Days to 50% Flowering | 42.17 | 40.43 | 38.97 | 39.86 | 43.56 | 43.89 | 40.25 | 41.80 | 41.67 | 42.67 |
| 2 | Days to Maturity | 61.29 | 58.78 | 66.50 | 61.08 | 67.11 | 66.58 | 63.50 | 60.90 | 63.39 | 68.33 |
| 3 | Plant Height | 51.48 | 56.76 | 59.81 | 72.09 | 54.65 | 67.38 | 61.05 | 70.37 | 74.80 | 67.73 |
| 4 | No. of Primary Branches per Plant | 4.44 | 4.19 | 3.45 | 3.45 | 2.86 | 2.95 | 5.47 | 4.63 | 3.92 | 4.13 |
| 5 | No. of Clusters per Plant | 7.06 | 6.14 | 5.04 | 6.69 | 8.95 | 4.96 | 4.57 | 8.09 | 4.78 | 6.20 |
| 6 | No. of Pods per Plant | 21.98 | 15.50 | 14.88 | 22.58 | 21.15 | 13.97 | 18.12 | 23.79 | 13.38 | 13.47 |
| 7 | No. of Seeds per pod | 9.68 | 11.67 | 11.52 | 10.86 | 11.46 | 11.43 | 11.92 | 9.73 | 6.59 | 22.07 |
| 8 | Pod length | 6.47 | 7.22 | 7.50 | 7.09 | 6.90 | 7.04 | 8.98 | 7.03 | 7.60 | 6.75 |
| 9 | Seed Index | 2.89 | 3.10 | 3.45 | 3.23 | 3.14 | 3.17 | 3.49 | 3.19 | 4.13 | 3.33 |
| 10 | Biological yield | 19.26 | 18.12 | 19.90 | 20.07 | 20.10 | 15.15 | 21.70 | 26.70 | 20.42 | 22.38 |
| 11 | Harvest Index | 31.61 | 30.46 | 27.02 | 36.48 | 31.76 | 40.09 | 23.67 | 25.52 | 18.76 | 26.73 |
| 12 | Seed yield per plant | 6.02 | 5.42 | 5.24 | 7.09 | 6.33 | 5.94 | 4.93 | 6.74 | 3.68 | 5.96 |

Conclusion

The results from the present investigation concludes that significant differences recorded for all the characters among the 100 greengram genotypes included in the study, indicating presence of sufficient variation among them. High GCV and PCV were recorded for number of primary branches per plant and number of clusters per plant. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering and number of clusters per plant. Average inter cluster was maximum between the cluster III and IV, cluster I and IV, cluster II and IV. The cluster means for different morphological traits revealed substantial genetic variability for all the traits. In the present experimental material, cluster IV showed the maximum cluster mean for more number of characters and also it is more diversified with other clusters. So the genotypes from this cluster should be used in hybridization programme for improvement of these traits. The genotypes present in cluster I, II, III and IV provide a broad spectrum of variability in segregating generations and may be used as parents in future hybridization programme to develop desirable genotypes, for yield improvement in greengram.

References

- Ahmad H, Syed MR, Manzoor AR, Mushtaq A, Gul Z, Shabeer AG *et al.* Estimation of Genetic Divergence in Mungbean (*Vigna radiata* L.) under Temperate Ecology of Kashmir. *Research & Reviews: Journal of Botanical Sciences.* 2016; 5(1):29-33.
- Annual Report. GOI, Ministry of agriculture and farmers welfare, Directorate of Pulses development, 2017-18. DPD/PUB/TR/19/2017-18.
- Azam MG, Hossain MA, Alam MS, Rahman KS, Hossain M. Genetic variability, heritability and correlation path analysis in mungbean (*Vigna radiata* L. Wilczek). *Bangladesh Journal of Agriculture Research.* 2018; 43(3):407-416.
- Chandra GS, Lavanya GR, Kulkarni SD. Studies on Genetic diversity in Greengram (*Vigna radiata* L. Wilczek) for seed yield characters. *Journal of Pharmacognosy and Phytochemistry.* 2017; 6(6):1765-1767.
- Garje UA, Bhailume MS, Nagawade DR. Genetic diversity analysis of greengram (*Vigna radiata* (L.) Wilczek). *The Bioscan.* 2013; 8(4):1477-1480.
- Garje UA, Bhailume MS, Nagawade DR, Sachin DP. Genetic association and Path coefficient analysis in greengram [*Vigna radiata* (L.) Wilczek]. *Journal of Food Legumes.* 2014; 27(2):151-154.
- Gokulakrishnan J, Sunil KB, Prakash M. Studies on Genetic Diversity in mungbean (*Vigna radiata* L.). *Legume Research.* 2012; 35(1):50-52.
- Gomez KA, Gomez AA. *Statistical Procedure for Agricultural Research.* 2nd Edition, J Wiley and Sons, New York, 1984. ISBN-10:0471870927.
- Kumhar SR, Chaudhary BR. Genetic Diversity and Variability in Mungbean (*Vigna radiata* (L.) Wilczek). *Journal of Plant Genetic Resources.* 2007; 20(2):122-125.
- Lavanya GR. Evaluation of mungbean germplasm for genetic variability. *Indian Journal of Plant Genetic Resources.* 2006; 19(1):104-106.
- Makeen K, Garad A, Jan A, Singh KA. Genetic variability and correlation studies on yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *Journal of Agronomy.* 2007; 6(1):216-218.
- Pandiyam M, Subbalakshmi B, Jebaraj. Genetic variability in greengram (*Vigna radiata* (L.) Wilczek). *International Journal of Plant Sciences.* 2006; 1(1):72-75.
- Prasanna LB, Rao PJM, Murthy KGK, Prakash KK, Yamini KN, Srividhya A. Genetic diversity and molecular characterization of mungbean genotypes (*Vigna radiata* (L.) Wilczek). *International Journal of Applied Biology and Pharmaceutical Technology.* 2013; 4(4):151-160.
- Rao. *Advanced statistical methods in biometrical research.* John Wiley and Sons Inc. New York, 1952, 326-272.
- Singh RK, Chaudhury BD. Biometrical methods of quantitative genetic analysis. *Haryana Journal of Horticulture Science.* 1985; 12:151-158.
- Sreethy TS, Lavanya GR, Arya P, Jahagirdar JE. Genetic Variability, Trait Association and Path analysis of yield and yield components in greengram (*Vigna radiata* (L.) Wilczek). *Research on Crops.* 2017; 18(4):711-717.
- Yimram T, Somta P, Srinivas P. Genetic variation in cultivated mungbean germplasm and its implication in breeding for high yield. *Field Crops Research.* 2009; 112:260-266.