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G Sarath Chandra
Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, Uttar Pradesh, India

G Roopa Lavanya
Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, Uttar Pradesh, India

SD Kulkarni
Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, Uttar Pradesh, India

Correspondence
G Sarath Chandra
Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, Uttar Pradesh, India

Studies on Genetic diversity in Greengram (*Vigna radiata* L. Wilczek*)* for seed yield characters

G Sarath Chandra, G Roopa Lavanya and SD Kulkarni

Abstract
Forty genotypes of greengram used to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. The data for twelve important quantitative characters recorded from the genotypes raised in Randomized Block Design having three replications. Pods per plant had maximum phenotypic and genotypic Coefficient of Variation (PCV and GCV), followed by clusters per plant. High heritability (broad sense) was recorded for plant height. High heritability coupled with high genetic advance was observed for plant height and biological yield per suggesting that, the role of additive gene effect and possibilities of achieving high genetic progress through selection. Forty greengram genotypes were grouped into seven clusters. Cluster I and cluster VII were large with nine genotypes each. Maximum inter-cluster distance was observed between cluster VI and VII, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters *viz*., seed yield per plant (g), days to 50% flowering, and plant height (cm) contributed maximum in manifestation of genetic diversity.

Keywords: Greengram, Heritability, Genetic advance, Cluster analysis, Divergence

Introduction
Greengram (*Vigna radiata* L. Wilczek, 2n=22, Fabaceae) popularly known as mungbean or golden gram, is an important pulse crop which is widely cultivated and consumed throughout India. Greengram is highly nutritive and it constitutes an important source of protein (23.6 percent) with carbohydrate (58 percent). India is the largest producer and consumer of greengram in the world. As greengram is a self-pollinated species considerable variation exists among the greengram cultivars and also within its related species (Bisht *et al*., 2005) [1]. Genetic improvement mainly depends upon the amount of genetic variability present in the base population and serves as a valuable source of base population for providing wide variability. One of the constraints listed for lack of breakthrough in greengram production has been the deficit of genetic variability for high yield potential (Ramanujam, 1978) [10]. Inclusion of diverse parents in hybridization programme serves the purpose of combining desirable recombinations. The major objectives of this investigation were to classify the available greengram germplasm into distinct groups on the basis of their genetic diversity and to identify diverse genotypes useful in hybridization programme for the development of better recombinants that will lead to the evolution of varieties with improved plant characters.

Materials and Methods
Forty greengram genotypes, received from Indian Institute of Pulse Research (Kanpur), Rajasthan Agriculture Research Institute, Durgapura (Rajasthan) and Agriculture Research Station, Badnapur (Maharashtra) were evaluated on the basis of quantitative characters, in Research Farm, SHUATS, Allahabad, during *kharif*, 2016 in a Randomized Block Design with three replications. Data were recorded on five randomly tagged plants for characters *viz*., 50% flowering, plant height, number of branches, days to maturity, number of clusters , number of pods, pod length, number of seeds per pod, biological yield, harvest index, seed index and seed yield per plant. The experimental data was analyzed statistically by the method of analysis of variance for single factor (Gomez and Gomez, 1984) [4] and different genetic parameters were estimated. Mahalanobis (1936) [7] defined the distance between two populations as D^2 which was obtained by Tochers method, described by Rao (1952) [11]. Contribution of individual characters towards divergence was estimated according to the method described by Singh and Chaudhary (1985) [12].

Results and Discussions
The analysis of variance revealed significant differences among the accessions for all the

characters studied, indicating the existence of a wide genetic divergence among them. Environment plays an important role in the expression of phenotype and genotype, fact which are inferred, form phenotypic observation. Hence, variability can be observed through biometric parameters like genotypic coefficient of variation, heritability (broad sense) and genetic advance. This would be of great help to breeder in evolving a selection programs for genetic improvement of crop plant. On an average, the high magnitude of GCV and PCV were recorded for pods per plant, branches per plant, clusters per plant and seed yield, suggesting sufficient variability and thus scope for genetic improvement through selection for these traits. Similar finding was also reported by Neelavati and Govindarasu (2010) [8]. High heritability were recorded for height of the plant, seed yield, seed index, pods per plant and 50%flowering, indicating that these traits are likely to be controlled by additive genetic component. Wani *et al.* (2007) **[14]** reported high heritability coupled with high genetic advance for number of pod per plant, plant height and harvest index, suggested the additive genetic control in the inheritance of these characters. Das *et al.* (1998) [3], Islam *et al.* (1999) [5], Loganathan *et al.* (2001a) [6] and Ram *et al.* (1997) [9] also reported high heritability for plant height, number of seeds per pod, number of pods per plant and harvest index

Based on D^2 values, 40 genotypes were grouped into seven clusters on the assumption that genotypes within the cluster have similar D^2 values among themselves. Cluster I and VII constitute nine genotypes, forming the large clusters followed by cluster V constitute seven genotypes. The pattern of group constellation proved the existence of significant amount of variability. Wide diversity was also reported by earlier workers, where, Das *et al.* (2010) [2] grouped 23 genotypes in eight clusters. The clustering pattern of the genotypes showed that genetic diversity was not related to geographic diversity. Such a type of constellation of germplasm proves that the collection made were genetically viable for different characters. The clustering pattern of the strains revealed that there was divergence between clusters.

The average intra cluster distance ranged from 32.31 to 55.86. Maximum intra-cluster distance was recorded for cluster IV (55.86) followed by cluster VII (53.80) while the minimum intra cluster distance was recorded for cluster V (32.31). The inter cluster D^2 value was maximum between cluster VI and VII (229.952) followed by cluster I and VI (162.05), suggesting that the genotypes present in these clusters may be used as parents for hybridization programme to develop desirable type as heterosis can be best exploited and chance of getting transgressive segregants are maximum when diverse lines are crossed (Lal *et al.,* 2001). On the basis of yield performance and some specialized characters, advance breeding lines, KM-1405, KM-1408 and KM-2195 from cluster VII, RMG-991, RMG-1014 from cluster III, may be selected as being the most diverse and high yielding lines. The probability of getting better segregates and promising recombinants will be more, if crosses are attempted among these lines.

The percent contribution of twelve characters to total genetic divergence is presented in table 3. High contribution in the manifestation of genetic divergence was exhibited by seed yield (26.79%) followed by days to 50% flowering (23.08%) and plant height (18.85%), suggesting scope for improvement in these characters. In other words, selection for these characters may be rewarding. The contribution of days to maturity (1.92%), seeds/pod (1.28%), clusters per plant (1.03%), and pod length (0.90%) was least to genetic diversity among all twelve characters; in contrast Umadevi and Ganesan (2007) [13] reported that seed index and biological yield had the greater contribution to genetic diversity.

Table 1: Distribution of 40 genotypes of greengram into different clusters.

Cluster No.	No. of genotypes	Genotypes included
I	9	KM-1421, KM-1422, KM-1401, K-851, RMG-992, IPM-02-3, IPM-02-14, MSG-118, DGG-3.
II	6	KM-1414, RMG-1083, RMG-1047, ML-2029, DGG-6, RMG-1027.
III	4	KM-1404, KM1406, RMG-991, RMG-1014.
IV	3	KM-1413, KM-1423, SAMRAT.
V	7	PUSA-871, RMG-1039, RMG-1016, RMG-975, RMG-1092, RMG-1028, MH-810.
VI	2	RMG-1093, VGG-05.
VII	9	KM-1405, KM-2241, KM-1409, KM-1410, KM-1412, KM-1415, T-44, KM-1408, KM-2195.

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

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster
1 Cluster	47.79	73.864	80.748	94.049	70.875	162.057	89.129
2 Cluster		40.809	113.115	103.421	78.311	109.363	92.901
3 Cluster			46.026	87.352	82.955	144.923	107.363
4 Cluster				55.867	106.287	142.207	111.409
5 Cluster					32.31	89.597	147.410
6 Cluster						44.830	229.952
7 Cluster							53.808

Table 3. The percent contribution of different quantitative characters to total genetic divergence.

S. No.	Source	Contribution (%)
1	Days to 50% flowering	23.08
2	Plant height	18.85
3	Number of Primary Branches/ Plant	2.44
4	Number of Clusters/ Plant	1.03
5	Number of Pods/ Plant	8.85
6	Pod length(cm)	0.90
7	Seed /pod	1.28
8	Days to maturity	1.92

9	Seed index	12.69
10	Seed yield	26.79
11	Biological yield	2.18
12	Harvest index	1.92

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