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Assessment of genetic variability and diversity in segregating generations of greengram [*Vigna radiata* L. Wilczek]

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Abstract

An experiment was conducted to evaluate the genetic variability and diversity in segregating lines of green gram of the cross KKM-3 (High yielding) × IPM 205-7 (Early maturing, YMV resistance). High phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) were recorded for seed yield per plant, primary branches per plant and secondary branches per plant and moderate for number of pods per cluster, number of seeds per pod, plant height, number of clusters per plant, number of pods per plant, 100 seed weight and pod length, indicating that the selection for these traits will be effective. High broad-sense heritability (h^2_{bs}) and genetic advance as *per cent* mean (GAM) was recorded for all the growth and yield traits confirming the additive gene action, except for number of clusters per plant. In contrast, high heritability (84.17) along with moderate GAM (12.76) was observed for days to 50% flowering signifying the role of non-fixable genetic variance. Based on the Mahalanobis' D^2 statistics, F_3 progeny lines were classified into 9 clusters. The greater intra-cluster D^2 values were noticed in cluster VII. The greater inter-cluster distance was found between clusters VIII and IX, followed by between clusters I and VIII, suggesting that the genetic architecture of the progeny lines in one cluster differs entirely from those included in other clusters. The trait number of pods per plant contributed the most towards the overall genetic divergence, followed by plant height. Cluster I can be selected for superior segregants with high yielding and early maturing types.

Keywords: Green gram, genetic variability, diversity

Introduction

Green gram [*Vigna radiata* (L.) Wilczek] is also known as mungbean or moong, is a leguminous plant species belonging to the Fabaceae family. It is a self-pollinated diploid ($2n=2x=22$) crop with typical papilionaceous flower bearing 5 sepals, 5 petals, 10 diadelphous (9+1) stamens and monocarpellary ovary with hairy style. In India, mungbean is grown in about 4.5 million hectares with the total production of 2.64 million tonnes and productivity of 548 kg/ha (Anon., 2020-21) ^[1].

Green gram is considered a hardy pulse crop and grows well in a hot and dry climate and its cultivation improves soil fertility by adding about 30-40 kg N/ha after the harvest of the crop. Therefore, the succeeding crop (usually a cereal) requires approximately 25% less nitrogen application (Mbeyagala *et al.*, 2017) ^[6]. The highly self-pollinated nature of this crop reduces the natural variability, which ultimately narrows down the effects of the selection process. The lack of genetic variability for high yield potential is the major constraint to achieving a major mungbean production breakthrough (Ramanujam, 1977) ^[10].

Investigation and a better understanding of the variability existing in a population constitute a base for efficient and effective breeding work (Bello *et al.*, 2012). Genetic diversity analysis is a powerful tool in quantifying the degree of divergence between biological populations and the relative contribution of different components to total divergence. Grouping of mungbean genotypes based on genetic variation for different characters will enable breeders for better selections. This paper deals with the above aspects for seed yield and yield components in F_3 generations of greengram.

Materials and Methods

The experiment was laid out at research plots of the College of Agriculture, Shivamogga. F_3 generation of the cross KKM-3 × IPM 205-7 was raised on a plant-to-row progeny basis in an

augmented design with six blocks. Each block was comprised of 5 F_3 progeny lines, parental lines and check variety. Each progeny was sown in a single row of 3 m length with 30 cm spacing between rows and 10 cm spacing between plants in a row on 6th July *Kharif* 2020. Each progeny row consists of 10 plants. All the recommended field management practices were followed to raise a healthy and better crop. The observations were recorded on F_3 families on individual plant basis on growth and yield contributing traits. Genetic parameters like mean, range, genotypic and phenotypic coefficient of variation, heritability, genetic advance as *per cent* mean, diversity analysis were calculated as per the standard procedure.

Results And Discussions

Analysis of variance between F_3 families revealed highly significant differences among the F_3 progenies for all characters under study, indicating the existence of sufficient genetic variability within families and between families and scope for improvement (Table 1). The present findings were in line with Narasimhulu *et al.* (2013) [8], Muralidhara *et al.* (2016).

Genetic variability parameters

From the results of the genetic parameters (Table 2), PCV values were higher than their corresponding GCV values for all the component traits. The difference between them was less, defining less influence of environment in expression of those characters inferring phenotypic selection may be given due consideration. However, the difference was relatively higher in the case of the number of primary branches per plant, the number of clusters per plant, hundred seed weight, indicating a significant effect of the environment on these traits where other variability parameters like heritability may also be considered for selection. These results are following Narasimhulu *et al.* (2013) [8], Muralidhara *et al.* (2016) [7].

High PCV and GCV values for seed yield per plant, secondary branches, moderate for number of clusters per plant, number of pods per cluster, number of pods per plant, plant height, number of seeds per pod, pod length and hundred seed weight, indicating that the practicing selection for these traits will be effective. In contrast, lesser extent of genetic variability exhibited by days to 50 *per cent* flowering, indicating that the selection for this character will be relatively less effective. These findings were in close agreement with the reports of Rao *et al.* (2006) [11], Narasimhulu *et al.* (2013) [8], Muralidhara *et al.* (2016) [7].

GCV gives a measure of variability present in a particular character. However, it does not determine the proportion of heritable variation present in the total variation. Hence, heritability in combination with genetic advance is considered for finding out heritable variation existing in character with a greater degree of accuracy (Dudley and Moll, 1969) [4].

High heritability coupled with high genetic advance as percent of mean was noticed for the number of seeds per pod, plant height, number of pods per plant, number of primary branches per plant, number of pods per cluster, seed yield per plant, hundred seed weight, number of secondary branches per plant, pod length confirming the additive gene action hence effective selection can be made for these traits. Whereas high heritability along with moderate GAM was observed for days to 50 *per cent* flowering, indicating the role of non-fixable genetic variance. These results are closely in

agreement with Titumeer *et al.* (2014) [13], Muralidhara *et al.* (2016) [7], Abhisheka and Mogali (2020) [2], Prithviraj and Murthy (2020) [9].

Genetic divergence

Based on their level of divergence, F_3 population was classified into nine different clusters. Cluster II emerged as the largest cluster with 18 progenies, followed by 6 progenies in cluster I, cluster VI with 3 progenies, cluster VII with 2 progenies, clusters III, IV, V, VIII and IX each with 1 progeny. The details are presented in figure 1.

The greater intra-cluster D^2 values were noticed in cluster VII. The intra-cluster distances for clusters III, IV, V, VIII and IX were found to be zero. The genotypes with close relatedness fall into the same cluster, owing to be less divergent than those positioned in a different cluster. The greater inter-cluster D^2 values were noticed between clusters VIII and IX, followed by between clusters I and VIII, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. The details are presented in figure 2.

Contribution of individual character towards total divergence

The trait number of pods per plant contributed the most towards the overall genetic divergence with 50.09%, followed by plant height (33.51%). These findings were in line with the findings of Garje (2013) [5], Chandra *et al.* (2017) [3], Saideah *et al.* (2021) [12]. Details are presented in figure 3.

Cluster means revealed the presence of considerable differences in the mean values of different characters. The distribution of the highest and lowest mean values for various characters in a distinct cluster indicated the traits contributing to the overall divergence (Table 3).

Cluster means for various characters

The mean cluster values for number of days to 50 *percent* flowering ranged from 26 to 39 days, where the progenies from cluster III were early flowering and progenies from cluster VIII were late to flower.

Cluster means for the trait plant height ranged from 22.10 to 66.50 cm, where the progenies belonging to cluster IX were shorter in contrast to the progenies from cluster VIII, which were taller.

Cluster means for number of primary branches per plant ranged from 1.87 to 2.70, where the progenies from cluster VI had a low number of primary branches compared to the progenies belonging to clusters I and VII, which had fewer primary branches more primary branches per plant.

Cluster means for number of secondary branches per plant ranged from 4.13 to 6.80, where the progenies from cluster VI were having a low number of secondary branches, whereas the progenies from cluster III had more number of secondary branches per plant.

Cluster means for number of clusters per plant ranged from 4.80 to 10.20. The progenies from cluster VIII had the lowest number of clusters; in contrast, the progenies belonging to cluster III had more number of clusters per plant.

Cluster means for number of pods per cluster ranged from 3.80 to 5.64, where the progenies belonging to cluster IV had fewer pods per cluster compared to the progenies from the cluster I had more pods per cluster.

Cluster means for number of pods per plant ranged from

15.60 to 40.54, where the progenies from cluster VIII had fewer number of pods per plant, compared to the progenies belonging to cluster I had more number of pods per plant.

The cluster means for the trait pod length ranged from 6.14 to 9.29 cm, where the progenies belonging to cluster IX had less pod length than the progenies from cluster I, where they had more pod length.

Cluster means for number of seeds per pod ranged from 7.80 to 13.30, where the progenies grouped into cluster III had less number of seeds per pod compared to the progenies belonging to cluster I had more number of seeds per pod.

Cluster means for the trait hundred seed weight ranged from 3.10 to 4.41 g. The progenies belonging to cluster V had less hundred seed weight when compared to the progenies from cluster I had more hundred seed weight.

Cluster means for seed yield per plant ranged from 2.77 to 8.88 g, where the progenies of cluster II had less seed yield per plant, compared to the progenies from cluster I had more seed yield per plant.

The F₃ progenies belonging to clusters I and III were found to be early flowering. The F₃ plants falling into the cluster I had a greater number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight and seed yield per plant. Hence, cluster I can be selected for superior segregants with high yielding and early maturing types. From both the crosses, China mung and IPM 205-7 were more divergent in nature through diversity analysis.

Superior segregants identified for yield and yield attributing traits: According to the findings, F₃ progeny lines viz., 32, 9, 25, 12 contributed significantly more number of pods per plant and significantly higher seed yield per plant compared to better parent KKM-3. However, other yield attributing traits like pod length, number of seeds per pod and hundred seed weight were on par with the parental lines. Hence, these progeny lines have been identified as superior segregants for yield and its contributing traits.

Table 1: ANOVA for seed yield and its component traits for F₃ population (KKM-3 × IPM 205-7) in Greengram

Source of Variation	Degrees of freedom	Mean Sum of Square										
		DDF	PH	PBP	SBP	NCP	NPC	NPP	PL	NSP	100SW	SYP
Blocks	5	1.62	0.67	0.09	0.15	0.03	0.06	6.06	0.03	0.1	0.07	0.12
Entries (F ₃ families + Checks)	33	20.02 **	3.21 **	0.85 **	63.36**	2.2 **	0.23 **	226.02 **	1.85 **	1.73 **	0.39 **	1.31 **
F ₃ families	29	4.87 **	35.56 **	0.21 **	1.82 **	1.5 *	0.61 **	17.13 **	0.94 **	1.74 **	0.26 **	1.03 **
Checks	3	135.13 **	1531.71 **	0.22 *	0.65 *	17.28 **	1.94 **	51.33 **	9.86 **	1.92 **	0.41 **	1.92 **
Checks vs. F ₃ families	1	131.74 **	1819.22 **	1.32 **	2.29 **	9.07 **	5.38 **	1453.34 **	5.31 **	25.4 **	3.87 **	8.63 **
Error	15	0.77	3.29	0.04	0.12	0.67	0.05	0.63	0.03	0.14	0.06	0.12

Significant @ P=0.05 level; **Significant @ P=0.01 level

DDF = Days to 50% flowering

NCP = Number of cluster per plant

NSP = Number of seeds per pod

PH = Plant height (cm)

NPC = Number of pods per cluster

100 SW = 100 Seed weight

PBP = Primary branches per plant

NPP = Number of pods per plant

SYP = Seed yield per plant (g)

SBP = Secondary branches per plant PL = Pod length (cm)

Table 2: Estimates of parameters specifying variability for seed yield and its component traits in F₃ families (KKM-3 × IPM 205-7) of greengram

Sl. No.	Traits	Mean±SE	Range		GCV (%)	PCV (%)	h ² (bs) (%)	GAM	CV
			Lowest	Highest					
1	Days to 50% flowering	30.04±1.06	25.14	39.15	6.74	7.35	84.17	12.76	2.83
2	Plant height	40.43±2.19	28.19	66.32	14.05	14.75	90.75	27.61	4.1
3	Primary branches per plant	2.16±0.25	1.14	2.99	18.76	21.09	79.14	34.43	9.2
4	Secondary branches per plant	4.91±0.43	3.15	8.65	26.55	27.5	93.18	52.87	7.39
5	Number of clusters per plant	8.44±0.99	5.22	10.54	10.84	14.54	55.62	16.68	10.01
6	Number of pods per cluster	4.49±0.27	2.93	6.45	16.68	17.4	91.88	32.99	4.74
7	Number of pods per plant	30.26±0.96	18.28	39.78	13.42	13.68	96.31	27.18	2.96
8	Pod length	7.68±0.22	6.19	9.68	12.39	12.62	96.3	25.07	2.36
9	Number of seeds per pod	8.48±0.45	6.17	10.58	14.91	15.54	92.03	29.51	4.17
10	100 Seed weight	3.62±0.3	2.6	4.66	12.41	14.19	76.52	22.39	6.55
11	Seed yield per plant	3.64±0.42	1.94	5.78	26.18	27.9	88.1	50.7	8.98

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

h²(bs) = Broad sense heritability

GAM = Genetic advance in per cent mean

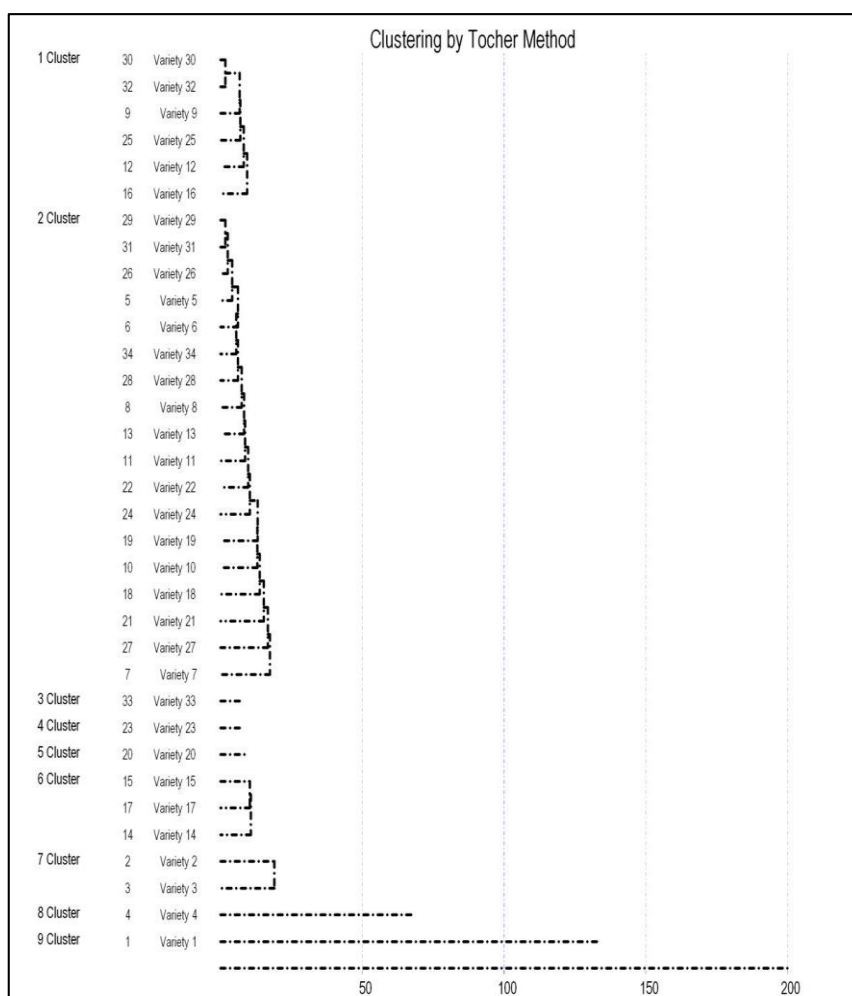


Fig 1: Clustering pattern of F₃ population (KKM-3 × IPM 205-7) based on D² values in greengram

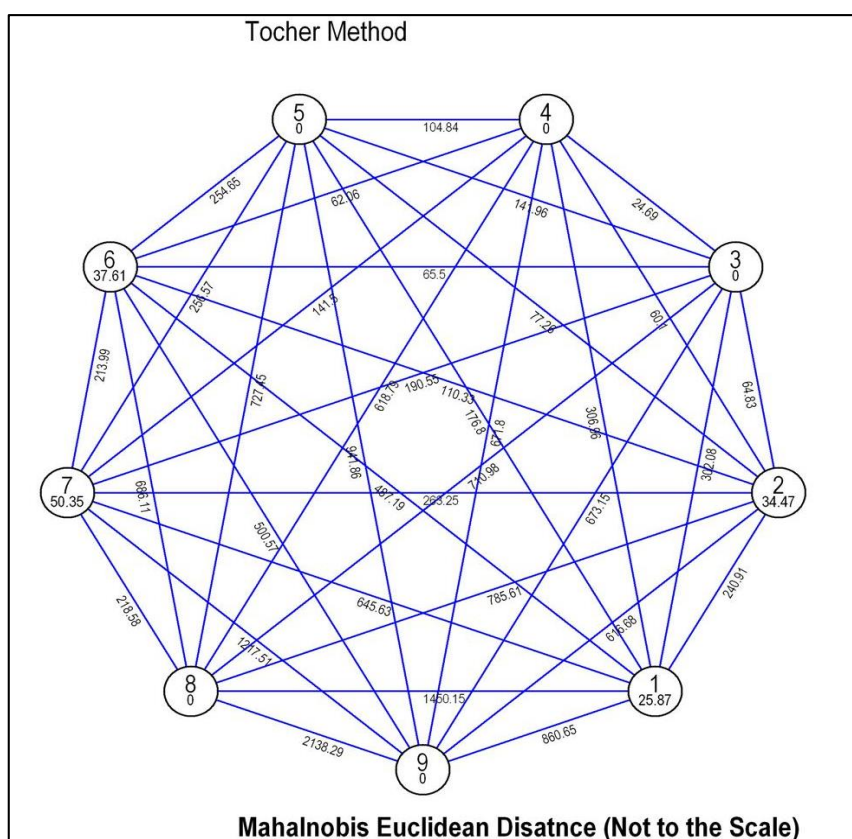


Fig 2: Average intra and inter cluster distances for yield and its components in F₃ population (KKM-3 × IPM 205-7) of Greengram

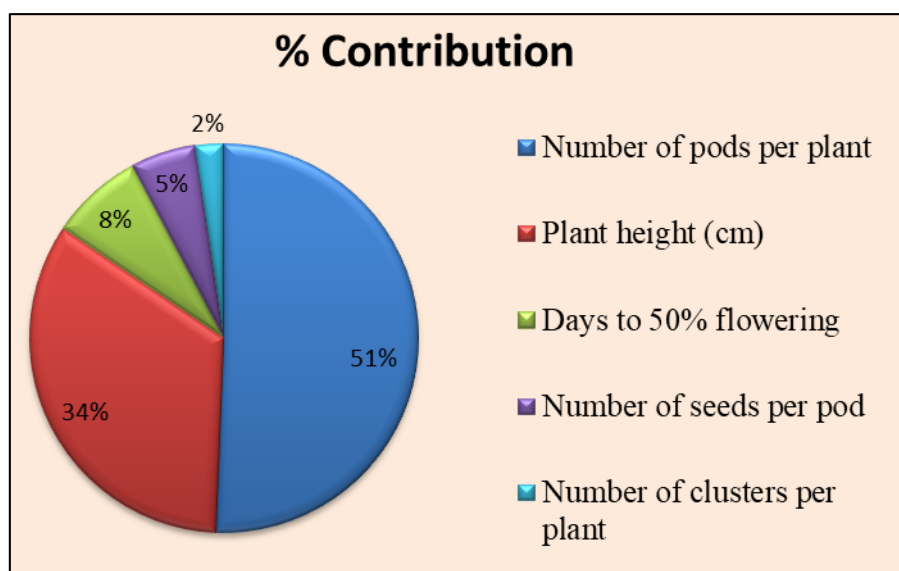


Fig 3: Percent contribution of different traits towards genetic diversity in F₃ population (KKM-3 × IPM 205-7) of greengram

Table 3: Cluster means for yield and yield attributing traits in F₃ population (KKM-3 × IPM 205-7) of Greengram

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Days to 50% flowering	27.32	30.82	26.00	28.00	32.50	28.37	31.50	39.00	28.00
Plant height	42.08	44.41	46.90	47.30	48.80	43.93	56.45	66.50	22.10
Primary branches per plant	2.50	2.02	2.00	2.40	2.40	1.87	2.70	2.20	2.40
Secondary branches per plant	6.60	4.46	6.80	5.20	4.60	4.13	4.70	4.20	4.60
Number of clusters per plant	10.02	8.51	10.20	8.90	6.95	9.04	7.50	4.80	8.50
Number of pods per cluster	5.64	3.97	4.60	3.80	4.60	4.73	5.30	4.68	5.20
Number of pods per plant	40.54	29.65	26.50	25.70	34.50	21.05	21.35	15.60	20.42
Pod length	9.29	7.16	7.40	6.86	6.86	7.43	9.10	8.30	6.14
Number of seeds per pod	13.30	8.32	7.80	11.60	11.80	7.92	11.00	9.20	9.82
100 seed weight	4.41	3.37	3.60	3.30	3.10	3.13	4.24	4.12	3.47
Seed yield per plant	8.88	2.77	3.10	3.25	3.12	2.78	5.04	3.14	4.89

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