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Genetic distance among mungbean germplasm pertaining to grain yield and yield components

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Abstract
Sixty greengram germplasm lines were subjected to multivariate analysis through Mahalanobis' D^2 statistics (Tocher's method) and 60 genotypes were grouped into nine clusters. Cluster III was the largest with 19 genotypes, followed by cluster I having 17 genotypes, cluster II and VII with eight genotypes, cluster V having 5 genotypes and clusters IV, VI, VIII and IX were solitary clusters. The maximum inter-cluster distance was between cluster VIII and IV, followed by cluster VIII and V. It shows that there is wide genetic diversity between the clusters. On the basis of divergence between clusters, superior F_1s or their transgressive segregants can be obtained by crossing between the genotypes belonging to cluster VIII and cluster IV and also between genotypes belonging to cluster VIII and cluster V which are having maximum inter cluster distance between them. Further such genotypes from above clusters which are having better *per se* are to be considered for hybridization programme.

Keywords: D^2 statistics, genetic divergence and mungbean

Introduction
Mungbean (*Vigna radiata* L. wilczeck) is a highly self-pollinating diploid plant with 2n = 2x = 22, chromosome number. The green gram (*Vigna radiata* L. Wilczek) is one of the important pulse crop because of its adaptation to short growth duration, low water requirement, soil fertility and is favoured for consumption due to its easy digestibility and low production of flatulence (Shil and Bandopadhyay, 2007) [13]. It is one of the protein rich legume and easily digestable pulse. As a short duration crop, it is suitable and fit for many crop rotations. It is a good source of Thiamine, Riboflavin and Vitamin C (Ascorbic acid). It occupies an important position due to its high seed protein content (22-24%) and it has the ability to restore the soil fertility through symbiotic nitrogen fixation (Malik *et al*., 1987) [10].

The success of breeding programme lies on the fact that the parents involved in any particular cross should be genetically divergent. The choice of parents with higher amount of genetic diversity is of greater importance in breeding programme. The crosses between the parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981) [3]. Mahalanobi D^2 statistics measures the degree of diversification and determines the relative contribution of each component character to total divergence (Mahalanobis, 1936) [8].

Materials and Methods
Present experiment was conducted with sixty mungbean germplasm lines along with four checks were evaluated in Augmented Randomized Complete Block Design (ARCBD), at Advanced P.G. Centre, Lam, Guntur, Andhra Pradesh, during *Kharif*, 2018-19. Total genetic material was laid out in five blocks, in each block four checks were repeated. Commercial spacing of 30x10 cm for between and within the rows, respectively with a row length of 4m. Standard agronomic practices and recommended fertilizer doses were applied for normal crop growth. Data was recorded for randomly selected five plants in each entry for the traits *viz.*, days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, test weight and grain yield per plant. In case of the traits, days to 50% flowering and days to maturity data was recorded on plot basis.

Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis (1936) [8]. The genotypes were grouped on the basis of minimum generalized distance using Tochers' method as described by Rao (1952) [11].

Results and Discussion

Univariate analysis of variance revealed the significant difference for nine out of eleven characters under study in the 60 mungbean genotypes. This significance of difference among 60 germplasm lines of mungbean for majority of characters justify further calculation of D^2 values. To estimate the D^2 values, correlated means of characters were transformed into uncorrelated variables using Pivotal Condensation Method. It measures the degree of diversification and determines the relative contribution of each component character to total divergence. The D^2 values between any two genotypes was obtained as the sum of squares of the differences of their corresponding uncorrelated values. Thus, D^2 values were obtained for all the possible 1770 pairs of genotypes.

The percent contribution of all the 11 characters in the 60 genotypes towards genetic divergence is presented in table 1. Among the characters studied, pods per plant (56.44%) showed maximum contribution followed by days to 50% flowering (51.00%), seeds per pod (12.66%), test weight (8.70%), pod length (4.80%), clusters per plant (4.75%), plant height (4.46%), days to maturity (4.00%), pods per cluster (3.39%), grain yield per plant (2.82%) branches per plant (1.07%).

The 60 genotypes were grouped into nine clusters using the Tocher's method (Table 2), with the criterion that the intra-cluster average D^2values should be less than the inter-cluster D^2values. The dendrogram showing relationship among all the genotypes is present in figure 1. The distribution of 60 genotypes into nine clusters was at random with maximum number of genotypes in cluster III (19 genotypes) followed by cluster I is having 17 genotypes, cluster II and VII with eight genotypes, cluster V is having 5 genotypes and clusters IV, VI, VIII and IX were solitary clusters (hence no intra-cluster distances / D^2values). The formation of distinct solitary cluster may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes must be responsible for this genetic diversity (Arunachalam and Ram, 1964) [2].

The average intra and inter-cluster D^2 values were estimated as per the procedure given by Singh and Chaudhary (1977) [14]. and are presented in the table 3 and figure 2. The nearest and farthest cluster for each of the nine clusters are indicated in table 4.Inter-cluster divergence expresses the diversification among clusters (group of genotypes resembling each other, hence with low intra-cluster divergence). Intra-cluster D^2 values ranged from 0.00 (cluster IV, VI, VIII and IX) to 48.61 (cluster VII). The intra-cluster distance indicated the diversity among the genotypes grouped in that clusters. Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured.

General notion exists that the larger is the divergence between the parental genotypes, the higher will be the heterosis in crosses (Falconer, 1964) [4]. Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced. In the present study, inter-cluster distances were worked out considering 11 characters and these distances ranged from 26.69 (between cluster I and VI) to 276.14 (between cluster IV and VIII).

Cluster I consist of 17 genotypes. It is nearest to cluster VI (26.29) followed by cluster VII (37.27) and was farthest from cluster VIII (139.52) followed by cluster IX (99.53).Cluster II is with 8 genotypes and its nearest cluster is cluster VIII (37.19) followed by cluster VI (44.85) while the farthest is cluster V (235.19) followed by cluster IV (226.72).Cluster III with 19 genotypes was the largest of all clusters. It was nearest to cluster IV (43.70) followed by cluster VI (47.29) and it was farthest from cluster VIII (252.00) followed by cluster II (185.81). Cluster IV was monogenotypic (OBGG-58). It was nearest to the cluster V (36.79) followed by cluster III (43.70) and was farthest from cluster VIII (276.14) followed by cluster II (226.72). Cluster V with 5 genotypes. It was closest to the cluster IV (36.79) followed by cluster III (59.21) and it was farthest from cluster VIII (255.05) followed by cluster II (235.19).

Cluster VI was monogenotypic (VGG 16-027). It was closest to cluster I (26.29) followed by cluster VII (29.91) and farthest from cluster VI (104.40) followed by cluster IV (83.05). Cluster VII with 8 genotypes. It was closest to the cluster VI (29.19) followed by cluster I (37.27) and farthest from cluster V (120.92) followed by cluster VIII (115.87). Cluster VIII was again monogenotypic (MGG 385). It was closest to the cluster II (37.19) followed by cluster VI (57.34) and farthest from cluster IV (276.14) followed by cluster V (255.05).Cluster IX was also monogenotypic (WGG 42) as that of cluster IV, VI and VIII. It was closest to the cluster VI (58.61) followed by cluster VIII (71.60) and farthest from cluster III (157.08) and cluster IV (137.34).

The maximum inter-cluster distance was between cluster VIII and IV (276.14), followed by cluster VIII and V (255.05), cluster VIII and III (252.00), cluster V and II (235.19), cluster IV and II (226.72), cluster III and cluster II (185.81) and cluster IX and III (157.08). This suggested that there is wide genetic diversity between these clusters. The germplasm lines taken from the Regional Agricultural Research Station, Lam farm, Guntur, Andhra Pradesh (from same geographical area) were grouped into different clusters *i.e.*, cluster I, II, III, V and VII. Similarly, germplasm lines OBGG 56 (cluster III), OBBGG 57 (cluster I) and OBGG 58 (cluster IV) were distributed into different clusters, which are taken from same geographical area *i.e.*,Berhampur, Orissa. This indicate that geographical divergence and genetic diversity are not correlated. These results are in accordance with those of Gokulakrishnan *et al.*, (2012) [6] and Ahmad *et al.*, (2016) [1].

Cluster means indicate average performance of all genotypes present in a particular cluster. The cluster mean values for 11 characters are presented in table 5. Days to 50% flowering had a range of 30.33 days for cluster IX to 36.67 for cluster VI, plant height had a range of 40.48 cm for cluster V to 56.92 cm for cluster VII, branches per plant had a range of 4.40 for cluster VI to 6.20 for cluster VIII, days to maturity had a range of 62.33 days for cluster IX to 69.91days for cluster III, clusters per plant had a range of 3.40 for cluster V to 11.40 for cluster VIII, pods per cluster had a range of 2.32 for cluster V to 4.00 for cluster IV and IX, pods per plant had a range of 5.60 for cluster IV to 34.20 for cluster VIII, pod length had a range of 6.54 for cluster I and III to 9.31 for cluster IX, seeds per pod had a range of 7.31 for cluster I to 13.60 for cluster VIII, test weight had a range of 3.50 for cluster VI to 5.30 for cluster IX and grain yield per plant had a range of 4.49 for cluster III to 6.90 for cluster IX.

For a successful breeding programme, selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants. In the present investigation it can be inferred that, superior F_1s or their transgressive segregants can be obtained by crossing between the genotypes belonging to cluster VIII and cluster IV and also between genotypes belonging to cluster VIII and cluster V which are having maximum inter cluster distance between them. Further such genotypes from above clusters which are having better *per se* are to be considered for hybridization programme. However, combining ability of the selected lines and gene action of the trait in question will finally decide the success of hybridization. The success and usefulness of Mahalanobis' D^2analysis in quantifying genetic divergence in mungbean was already indicated by Gokulakrishnan *et al.,* (2012) [6], Gadakh *et al.,* (2013) [5], Ahmad *et al.,* (2016) [1], Jeeva and Saravanan (2017) [7], Sunayana *et al.,* (2017) [15], Mahalingam *et al.,* (2018) [9] and Saady *et al.,* (2018) [12].

Table 1: Contribution of different characters towards genetic divergence in 60 greengram (*Vigna radiata* L. Wilzeck) genotypes

S. No.	Source	No. of times ranked first	Per cent contribution
1	Days to 50% flowering	9	51%
2	Days to maturity	7	4%
3	Plant height (cm)	79	4.46%
4	Branches per plant	19	1.07%
5	Clusters per plant	84	4.75%
6	Pods per cluster	60	3.39%
7	Pods per plant	999	56.44%
8	Pod length (cm)	85	4.8%
9	Seeds per pod	224	12.66%
10	Test weight (g)	154	8.7%
11	Grain yield per plant (g)	50	2.82%

Table 2: Clustering pattern of 60greengram (*Vigna radiata* L. Wilzeck) genotypes by Tocher's method

Cluster No.	No. of genotypes	Name of genotype (S)
I	17	LGG 555, LGG 616, NVL 722, RM 16-2, LGG 650, LGG 603, LGG 634, OBGG 57, CO 6, PM 112, LGG 632, TARM 1, LGG 627, Pusa 0972, LGG 639, MGG 387, LGG 605
II	08	LGG 626, LGG 630, VGG 036, COGG 13-39, LGG 647, LGG 586, AGG 35, VGG 15-30
III	19	LGG 509, LGG 610, LGG602, LGG 636, RM 16-9, LGG 600, LGG 615, LGG 617, PM 110, LGG 629, LGG 625, LGG 604, LGG 609, SMP 17-16, VBN(G8-2), OBGG 56, LGG 644, LGG 576, SMP 17-14
IV	01	OBGG 58
V	05	LGG 595, TLM 24, Pusa Vishal, LGG 578, PM 5
VI	01	VGG 16-027
VII	08	LGG 607, VGG 16-057, LGG 603, LGG 631, LGG 407, RM 16-3, GGG 1, PM 115
VIII	01	MGG 385
IX	01	WGG 42

Table 3: Average intra and inter-cluster distances (D^2 values) among eight clusters of 60 grain yield in greengram (*Vignaradiata* L. wilczeck) genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	17.19	80.05	48.34	75.58	95.41	26.29	37.27	139.52	99.53
II		22.54	185.81	226.72	235.19	44.85	74.61	37.19	94.71
III			28.17	43.70	59.21	47.29	80.19	252.00	157.08
IV				0.00	36.79	83.05	100.91	276.14	137.34
V					25.02	104.40	120.92	255.05	120.64
VI						0.00	29.91	57.34	58.61
VII							48.61	115.87	82.06
VIII								0.00	71.60
IX									0.00

Table 4: The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 60 greengram genotypes

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	VI (26.29)	VIII (139.52)
II	VIII (37.19)	V (235.19)
III	IV (43.70)	VIII (252.00)
IV	V (36.79)	VIII (276.14)
V	IV (36.79)	VIII (255.05)
VI	I (26.29)	V (104.40)
VII	VI (29.91)	V (120.92)
VIII	II (37.19)	IV (276.14)
IX	VI (58.61)	III (157.08)

Table 5: Mean values of eight clusters estimated by Tocher's method in 60 grain yield in greengram (*Vignaradiata* L. wilczeck) genotypes

Cluster no.	Days to 50% flowering	Plant Height	Branches per plant	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	Test weight	Grain yield per plant
I	33.69	50.16	4.83	68.42	6.49	3.12	18.64	6.54	7.31	3.63	5.81
II	34.04	51.83	5.63	68.54	10.43	3.71	31.79	6.99	9.50	3.66	6.84
III	34.02	54.29	4.46	69.91	4.08	2.73	10.59	6.54	8.07	3.72	4.49

IV	32.00	47.00	4.80	66.67	4.20	4.00	5.60	6.60	10.60	4.40	6.16
V	32.67	40.48	5.12	67.20	3.40	2.32	7.76	7.99	11.64	5.02	4.54
VI	36.67	48.60	4.40	68.00	7.60	3.80	22.20	7.32	10.40	3.50	6.64
VII	33.13	56.92	4.83	67.83	5.88	3.65	21.41	6.71	8.83	3.85	6.31
VIII	35.00	54.00	6.20	67.67	11.40	3.60	34.20	8.64	13.60	4.20	6.86
IX	30.33	43.20	5.80	62.33	4.20	4.00	24.00	9.31	12.20	5.30	6.90

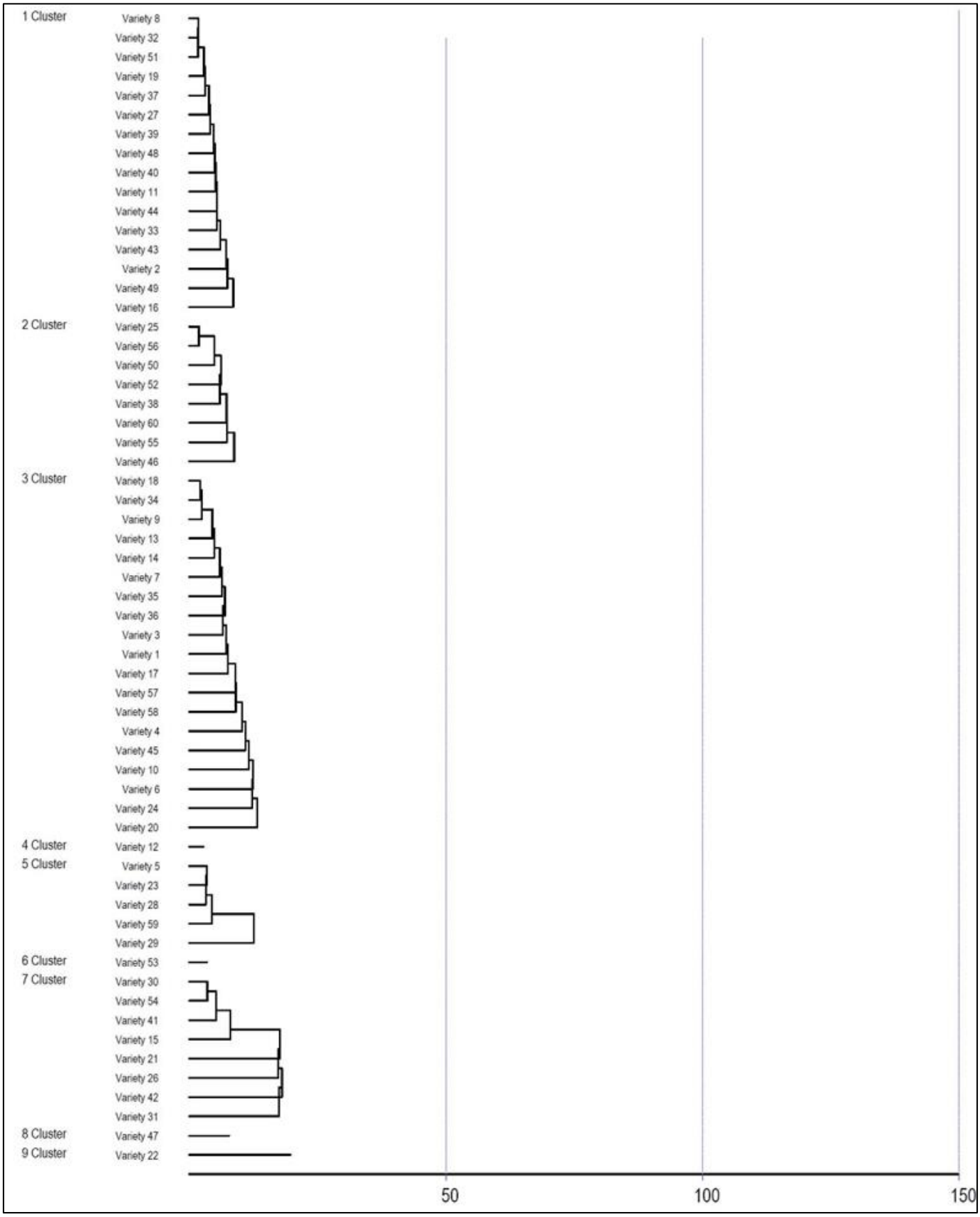

Fig 1: Dendrogram showing relationship among 60 greengram (*Vigna radiata* L. Wilczek) genotypes in nine clusters based on Mahalanobis' D^2 values

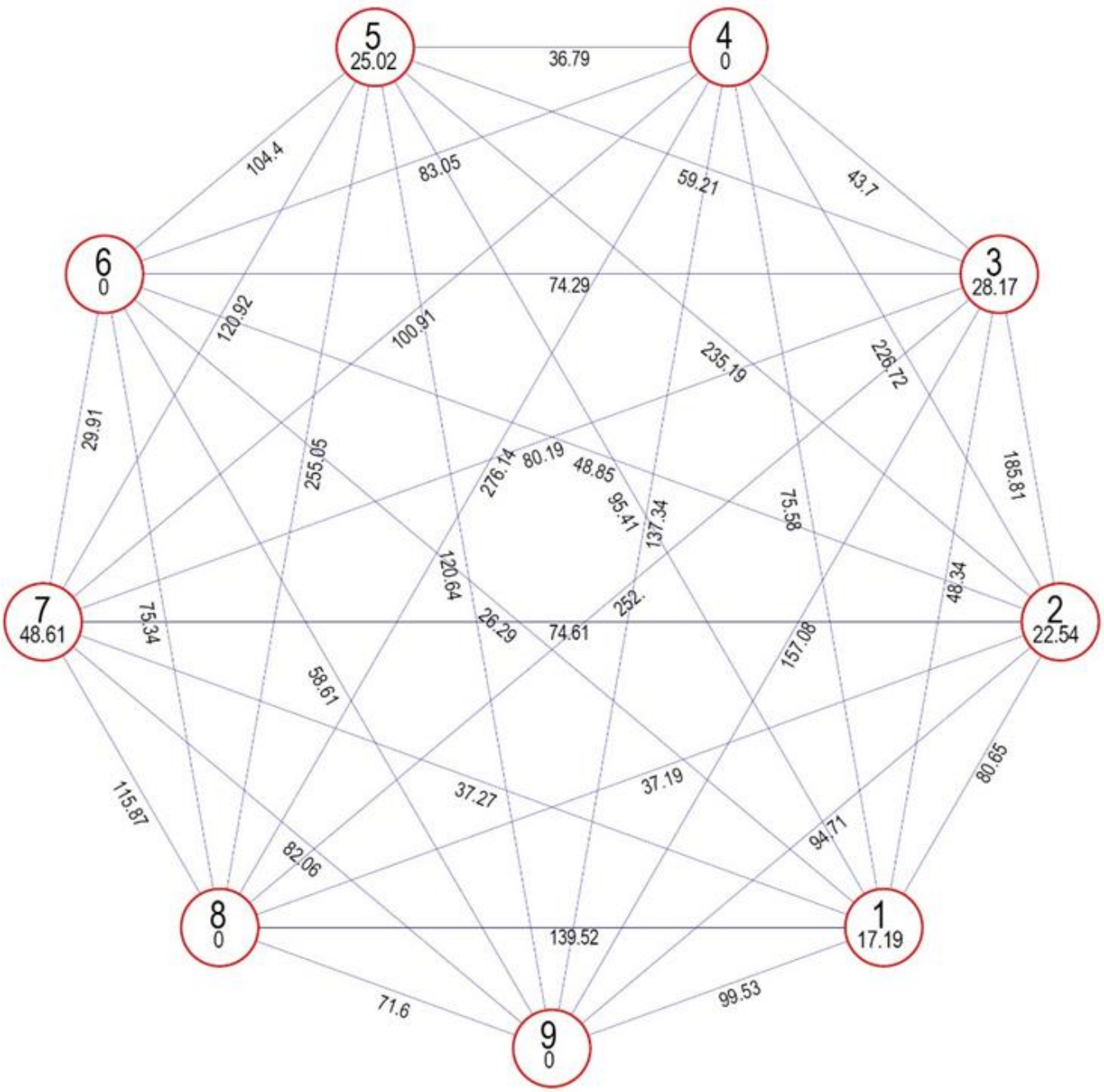

Fig 2: Intra and inter-cluster distance of 60 greengram (*Vigna radiata* L. Wilczek) genotypes in nine clusters based on tocher's method

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