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Genetic divergence studies on yield, physiological and nutritional traits in pearl millet [*Pennisetum glaucum* (L.) R Br.]

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Abstract
Present investigation was made to study the nature and magnitude of genetic divergence in 42 pearl millet genotypes were evaluated in randomized block design for twenty two physiological, nutritional and yield related traits using multivariate analysis through Mahalanobis, D^2 statistics. The analysis suggested considerable genetic divergence among the material. D^2 statistics resulted in ten clusters. Based on relative magnitude of D^2, the genotypes were grouped into ten different non-overlapping clusters. Cluster I, having 11 genotypes, emerged with highest number of entries followed by cluster III which had 10 genotypes. Nine genotypes were observed in cluster II and Cluster IV had six genotypes, while clusters V, VI, VII, VIII, IX and X had one genotype each. The maximum intra-cluster distance was observed for cluster II followed by cluster IV, cluster III and cluster I. The maximum inter-cluster D^2 value was recorded between cluster III and VII followed by between cluster III and V and cluster III and VI. Among the 22 characters studied highest contribution in manifestation of genetic divergence was exhibited by LAI at 60 DAS followed by LAD, Fe content, Zn content, protein content, days to maturity, green fodder yield plot^{-1}, plant height, 1000 - grain weight and panicle length.

Keywords: Genetic divergence, D^2, pearl millet, magnitude, clusters

Introduction
Pearl millet [*Pennisetum glaucum* (L.) R. Br.] Belongs to the family poaceae (graminae) and genus *Pennisetum*. It is diploid (2x = 14) in nature and is commonly known as cattail millet or bulrush millet in English (Adam, 1996) [1]. It is the third most important cereal crop in India, after rice and wheat. It is one of the major warm season coarse grain cereals with C4 mechanism grown in the arid and semi-arid tropical regions of Asia and Africa. It is the major source of nutritious food for poorest people as well as feed and fodder for livestock in rainfed regions of the country. It is rightly termed as nutricereal because of high protein content with balanced amino acids, carbohydrates and fat. It is rated as good source of fodder owing to its prolific regeneration capacity, good growth, heavy tillering, leafiness, succulent stem and has capacity to provide nutrients. Green fodder is more palatable because it does not have HCN (hydrogen cyanide) content as that of sorghum (Lakshmana, 2008) [2]. Therefore, there is an immediate need to breed stable pearl millet cultivars with high yielding coupled with better nutritional quality. It is endowed with huge amount of variability for micronutrients especially for grain Fe and Zn content. Micronutrient enrichment in pearl millet is possible by identifying stable genotypes for high levels of micronutrients and utilizing them in breeding programme.
There is wide genetic diversity available and characterizing these resources is prerequisite for the genetic improvement
Of its cultivars. The generalized distance concept of Mahalanobis' is based on multivariate analysis of quantitative traits. It is used to measure the genetic divergence and to classify the genetic stock into distinct groups. Intercrossing between more divergent parents is expected to generate a broad spectrum of variability and selection to be adopted in the segregating generations. Considering this, the present study was taken up in pearl millet to understand the diversity available in the genetic stocks.

Materials and Methods

Forty two genotypes of pearl millet were grown in a randomized block design with three replications during *kharif*, 2018 at Sri Venkateswara Agricultural College dry land farm, Tirupati. Each genotype was sown in one row of 3m length with a spacing of 50 cm between rows and 12 cm between plants within the row. The data were recorded on five competitive plants taken from each replication for plant height, no. of productive tillers plant^{-1}, panicle length, panicle girth, 1000 - grain weight, grain yield plant^{-1}, green fodder yield plant^{-1}, specific leaf area at 40 DAS, SPAD chlorophyll meter reading at 40 DAS, leaf area index at 40 DAS, leaf area duration, harvest index, iron content, zinc content and protein content. The characters *viz*., days to 50% flowering and days to maturity were recorded on per plot basis. The mean data recorded on five random plants per entry in each plot were subjected to analysis of variance as well as multivariate analysis of D2 statistics according to Mahalanobis' (Mahalanobis, 1936) [3] The genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (Rao, 1952) [4].

Results and Discussion

The analysis of variance showed highly significant differences among the genotypes for 22 characters studied. Wilk's criterion has shown highly significant differences among the genotypes for the aggregate effect of all the characters. The Mahalanobis D^2 cluster analysis grouped all the 42 pearl millet accessions of the present investigation into ten distinct non- overlapping clusters (Table 1 and Fig. 1). The discrimination of genotypes into discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregants for seed yield, physiological and other nutritional characters. Intra-cluster average D^2 values ranged from 0.00 to 145.42. Among the clusters, cluster II had the maximum intra cluster distance (145.42) followed by cluster IV (143.38), cluster III (137.95) and cluster I (95.99), while the clusters V, VI, VII, VIII, IX and X recorded zero values as they included only single genotype in each of them. The maximum inter-cluster D^2 value was recorded between cluster III and VII (1405.20) followed by between cluster III and V (1292.45) and cluster III and VI (1220.88), while the minimum D^2 value was found between cluster V and VI (106.62) followed by between cluster V and VII (107.24) and cluster VI and VII (113.43) (Table 2 and Fig.2). High value of inter- cluster distance points out towards high amount of diversity between the clusters involved. Cluster I includes a large number of genotypes i.e. 11 genotypes followed by cluster III which had 10 genotypes. Nine genotypes were observed in cluster II and Cluster IV had six genotypes, while clusters V, VI, VII, VIII, IX and X had one genotype each the cluster means of different characters in various clusters gives clear idea about parent selection for improvement of various traits. (Table 3 and 4). Early flowering was observed in the genotypes of cluster IV (44.39 days), while delayed flowering in the genotypes of cluster X (54.00 days). Days to maturity ranged from 72.00 days in cluster VIII to 97.67 days in cluster VI.

The genotypes of cluster IX were taller in height (183.77 cm), while that of cluster III were shorter in height (91.61 cm). Similarly, number of productive tillers plant^{-1} ranged from 1.99 in cluster VI to 3.48 in cluster III and IV, whereas, anicle length was highest in cluster VII (36.77 cm) and shortest in cluster VIII (15.17 cm). The panicle girth ranged from 2.76 cm in. cluster IX to 4.37 cm in cluster V. Thousand grain weight ranged from 10.08 g in cluster X to 17.36 g in cluster VII. The genotypes of cluster VII recorded high grain yield plant^{-1} (49.27 g), while genotypes of cluster X recorded low grain yield plant^{-1} (25.28 g). The genotypes of cluster IV showed high grain yield plot^{-1}(3817.47 kg ha^{-1}), while the genotypes of cluster X showed low grain yield plot^{-1} (1197.29 kg ha^{-1}). The genotypes in cluster IV recorded high green fodder yield plant^{-1} (0.15 kg), while genotypes in cluster III recorded low green fodder yield plant^{-1}(0.08 kg). The genotypes in cluster VIII recorded high green fodder yield plot-1 (30380.71 kg ha-1), while genotypes in cluster III recorded low green fodder yield plot-1 (13477.15 kg ha-1). The cluster means for each of eleven physiological and nutritional characters are presented in Table 4. The cluster mean for SLA at 40 DAS was maximum in cluster IX (189.36 cm2g-1) and was minimum in cluster II (155.60 cm2g-1) and at 60 DAS was maximum in cluster IX (230.08 cm2g-1) and was minimum in cluster V (181.73 cm2g-1). The SCMR at 40 DAS was maximum in cluster IV (49.74) and minimum in cluster IX (33.23). The SCMR at 60 DAS was maximum in cluster IV (55.45) and was minimum in cluster VIII (45.72). The high and low values for LAI at 40 DAS ranged from cluster III (0.80) to cluster VII (2.02), whereas, LAI at 60 DAS ranged from cluster III (1.31) to cluster VI (2.30). Leaf Area Duration was maximum in cluster VI (1331.07 cm2 day-1) and was minimum in cluster III (492.97 cm2 day-1). Harvest index was maximum in cluster VIII (55.25%) and was minimum in cluster VI (43.08%). The genotype in cluster X recorded high Fe content (160.33 ppm), while genotypes in cluster IX recorded low Fe content (47.00 ppm). Zinc content was maximum in cluster VIII (34.00 ppm) and minimum in cluster VII (18.00 ppm). Protein content was maximum in cluster X (19.16%) and was minimum in cluster VIII (9.80%). The cluster means of different characters help the breeder to know the performance of genotypes with better mean performance against cluster means. The following clusters registered higher cluster mean values for the traits studied and genotypes of outstanding mean performance from the selected clusters may serve as potential parents for hybridization programme. In this study, it is found that the cluster means for different characters showed considerable differences between the clusters for all the characters. Cluster VII registered maximum values for panicle length, 1000 - grain weight and grain yield plant^{-1}. Cluster IV recorded maximum values for number of productive tillers plant^{-1}, grain yield plot^{-1} and green fodder yield plant^{-1} and minimum values for days to 50% flowering. Cluster V recorded maximum value for panicle girth. Further, Cluster VIII recorded maximum value for green fodder yield plot^{-1} and minimum values for days to maturity. Cluster III recorded minimum values for plant height. Inter- crossing the genotypes from these clusters could be suggested to generate wide range of variability subsequently followed by effective selection for improving these characters.

The above discussion showed wide variation between clusters. The discrimination of genotypes into discrete clusters suggested presence of high degree of genetic diversity in the

material evaluated. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregants for seed yield and other important characters. Among all the characters studied, LAI at
60 DAS contributed the maximum (30.68%) towards the divergence by taking first rank in 277 times out of 861 combinations, followed by LAD (30.34% with 274 times ranked first), Fe content (10.19% with 92 times ranked first), Zn content (8.86% with 80 times ranked first), protein content (5.87% with 53 times ranked first), days to maturity (3.65% with 33 times ranked first), green fodder yield plot^{-1} (3.43% with 31 times ranked first), plant height (2.21% with 20 times ranked first), 1000 - grain weight (1.99% with 18 times ranked first) and panicle length (0.66% with 6 times ranked first) (Table 4). It is important to establish a breeding programme for biofortification for grain iron content which is helpful for the people to overcome malnutrition.

Table 1: Cluster composition of pearl millet genotypes (Tocher's method)

Cluster number	No. of genotypes	Genotypes
I	11	ICHiFe-2, ICHiFe-11, ICHiFe-13, ICHiFe-14, ICHiFe-15, ICHiFe-16, ICHiFe-21, ATP-5, ATP-6, ATP-17, ATP-18
II	9	ICHiFe-10, ICHiFe-19, ATP-3, ATP-7, ATP-9, ATP-13, ATP-14, ATP-15, ATP-16
III	10	ICHiFe-3, ICHiFe-4, ICHiFe-5, ICHiFe-6, ICHiFe-7, ICHiFe-8, ICHiFe-9, ICHiFe-12, ATP-1, ATP-2
IV	6	ICHiFe-1, ATP-10, ATP-11, ATP-12, ABV-04, Dhanashakti
V	1	ATP-4
VI	1	ICHiFe-20
VII	1	ATP-8
VIII	1	ICHiFe-17
IX	1	ICHiFe-18
X	1	ICHiFe-22

Table 2: Inter and Intra cluster (diagonal) average of D^2 and D values (in parentheses) of 10 clusters in pearl millet genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
Cluster 1	95.99 (9.79)	190.01 (13.78)	347.90 (18.65)	170.87 (13.07)	452.76 (21.28)	415.82 (20.39)	546.35 (23.37)	291.27 (17.06)	192.69 (13.88)	193.38 (13.91)
Cluster 2		145.42 (12.06)	691.79 (26.30)	295.92 (17.20)	222.43 (14.91)	227.60 (15.09)	265.99 (16.31)	217.67 (14.75)	161.32 (12.70)	397.06 (19.93)
Cluster 3			137.95 (11.75)	326.21 (18.06)	1292.45 (35.95)	1220.88 (34.94)	1405.20 (37.49)	837.41 (28.94)	706.74 (26.58)	264.44 (16.26)
Cluster 4				143.38 (11.97)	662.62 (25.74)	635.76 (25.21)	722.88 (26.89)	404.05 (20.10)	296.13 (17.21)	304.52 (17.45)
Cluster 5					0.00 (0.00)	106.62 (10.33)	107.24 (10.36)	226.76 (15.06)	229.89 (15.16)	749.16 (27.37)
Cluster 6						0.00 (0.00)	113.43 (10.65)	167.59 (12.95)	281.03 (16.76)	651.09 (25.52)
Cluster 7							0.00 (0.00)	323.67 (17.99)	309.43 (17.59)	871.03 (29.51)
Cluster 8								0.00 (0.00)	290.45 (17.04)	427.00 (20.66)
Cluster 9									0.00 (0.00)	439.92 (20.97)
Cluster 10										0.00 (0.00)

Table 3: Cluster means with respect to grain yield and yield component characters in pearl millet genotypes

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers plant^{-1}	Panicle length (cm)	Panicle girth (cm)	1000 - grain weight (g)	Grain yield plant^{-1} (g)	Grain yield plot^{-1} (kg ha^{-1})	Green fodder yield plant^{-1} (kg)	Green fodder yield plot^{-1} (kg ha^{-1})
Cluster 1	49.23	90.36	127.06	2.51	20.04	3.55	12.25	36.89	2544.79	0.11	17791.55
Cluster 2	51.15	87.22	129.11	2.85	24.95	3.59	13.18	45.06	2892.58	0.13	21211.61
Cluster 3	48.73	89.90	91.61	3.48	17.59	3.39	15.11	35.77	2128.95	0.08	13477.15
Cluster 4	44.39	82.56	138.29	3.48	23.36	3.85	16.40	48.58	3817.47	0.15	21553.14
Cluster 5	51.00	78.33	149.97	2.19	27.17	4.37	10.44	40.79	2425.65	0.11	17135.75
Cluster 6	53.33	97.67	152.43	1.99	18.19	3.51	15.63	37.96	3037.18	0.13	22483.76
Cluster 7	50.33	95.00	120.13	2.63	36.77	3.54	17.36	49.27	3317.80	0.14	25535.70
Cluster 8	44.67	72.00	130.53	2.39	15.17	3.71	14.67	35.56	2784.38	0.10	30380.71
Cluster 9	51.00	84.00	183.77	2.32	26.84	2.76	14.32	34.09	2388.27	0.09	20644.13
Cluster 10	54.00	96.67	121.80	2.40	16.64	3.02	10.08	25.28	1197.29	0.08	17649.06

Table 4: Cluster means with respect to physiological and nutritional characters in pearl millet genotypes

Cluster No.	Specific Leaf Area at 40 DAS (cm^2g^{-1})	Specific Leaf Area at 60 DAS (cm^2g^{-1})	SCMR at 40 DAS	SCMR at 60 DAS	Leaf Area Index at 40 DAS	Leaf Area Index at 60 DAS	Leaf Area Duration (cm^2 day^{-1})	Harvest Index (%)	Fe content (ppm)	Zn content (ppm)	Protein content (%)
Cluster 1	165.88	199.29	46.36	54.57	1.27	1.73	823.51	46.92	84.79	26.79	11.48
Cluster 2	155.60	208.39	43.33	54.80	1.56	1.97	1032.26	48.55	73.89	24.59	13.10
Cluster 3	166.04	206.29	44.61	52.45	0.80	1.31	492.97	53.93	97.90	27.43	11.94
Cluster 4	166.06	219.29	49.74	55.45	1.14	1.60	746.60	50.92	65.00	26.83	13.67
Cluster 5	176.41	181.73	38.97	52.23	2.00	2.22	1220.19	47.66	81.00	26.00	12.28
Cluster 6	176.83	217.37	40.62	48.84	1.86	2.30	1331.07	43.08	110.67	33.00	12.59
Cluster 7	182.39	203.15	42.97	49.77	2.02	2.26	1247.29	53.34	74.00	18.00	12.64
Cluster 8	172.72	191.35	39.28	45.72	1.69	2.06	1096.19	55.25	135.67	34.00	9.80
Cluster 9	189.36	230.08	33.23	48.47	1.66	1.84	1047.56	43.51	47.00	21.33	10.42
Cluster 10	178.79	211.32	37.75	46.44	1.00	1.69	731.55	45.40	160.33	26.33	19.16

Table 5: Contribution of different grain yield, physiological and nutritional characters to diversity in Pearl millet genotypes

S.N0.	Character	Contribution (%)	Times ranked first
1	Days to 50% flowering (days)	0.00	0
2	Days to maturity (days)	3.65	33
3	Plant height (cm)	2.21	20
4	No. of productive tillers $plant^{-1}$ (no.)	0.44	4
5	Panicle length (cm)	0.66	6
6	Panicle girth (cm)	0.11	1
7	1000 - grain weight (g)	1.99	18
8	Grain yield $plant^{-1}$ (g)	0.33	3
9	Grain yield $plot^{-1}$ (kg ha^{-1})	0.00	0
10	Green fodder yield $plant^{-1}$ (kg)	0.55	5
11	Green fodder yield $plot^{-1}$ (kg ha^{-1})	3.43	31
12	Specific Leaf Area at 40 DAS (cm^2g^{-1})	0.00	0
13	Specific Leaf Area at 60 DAS (cm^2g^{-1})	0.22	2
14	SCMR at 40 DAS	0.00	0
15	SCMR at 60 DAS	0.00	0
16	Leaf Area Index at 40 DAS	0.00	0
17	Leaf Area Index at 60 DAS	30.68	277
18	Leaf Area Duration (cm^2 day^{-1})	30.34	274
19	Harvest Index (%)	0.44	4
20	Fe content (ppm)	10.19	92
21	Zn content (ppm)	8.86	80
22	Protein content (%)	5.87	53

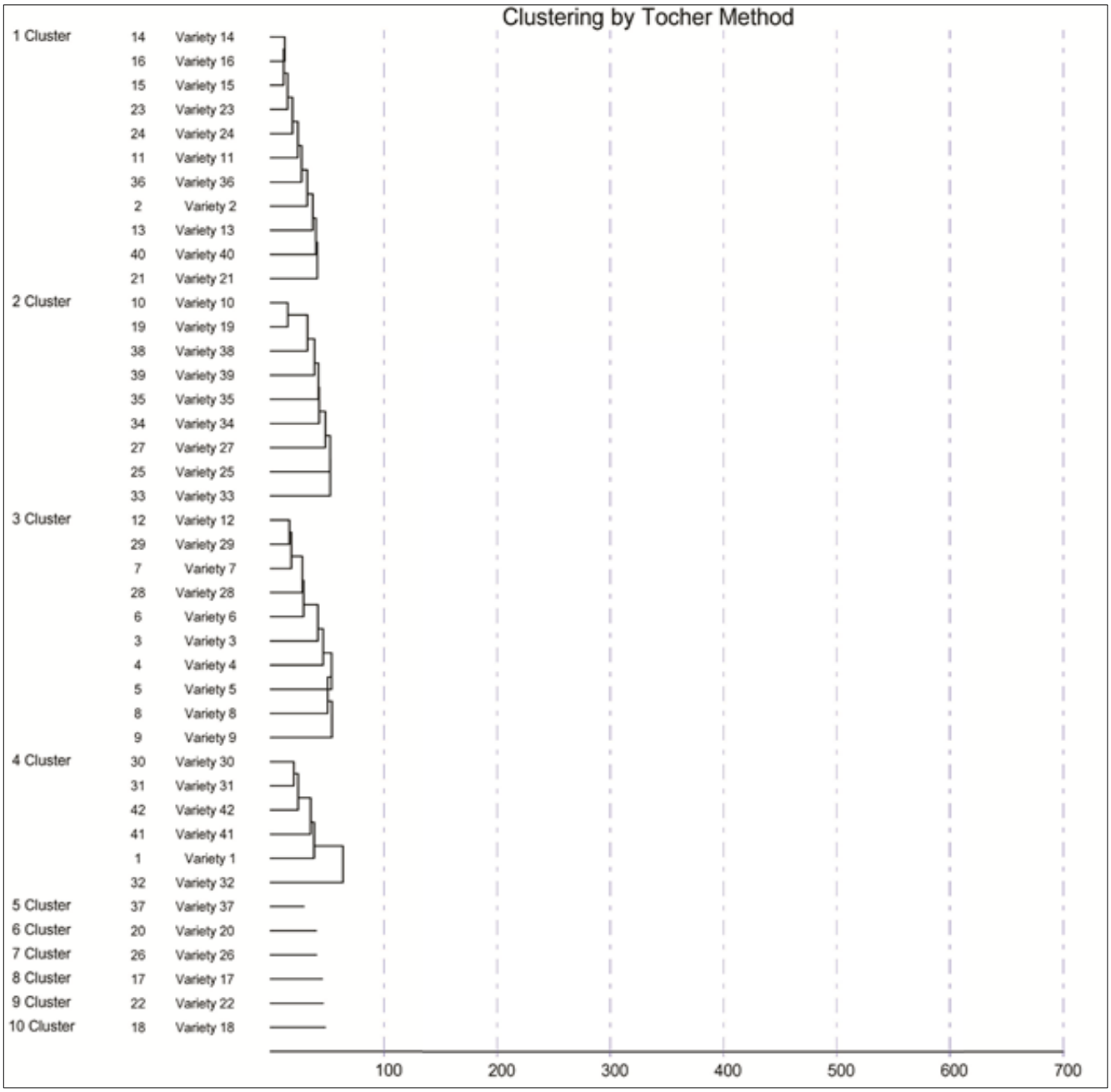

Fig 1: Dendrogram of 42 pearl millet genotypes obtained through Torcher's method of classification

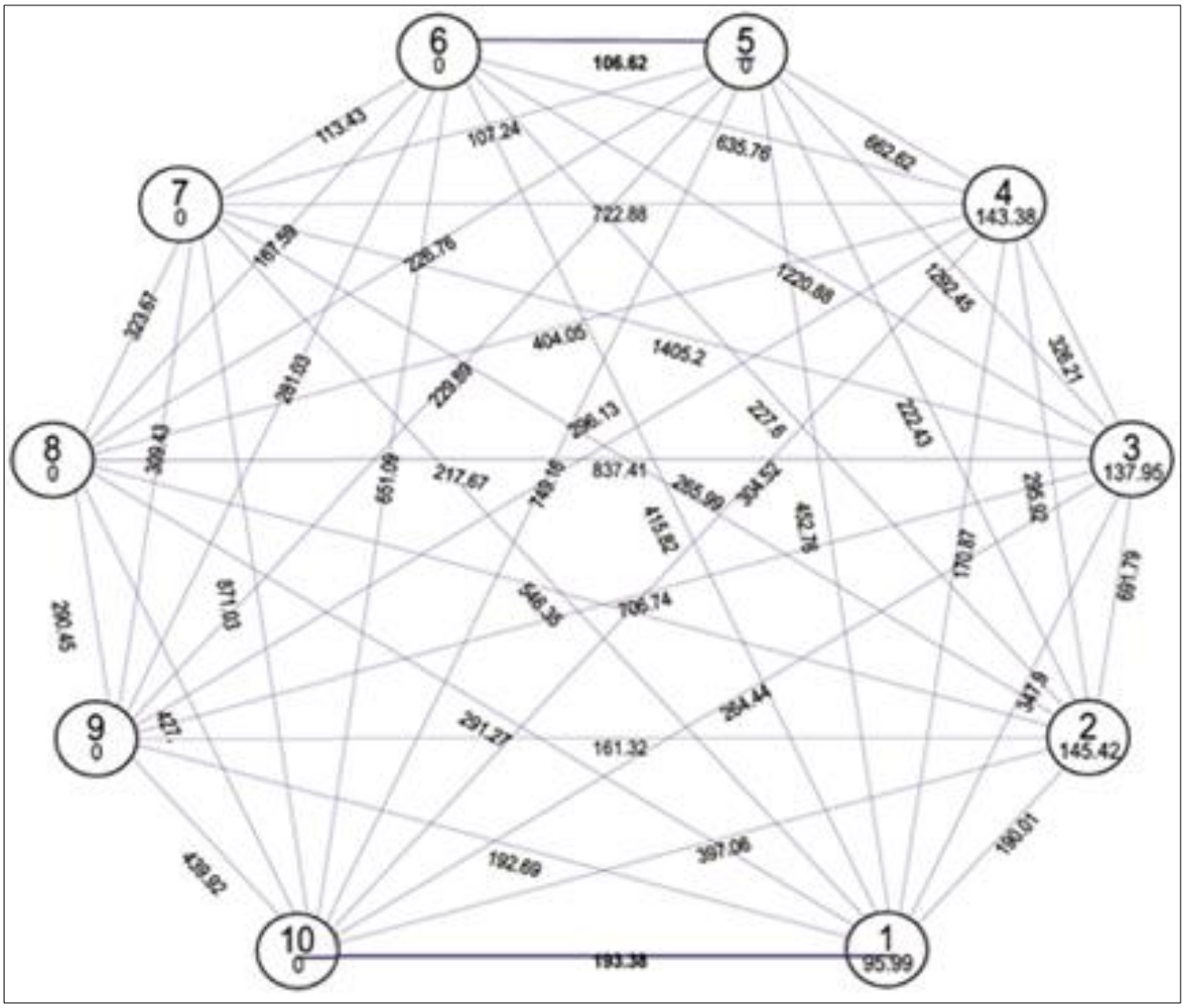

Fig 2: Intra-cluster (D) and inter-cluster distance (D^2) among ten clusters of pearl millet

Conclusion

By and large, based on the above discussion we can conclude that the genotypes from the cluster III and VII followed by cluster III and V were more divergent than any other clusters. Hence, the genotypes belonging to the distinct clusters (III and VII; III and V and III and VI) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregrants.

Based on the divergence analysis, the crosses *viz*., ATP-2 x ATP-8 (cluster III x cluster VII), ICHiFe-3 x ATP-4 (cluster III x cluster V) and ATP- 2 x ICHiFe-20 (cluster III x cluster VI) could be considered for obtaining a wide spectrum of variation among the segregants for high yield and nutritional traits. Hybridization among these genotypes drawn from widely divergent clusters with high yield potential are likely to produce more heterotic effect and also transgressive sergeants in subsequent generations. The inter-cluster distances were higher than the intra-cluster distances which indicate the existence of substantial diversity among the parents.

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