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Research Article

Assessment of genetic diversity using morphological traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract

The nature and magnitude of genetic diversity was assessed among 120 genotypes of pigeonpea along with three checks in augmented design during *Kharif,* 2011-12. The Non-hierarchical Euclidean cluster analysis grouped all the genotypes into twelve distinct non-overlapping clusters indicated existence of high degree of genetic diversity in the materials. The crossings between the members of diverse clusters separated by high inter-cluster distances are likely to throw desirable segregants. In this context, very high inter cluster distances were recorded between cluster VI and XII, cluster V and XII, cluster II and IX, cluster VI and XI, cluster II and VI and cluster V and IX. Considering the mean performance for different characters of genotypes belonging to diverse clusters, the promising genotypes for exploitation as parents in breeding programme were NDAGC 2011-4, NDAGC 2011-42 and NDAGC 2011-2 of cluster II; NDAGC 2011-18, NDAGC 2011-58, NDAGC 2011-34 and NDAGC 2011-27 of cluster V; NDAGC 2011-16, NDAGC 2011-41, NDAGC 2011-88, NDAGC 2011-104 and NDAGC 2011-103 of cluster VI; IC 525504 and Pusa 33 of cluster IX and IC 525456, IC 525408 and IC 525463 of cluster XII. It may be concluded that crosses between diverse genotypes belonging to clusters separated by high inter-cluster distances with desired means are likely to produce transgressive segregants may be advocated for developing high yielding pigeonpea varieties.

Key words
Pigeonpea [*Cajanus cajan* (L.) Millsp], genetic divergence, clustering pattern.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the second most important pulse crop of India after chickpea. It is commonly known as Arhar, Red gram and Tur. It has been recognized as a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low priced vegetarian foods. In fact, this crop has diversified uses such as food, feed, fodder and fuel. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals.

Success of crop improvement programme in any crop depends upon the extent of genetic variability and genetic diversity, association of characters, choice of parents for hybridization and selection procedure adopted. Compared to other food legumes breeding in pigeonpea has been more challenging due to various crop specific traits and highly sensitive nature to biotic and abiotic stresses. The final target of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield. This requires genetic amelioration through maximum utilization of allelic resources to develop ideal genotype.

The information about the nature and magnitude of genetic diversity existing in the available germplasm of a particular crop is crucial for selection of diverse parents, which upon hybridization may provide a wide spectrum of gene recombination for quantitatively inherited traits. Genetic diversity can be measured by different methods such as pedigree analysis, Mahalanobis-D^2 statistics, Nonhierarchical Euclidean cluster analysis and using molecular markers. Keeping in view, present experiment has been undertaken to study genetic diversity for selecting suitable parents for pigeonpea breeding programme aimed at isolating desirable segregants for seed yield and other important characters.

Materials and methods

One hundred twenty pigeonpea germplasm were evaluated in augmented design at research farm of genetics and plant breeding, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad during *Kharif* season of 2011. The experimental site is located at 26.47°N latitude, 82.12°E longitudes and an altitude of 113 m above mean sea level. This site is in the eastern Gangetic plains of India and has sandy loam soil texture. The experimental plot was sub-divided in to 10 blocks of 15 plots each. The three checks were allocated randomly to three plots in each block, while remaining 12 plots in a block were used for accommodating the unreplicated test genotypes. Each genotype was raised in single row plots of 4 m length with intra-row and inter-row spacing of 30 cm and 60 cm, respectively. All the recommended cultural practices were followed to raise a good crop.

The observations were recorded on five randomly selected competitive plants of a genotype in a plot in each replication for eleven characters. The characters studied were, days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest-index (%).

Genetic divergence among 123 genotypes planted in augmented design was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973).

Results and discussion

The study of genetic divergence among 120 pigeonpea genotypes and 3 checks was performed by employing Non-hierarchical Euclidean cluster analysis for eleven characters. The 123 genotypes were grouped into twelve different non-overlapping clusters (Table 1 & Fig.1). Cluster I, having 25 genotypes, emerged with highest number of entries followed by cluster VII with 18 genotypes. Cluster III, X, XI and VIII were represented by 17, 16, 11 and 10 genotypes, respectively. Cluster IV and VI were constituted by five genotypes each while Cluster II and XII possessed three entries each. Cluster XI contained eight genotypes. Cluster IX, comprising two genotypes, had least number of entries.

The maximum intra-cluster distance (Table 2 & Fig. 2) was found for cluster XII (23.94), followed by cluster IX (14.45), cluster II (10.57), cluster I (10.29), cluster IV (8.98), cluster XI (8.30), cluster VII (7.92) and cluster V (7.53). The minimum intra-cluster distance was recorded for cluster X (6.61), followed by cluster VIII (6.99). The highest inter-cluster distance was recorded between cluster VI and XII (83.04), followed by cluster V and XII (76.82), cluster II and IX (71.20), cluster VI and IX (69.94), cluster II and V (67.09), cluster II and VI (65.22) and cluster V and IX (63.74). The lowest inter-cluster distance was recorded between cluster VII and VIII (11.53), followed by cluster X and XI (11.77) and cluster VIII and X (12.61).

The intra-cluster group means for eleven characters (Table 3) revealed marked differences between the clusters in respects of cluster means for different characters. Cluster I, having 25 genotypes, showed second highest cluster means for plant height (174.48cm) and harvest-index (28.88%) besides having moderate to high mean performance for other characters. Cluster II with three genotypes recorded highest cluster means for seed yield per plant (64.09g), harvest-index (32.07%) and plant height (202.52cm) and second highest cluster means for secondary branches per plant (13.66), pods per plant (204.89), 100-seed weight (11.84g) and biological yield per plant (197.07g) besides having lowest cluster mean for seeds per pod (2.90). Cluster III, comprising 17 genotypes, exhibited highest cluster mean for days to maturity (255.22 days) and days to 50% flowering (150.35 days) and second lowest cluster mean for biological yield per plant (136.60g). The five genotypes of cluster IV were responsible for second highest cluster mean for days to 50% flowering (149.37 days) and second lowest cluster means for plant height (153.70cm) and seeds per pod (2.94). Cluster V possessing, XI genotypes, has second highest mean for days to maturity (253.11 days); lowest cluster means for plant height (153.36 cm), seed yield per plant (21.69g) and harvest-index (16.14%) and second lowest cluster means for primary branches per plant (3.10), secondary branches per plant (5.83) and pods per plant (80.75). The five genotypes of cluster VI produced highest cluster means for seeds per pod (4.19) and 100-seed weight (12.12g) and lowest cluster means for primary branches per plant (2.97), secondary branches per plant (5.72) and pods per plant (73.69). Cluster VII with 18 genotypes showed second lowest cluster means for days to 50% flowering (121.53 days), days to maturity (221.18 days) and harvest-index (17.90%) besides having moderate cluster means for remaining characters. The ten members of cluster VIII resulted second lowest cluster means for seed yield per plant (27.97g) along with low to moderate means for remaining characters. Cluster IX having least number of entries has second highest cluster mean for primary branches per plant (5.43) and lowest cluster mean for days to 50% flowering (110.67 days), days to maturity (133.42 days) and 100-seed weight (7.26g). Cluster X having 16 genotypes exhibited second highest cluster mean for seeds per pod (3.54) besides having moderate mean for most of the characters. The eight genotypes of cluster XI were characterized by highest cluster mean for primary branches per plant (5.59); lowest cluster mean for biological yield per plant (130.77g) and second lowest cluster mean for 100- seed weight (7.27g). The highest cluster means for secondary branches per plant (18.06), pods per plant (260.96) and biological yield per plant (199.46g) and second highest cluster mean for seed yield per plant (55.25g) were noted for cluster XII which was constituted by three genotypes.

The Non-hierarchical Euclidean cluster analysis grouped 120 pigeonpea germplasm lines and three checks of the present investigation into twelve distinct non-overlapping clusters. The discrimination of germplasm lines in to so many discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the pigeonpea materials (Katiyar *et al.*, 2004; Gupta *et. al.*, 2008; Sawant *et* *al.*, 2009; Bhadru, 2011; Pratap *et al.*, 2011). Presence of substantial genetic diversity among the germplasm lines 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.

The clustering pattern revealed that the genotypes of heterogeneous origin were frequently present in same cluster. Although the genotypes originated in same place or geographic region were also found to be grouped together in same cluster, the instances of grouping of genotypes of different origin or geographical regions in same cluster were observed in case of all the clusters. This indicated lack of any definite relationship or correlation between genetic diversity and geographic origin of the pigeonpea genotypes evaluated in the present study. Therefore, the selection of parental material for hybridization programme simply based on geographic diversity may not be rewarding exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances. This finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographic diversity in pigeonpea (Sawant *et al.*, 2009; Bhadru, 2011; Pratap *et al*., 2011).

Cluster I, having 25 genotypes, emerged with highest number of entries followed by cluster VII with 18 genotypes. Cluster III, X, XI and VIII were represented by 17, 16, 11 and 10 genotypes, respectively. Cluster IV and VI were constituted by five genotypes each while Cluster II and XII possessed three entries each. Cluster XI contained eight genotypes. Cluster IX, comprising two genotypes, had least number of entries.

The estimates of average intra- and inter-cluster distances for twelve clusters revealed that the genotypes present in a cluster have little genetic divergence from each other with respect to aggregate effect of 11 characters under study, while much more genetic diversity was observed between the genotypes belonging to different clusters. Since, high or optimum genetic divergence is desired between the parents of hybridization plan for obtaining higher frequency of desirable recombinants, the chances of obtaining good segregants by crossing the little diverse genotypes belonging same cluster are very low. In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. In present investigation, vary high inter cluster distances were recorded between cluster VI and XII, cluster V and XII, cluster II and IX, cluster VI and XI, cluster II and VI and cluster V and IX. The lowest inter cluster distance was observed between cluster VII and VIII, followed by cluster X and XI and cluster VIII and X. Thus, crossing between the genotypes of the above three cluster pairs having very low inter-cluster distances may not be rewarding owing to little genetic diversity among their genotypes.

The intra-cluster group means for eleven characters revealed marked differences between the clusters in respects of cluster means for different characters. Cluster I, having 25 genotypes, showed second highest cluster means for plant height and harvest-index besides having moderate to high mean performance for other characters. Cluster II with three genotypes recorded highest cluster means for seed yield per plant, harvest-index and plant height and second highest cluster means for secondary branches per plant, pods per plant, 100-seed weight and biological yield per plant besides having lowest cluster mean for seeds per pod. Cluster III, comprising 17 genotypes, exhibited highest cluster mean for days to maturity and days to 50% flowering and second lowest cluster mean for biological yield per plant. The five genotypes of cluster IV were responsible for second highest cluster mean for days to 50% flowering and second lowest cluster means for plant height and seeds per pod. Cluster V possessing, XI genotypes, has second highest mean for days to maturity; lowest cluster means for plant height, seed yield per plant and harvest-index and second lowest cluster means for primary branches per plant, secondary branches per plant and pods per plant. The five genotypes of cluster VI produced highest cluster means for seeds per pod and 100-seed weight and lowest cluster means for primary branches per plant, secondary branches per plant and pods per plant. Cluster VII with 18 genotypes showed second lowest cluster means for days to 50% flowering, days to maturity and harvest-index besides having moderate cluster means for remaining characters. The ten members of cluster VIII resulted second lowest cluster means for seed yield per plant along with low to moderate means for remaining characters. Cluster IX having least number of entries has second highest cluster mean for primary branches per plant and lowest cluster mean for days to 50% flowering, days to maturity and 100-seed weight. Cluster X having 16 genotypes exhibited second highest cluster mean for seeds per pod besides having moderate mean for most of the characters. The eight genotypes of cluster XI were characterized by highest cluster mean for primary branches per plant; lowest cluster mean for biological yield per plant and second lowest cluster mean for 100- seed weight. The highest cluster means for secondary branches per plant, pods per plant and biological yield per plant and second highest cluster mean for seed yield per plant were noted for cluster XII which was constituted by three genotypes.

The above discussion clearly shows wide variation from one cluster to another in respect of cluster means for eleven characters, which indicated that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in pigeonpea. Considering the mean performance for different characters of genotypes belonging to diverse clusters, the promising genotypes for exploitation as parents in hybridization programme were NDAGC 2011-4, NDAGC 2011-42 and NDAGC 2011-2 of cluster II; NDAGC 2011-18, NDAGC 2011-58, NDAGC 2011-34 and NDAGC 2011-27 of cluster V; NDAGC 2011-16, NDAGC 2011-41, NDAGC 2011-88, NDAGC 2011-104 and NDAGC 2011-103 of cluster VI; IC 525504 and PUSA 33 of cluster IX and IC 525456, IC 525408 and IC 525463 of cluster XII. These genotypes may be recommended for crossing with the genotypes of the clusters showing high inter cluster distances mentioned above for isolating transgressive segregants. However, caution should be exercised in selecting very diverse genotypes, because the frequency of heterotic crosses and magnitude of heterosis for yield and its components were found to be higher in crosses between parents with intermediate divergence than the extreme ones.

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Table 1. Clustering pattern of 123 pigeonpea genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 11 characters

Cluster number	No. of genotypes	Genotypes
I	25	IC 525418, IC 525403, IC 525438, NDAGC 2011-3, NDAGC 2011-82, NDA 2, NDAGC 2011-22, BAHAR, NDA 1, NDAGC 2011-85, NDGC 2011-20, NDAGC 2011-60, NDAGC 2011-40, NDAGC 2011-48, NDAGC 2011-44, NDAGC 2011-38, NDAGC 2011-47, NDAGC 2011-7, NDAGC 2011-43, NDAGC 2011-51, NDAGC 2011-90, NDAGC 2011-81, NDAGC 2011-61, NDAGC 2011- 87, NDAGC 2011-86.
II	3	NDAGC 2011-4, NDAGC 2011-42, NDAGC 2011-2.
III	17	NDAGC 2011-1, NDAGC 2011-31, NDAGC 2011-26, NDAGC 2011-5, NDAGC 2011-29, NDAGC 2011-28, NDAGC 2011-17, NDAGC 2011-89, NDAGC 2011-14, NDAGC 2011-39, NDAGC 2011-32, NDAGC 2011-45, NDAGC 2011-50, NDAGC 2011-15, NDAGC 2011-84, NDAGC 2011-46, NDAGC 2011-49.
IV	5	NDAGC 2011-6, NDAGC 2011-8, NDAGC 2011-33, NDAGC 2011-9, NDAGC 2011-21.
V	11	NDAGC 2011-67, NDAGC 2011-27, NDAGC 2011-30, NDAGC 2011-19, NDAGC 2011-34, NDAGC 2011-18, NDAGC 2011-23, NDAGC 2011-24, NDAGC 2011-37, NDAGC 2011-58, NDAGC 2011-25.
VI	5	NDAGC 2011-16, NDAGC 2011-41, NDAGC 2011-88, NDAGC 2011-104, NDAGC 2011-103
VII	18	IC 525486, IC525475, IC525500, IC525442, IC525448, IC525533, IC525415, IC525433, IC525414, IC525505, IC525472, IC525446, IC525494, IC525409, IC525434, IC525449, IC525540, IC525420.
VIII	10	IC525488, IC525460, IC525489, IC525440, IC525528, IC525464, IC525425, IC525439, IC525550 IC525430,
IX	2	IC525504, PUSA 33
X	16	IC525442, IC525455, IC525520, IC525445, IC525432, IC525490, IC525514, IC525421, IC525412, IC525484, IC525417, IC525526, IC525454, IC525465, IC525530, IC525466.
XI	8	IC 525441, IC 525410, IC 525536, IC 525521, IC 525406, IC 5225416, IC 525506, IC 525508
XII	3	IC 525456, IC 525408, IC 525463

Table 2. Estimates of average intra- and inter-cluster distances for 12 clusters in pigeonpea

Clusters	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**	**Cluster XI**	**Cluster XII**
Cluster I	**10.29**	20.61	16.67	24.31	31.81	28.84	23.83	26.12	54.29	17.11	22.95	35.67
Cluster II		**10.57**	41.29	47.10	67.09	65.22	43.35	52.25	71.20	34.90	39.59	33.20
Cluster III			**7.25**	13.35	14.32	15.54	20.60	14.18	54.54	15.74	20.56	53.83
Cluster IV				**8.98**	15.50	34.54	20.92	16.27	54.05	22.88	18.06	50.16
Cluster V					**7.53**	22.55	25.79	15.90	63.74	29.43	32.63	76.82
Cluster VI						**7.05**	35.45	25.37	69.94	26.21	42.30	83.04
Cluster VII							**7.92**	11.53	27.28	13.29	16.64	35.68
Cluster VIII								**6.99**	32.45	12.61	16.83	52.24
Cluster IX									**14.45**	28.42	31.52	48.16
Cluster X										**6.61**	11.77	34.15
Cluster XI											**8.30**	28.87
Cluster XII												**23.94**

*****Bold figure represent intra-cluster distances.

Table 3. Clusters means for 11 characters in pigeonpea

Clusters	Days to 50 % Flowering	Days to Maturity	Plant Height (cm)	Primary Branches/ Plant	Secondary Branches/ Plant	Pods/ Plant	Seeds/ Pod	100 Seed Weight (g)	Seed Yield/ Plant (g)	Biological Yield/ Plant (g)	Harvest Index (%)
Cluster I	147.63	250.81	174.48	4.35	10.26	147.10	3.30	11.37	51.78	179.71	28.88
Cluster II	147.23	250.09	202.52	4.22	13.66	204.89	2.90	11.64	64.09	197.07	32.07
Cluster III	150.35	255.22	166.53	3.47	9.35	108.34	3.46	9.52	33.30	136.60	24.64
Cluster IV	149.37	251.67	153.70	3.46	10.83	139.97	2.94	7.29	28.12	140.33	21.39
Cluster V	147.81	253.11	153.36	3.10	5.83	80.75	3.11	9.62	21.69	141.19	16.14
Cluster VI	149.30	252.20	164.21	2.97	5.72	73.69	4.19	12.12	33.57	137.07	24.86
Cluster VII	121.53	221.18	170.65	4.78	10.26	128.60	3.36	7.52	33.28	185.90	17.90
Cluster VIII	124.00	225.13	168.39	3.77	7.82	106.69	3.33	7.58	27.97	139.57	19.88
Cluster IX	110.67	133.42	171.58	5.43	11.27	136.32	3.38	7.26	37.38	162.67	22.80
Cluster X	122.44	222.82	173.89	4.77	10.13	129.14	3.54	9.03	41.36	145.15	28.53
Cluster XI	126.44	226.41	162.46	5.59	12.31	150.53	3.13	7.27	37.60	130.77	28.58
Cluster XII	122.57	222.98	172.40	7.07	18.06	207.96	3.08	9.25	55.25	199.46	27.55

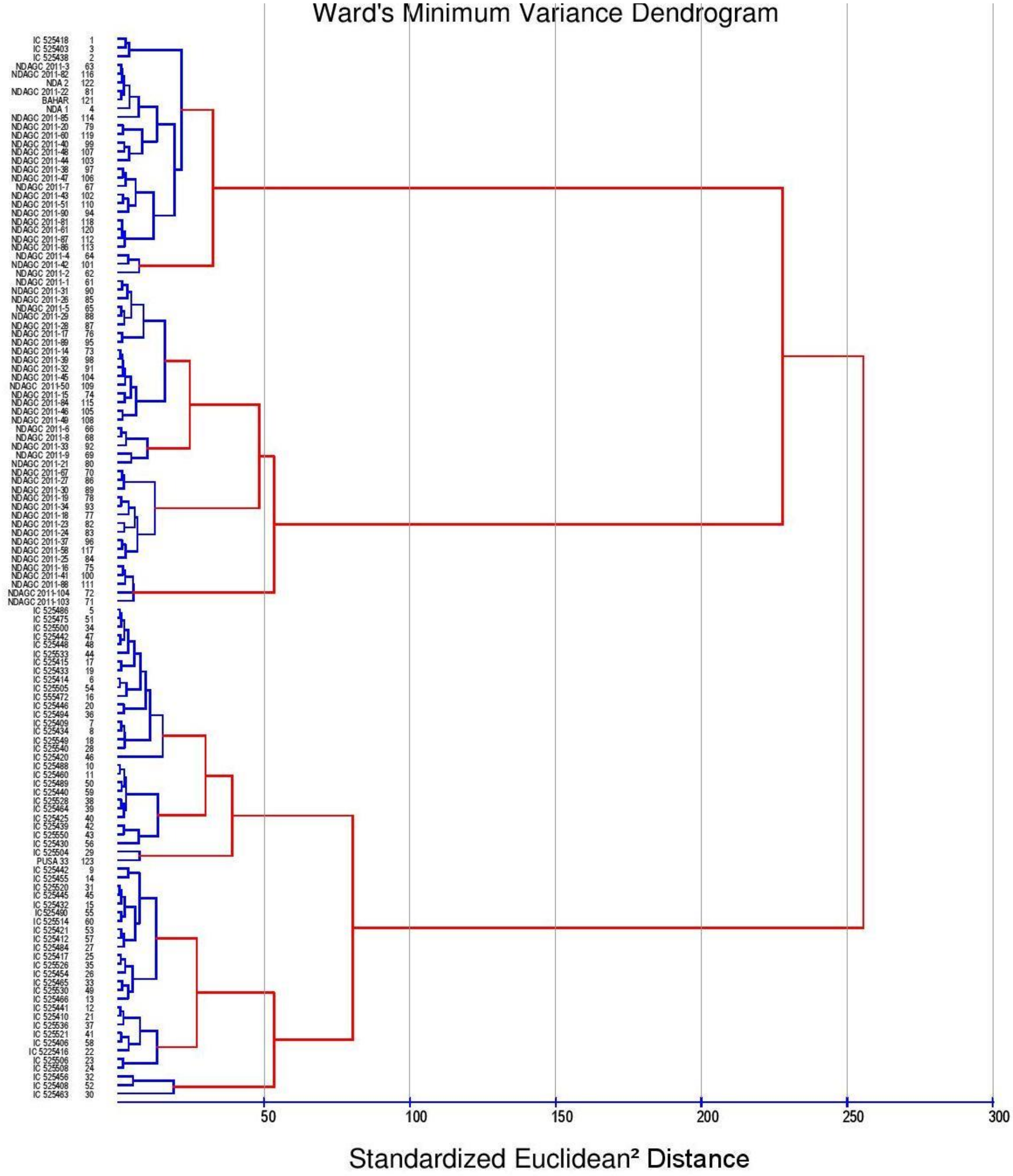

Fig. 1. Ward's Minimum Variance Dendrogram

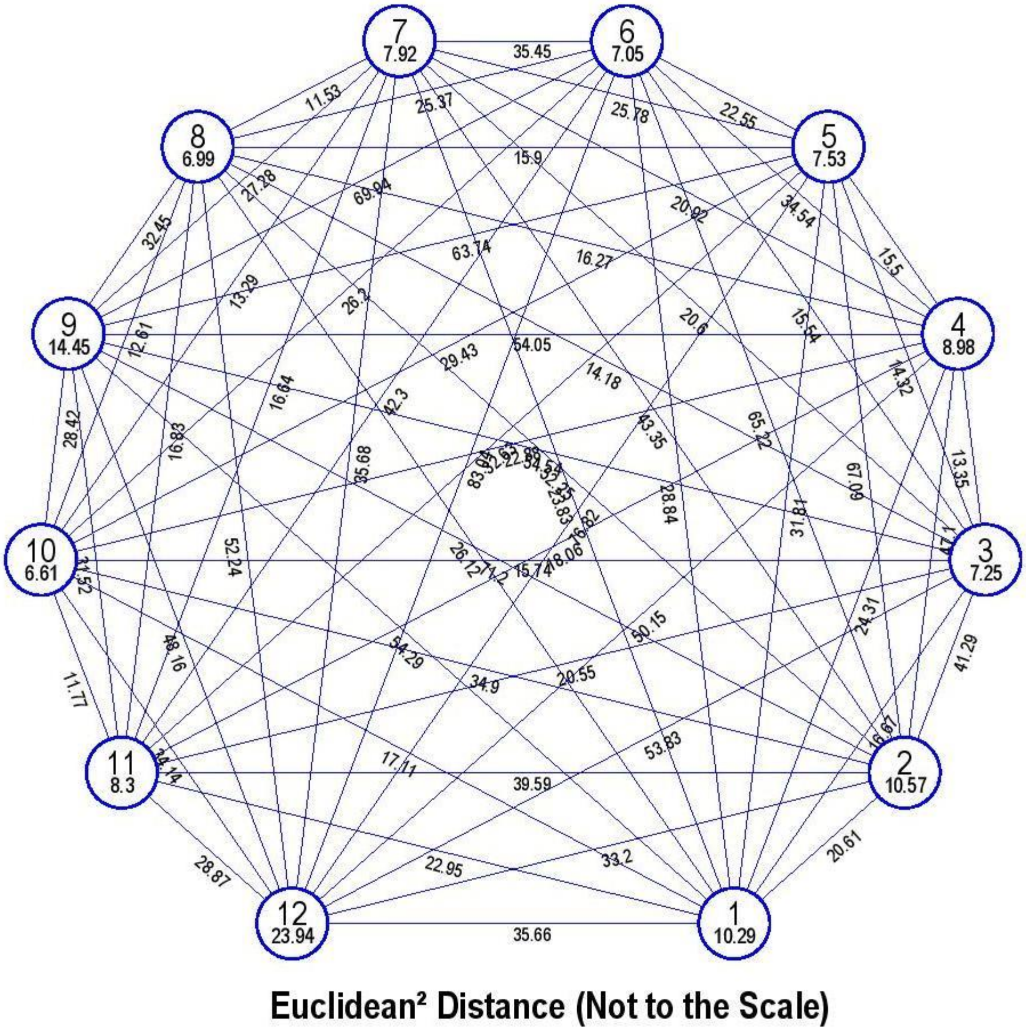

Fig. 2. Cluster diagram showing Euclidean^2 distance