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Genetic Divergence Studies in Roselle (*Hibiscus sabdariffa* L.)

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Genetic biodiversity among sixty genetically diversified genotypes of roselle (*Hibiscus sabdariffa* L.) for nine quantitative characters by Multivariate analysis revealed that the factors other than geographical diversity might have been responsible for grouping of genetic divergence. The clustering pattern revealed that the genotypes originating from different geographical regions got themselves grouped into different clusters. This indicated that the geographic biodiversity is not the only factor in determining genetic biodiversity. The genotypes with same geographic origin could have undergone change for different characters under selection during the process of evolution. The free clustering of the ecotypes suggested the influence of direction of selection pressure (applied) for realizing maximum yield in different ecosystems, the nicely evolved homeostatic devices would favour constancy of the associated characters and thus show indiscriminate clustering. The comparative study of efficacy of Tocher's method of grouping with Complete linkage dendrogram indicated the superiority of Complete linkage dendrogram over Tocher's method with a defined uniformity of index of homogeneity and optimum number of uniform clusters.

Key words: Roselle, *Hibiscus sabdariffa*, Complete linkage dendrogram, Tocher's method, index of homogeneity, Clustering.

Roselle *(Hibiscus sabdariffa* L.) is an important fibre yielding crop in India next to jute and the fibre is extracted from the bast region of stem. Fibre yield is quantitatively inherited and influenced by genetic factors as well as environments Genetic biodiversity is the diversity within species that allows a species the opportunity to evolve under changed environmental conditions. The variability observed among individuals (phenotypes) results partly from the interaction of genetic differences (genotypes) (Abdelatif *et al.* 2009). Quantification and classification (separation) of biological diversity present in a population of species is difficult.

Multivariate analysis by means of Mahalanobis's D_2 statistic is an useful tool in quantifying the degree of divergence between biological populations at genotypic level and to assess the relative contribution of different quantitative and qualitative characters to the total biodivergence (Pulli Bai *et al.* 2005a). Generally, the stopping rule for formation of any cluster is arbitrary and biodiversified genotypes are often wrongly clustered by tocher's method. There is no set formula to determine the best genotypes in various clusters formed, depending on the range and magnitude of variations in D_2 values. Complete linkage dendrogram (agglomerative method of hierarchical clustering approach) is a novel device for clustering the magnitude of biodiversity present in the biological populations. The comparative study of these two methods of clustering of the quantified biodiversity is essential for understanding different factors responsible for genetic biodivergence (Appalaswamy *et al.* 2003).

An attempt was made in the present investigation of study the genetic biodiversity with a comparative study of Tocher's method and Complete linkage dendrogram for effective quantification and grouping of biodiversity in sixty genotypes of roselle.

Materials and Methods

The sixty diversified genotypes (geographically and genetically) of roselle were studied in *kharif* (rainy season), 2011. The data collected on nine quantitative characters, i.e., days to 50 per cent flowering, plant height, basal stem diameter, number of nodes per plant, internodal length per plant, green plant weight per plant, fibre length per plant, fibre wood ratio and fibre yield per plant, were subjected to multivariate analysis given by Mahalanobis (1936). Grouping of the biodiversified genotypes into different clusters was done using two methods, namely, Tocher's technique (Rao, 1952) and Complete linkage dendrogram (Sneathe and Sokal, 1973) . The complete linkage dendrogram was based on the Mahalanobis Euclidean$_2$ distance.

Results and Discussion

The sixty genotypes were grouped into nine clusters using Tocher's method, where cluster I, II, III, IV and V consists of each with 19, 1, 14, 13 and 9

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Table 1. Homogenity index (Uniformity index) of clusters formed by the Tocher's and Complete linkage dendrogram methods in roselle.

Cluster number	Tocher's Method	Complete linkage dendrogram
I	0.579	0.590
II	———	0.456
III	0.604	0.611
IV	0.696	0.896
V	0.655	———
VI	———	0.547
VII	———	0.456
VIII	———	0.693
IX	———	———
Average	0.634	0.607

genotypes respectively. Whereas only single genotype were present in each of the clusters VI, VII, VIII and IX. While in Complete linkage dendrogram 15, 11, 16, two, one, five, six and four genotypes were grouped into the cluster I, cluster II, cluster III, cluster IV, cluster V, cluster VI, cluster VII and cluster VIII respectively (Table. 2, Fig. 1 & 2). It is clearly indicated the differentiation of clustering of genotypes into different clusters by these two methods. In the present investigation the pattern of clustering revealed that the genotypes originated from different geographical regions got themselves grouped into different clusters. Geographical biodiversity though important may not necessarily be the factor in determining genetic biodiversity.

The present study has shown that the factor other than geographical diversity might have been responsible for grouping of different genotypes. This could be due to the reason that ecotypes in a

Table 2. Cluster composition of genetic divergence of roselle (*Hibiscus sabdariffa* L.)

Cluster number	Tocher's method		Complete linkage dendrogram		Selection of genotypes in respective cluster		Selection of genotypes for further studies, based on comparative studies
	Number of genotypes	Origin(number of genotypes)	Number of genotypes	Origin(number of genotypes)	Tocher's method	Complete linkage dendrogram	
I	19	ARS, Amadalavalasa(A.P) (3) CRIJAF, Barrackpore(W.B) (2) Exotic (2) Indigenous local collection (12)	15	CRIJAF, Barrackpore(W.B) (2) Exotic (3) Indigenous local collection (8) Odisha (2)	AMV-5, AHS-163, R-92, R-129, AHS-188, AR-12, ER-1	AHS-161	
II	1	CRIJAF, Barrackpore(W.B) (1)	11	ARS, Amadalavalasa(A.P) (5) Exotic (1) Indigenous local collection (5)	R-83	AR-48, R-83, R-246	
III	14	Exotic (2) Indigenous local collection (9) Odisha (3)	16	ARS, Amadalavalasa(A.P) (2) CRIJAF, Barrackpore(W.B) (2) Exotic (2) Indigenous local collection (10)	R-134, JRRM-9-1, JRR-9, REX-1	R-200, ER-38, AHS-169, AMV-4, R-16, AR-190	AMV-5 R-83 JRR-9 ER-1
IV	13	ARS, Amadalavalasa(A.P) (4) Exotic (3) Indigenous local collection (6)	2	ARS, Amadalavalasa(A.P) (1) Indigenous local collection (1)	AHS-160, AR-71, R-28, CRIJAFR-8, AHS-172, AS-81-22, AMV-4	CRIJAFR-2, ER-1, ER-10	CRIJAFR-2 AHS-161 JRRM-9-2 AR-13
V	9	Exotic (1) Indigenous local collection (8)	1	CRIJAF, Barrackpore(W.B) (1)	CRIJAFR-2	AR-104, AR-19	
VI	1	ARS, Amadalavalasa(A.P) (1)	5	Exotic (1) Indigenous local collection (4)	AHS-161	AHS-188, R-129, AMV-5, AR-12	
VII	1	CRIJAF, Barrackpore(W.B) (1)	6	Exotic (1) Indigenous local collection (4) Odisha (1)	HS-4239	JRRM-9-2	
VIII	1	Indigenous local collection (1)	4	Indigenous local collection (4)	AR-13	HS-4270	
IX	1	CRIJAF, Barrackpore(W.B) (1)	---	---	HS-4270	---	

ARS – Agricultural Research Station, A.P – Andhra Pradesh, CRIJAF – Central Research Institute on Jute and Allied Fibres, W.B – West Bengal

particular habitat could have been evolved with different objectives and varied local situations and needs, thus giving importance to different characters. Therefore, ecotypes originating at the same place might have different genetic architecture. Likewise certain cultivars might possess similar characteristics even though their origins were different. Hence, genotypes with same geographical origin could have undergone change for different characters under selection during the process of evolution (Veerabadhiran *et al*., 1996).This shows that geographical biodiversity is not always related to genetic diversity and therefore is not adequate as an index of genetic diversity.

Moreover less number of clusters and grouping more number of genotypes into single cluster was observed in Tocher's method of clustering as compared to Complete linkage dendrogram. It is clearly indicated that the genotypes were grouped proportionately in case of Complete linkage dendrogram whereas by the Tocher's method, most of the genotypes were grouped into one or two clusters confined by intra-cluster D_2 values. There was little difference in case of inter-cluster D_2 values in both methods. Theoretically, the best method of clustering will be the one, which gives the more homogeneous clusters (minimum intra-cluster distance) along with maximum possible inter-cluster distance (Wahi and Kher, 1991). As none of these two procedures satisfy both the conditions uniformly, it was decided to form an index of homogeneity of clusters by taking the ratio of intra-cluster to inter-cluster distance to compare the efficiency of the two procedures. Lower the values of this index, the more homogeneous will be the clusters. The indices of homogeneity values were presented in Table.1.

Uniformity of index of homogeneity was observed in case of Complete linkage dendrogram whereas in Tocher's method, uniformity was lacking due to grouping of maximum number of genotypes into one or more clusters leaving other clusters with single with single genotypes. The comparative study of grouping of divergence by Tocher's method and Complete linkage dendrogram in roselle is essential for selecting biodivergent parental genotypes for effective creation of genetic

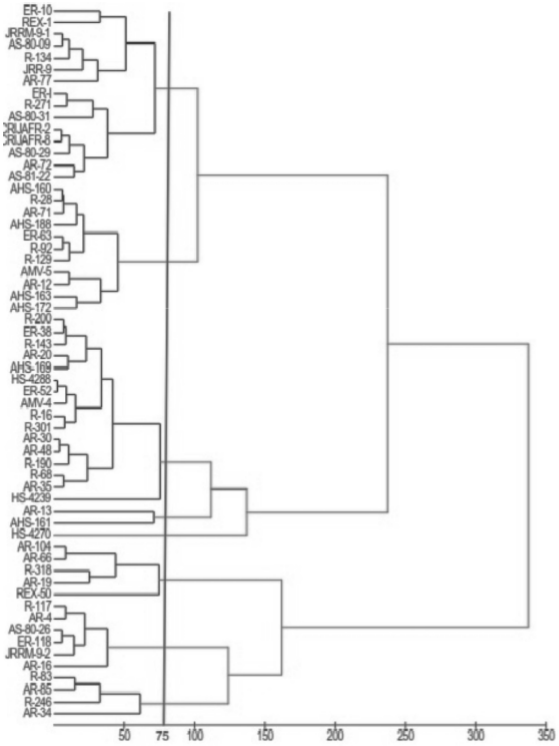

Fig. 1. Complete linkage dendrogram in roselle

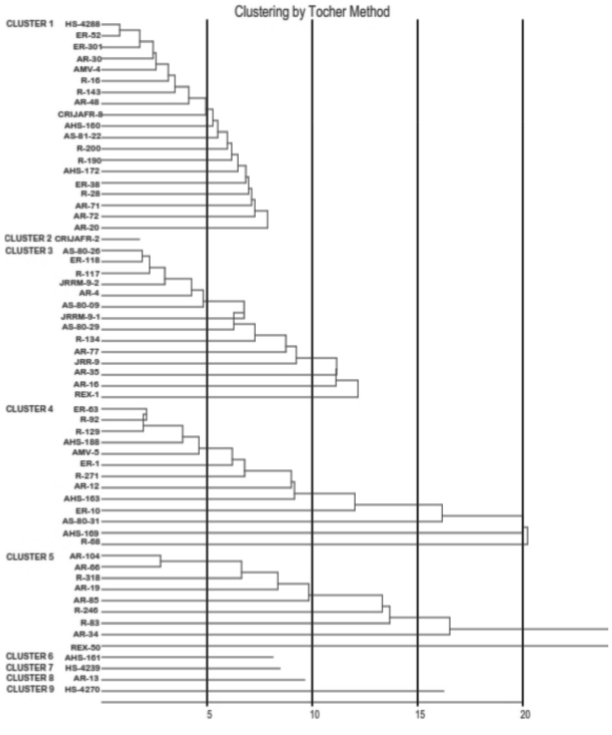

Fig. 2. Clustering by Tocher's method in roselle

biodiversity for crop improvement. In the present investigation, these biodivergent genotypes AMV-5, R-83, JRR-9, ER-1, CRIJAFR-2, AHS-161, JRRM-92 and AR-13 (Table.2) were found promising by comparative study of Tocher's method and Complete linkage dendrogram, may serve as potential parental genotypes for future hybridization programme.

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