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Genetic divergence studies for fibre yield and quality traits in roselle (*Hibiscus sabdariffa* L.)

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ABSTRACT

A field experiment was conducted with 67 genotypes of roselle at Agricultural Research Station, Amadalavalasa, Srikakulam district during *kharif* (2025) to assess the genetic divergence for eleven fibre yield and fibre quality traits. All the genotypes were grouped into five clusters based on Mahalanobis D^2 analysis using Tocher's method. Cluster I comprised of 46 genotypes followed by Cluster III with 10 genotypes, Cluster II with 8 genotypes, Cluster IV with 2 genotypes and Cluster V with a solitary genotype. The maximum inter-cluster distance was observed between clusters III and IV followed by clusters IV and V, indicating wider genetic diversity among these clusters. Cluster V recorded high mean values for green weight, fibre stick ratio, tenacity and fibre yield, whereas Cluster IV recorded highest mean value for plant height. Cluster II showed superiority for basal diameter and stick yield, while Cluster I recorded higher mean performance for fibre fineness. Among the eleven characters studied, days to 50 per cent flowering contributed maximum towards genetic divergence followed by defects, root content and tenacity. Based on cluster mean performance, AMV-10 (Cluster V) and genotypes HS-7910 and RIN-304 (Cluster IV) were identified as promising parents for fibre yield and fibre quality improvement. Hybridization between superior genotypes belonging to Clusters III and IV may be useful for generating wider variability and exploiting heterosis in roselle breeding programmes.

Key Words: *Genetic divergence, Mahalanobis' D^2 analysis, Roselle and Tocher's method*

Roselle (*Hibiscus sabdariffa* L.), a member of the Malvaceae family, is a versatile and important crop grown mainly in tropical and subtropical regions. It is a self-pollinating, herbaceous shrub with a chromosome number of 2n = 4x = 72 (Sabiel *et al*., 2014; Osman *et al*., 2011). Commonly known as roselle, it is cultivated for its edible calyces, leaves, seeds, bast fibre and paper pulp. The plant is referred to by various local names such as Karkade, Sorrel, Red Sorrel, Jamaican Sorrel, Indian Sorrel, Sour-Sour and Queensland Jelly Plant (Naim & Ahmed, 2010; Mahadevan *et al*., 2009). Roselle is an important medicinal plant possessing several therapeutic properties. Fresh calyces are rich in ascorbic acid, riboflavin, niacin, carotene, calcium and iron, while dry calyces exhibit antimicrobial and antioxidant activities due to the presence of phenolic compounds, flavonoids, gossypetin, hibiscetin and sabdaretin. Seeds of roselle have been found to be a good source of protein (Anokwuru *et al*., 2011).

The success of any crop improvement programme essentially depends on the nature and magnitude of genetic variability present in the crop. Improvement in yield is normally attained through exploitation of the genetically diverse parents for getting good hybrids. In this context, Mahalanobis D^2 statistic is an effective tool in quantifying the degree of divergence at genetic level and also provides quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). The present study was undertaken to assess the extent of genetic divergence among 67 roselle genotypes for fibre yield and fibre quality traits.

MATERIAL AND METHODS

The experimental material for genetic divergence studies comprised of 67 genotypes of roselle belonging to different regions of India. The material under study was made available at Agricultural Research Station, Amadalavalasa (Andhra Pradesh) through AINPJAF, CRIJAF and ICAR-NINFET, Kolkata. The experiment was laid out in Randomized Block Design with three replications during *kharif*

2025. Each genotype was sown in a single row of 4.0 m length with a spacing of 30 x 10 cm. The data was collected from 5 randomly selected plants in a row for each replication. All the fibre yield parameters were recorded at the time of harvesting. Fibre was extracted by standard method of retting. Data was recorded for 11 quantitative characters *viz*., days to 50 per cent flowering, plant height (cm), base diameter (mm), green weight (kg), stick yield (g), fibre stick ratio, root content (%), defects (%), tenacity (g/tex), fibre fineness (tex) and fibre yield (g). Mahalanobis D^2 statistic was used to assess the diversity among genotypes and they were grouped into different clusters using the Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among 67 genotypes for all the eleven characters studied, indicating the existence of substantial genetic variability among the genotypes. Based on Mahalanobis D^2 statistics, the 67 genotypes were grouped into five distinct clusters following Tocher's method considering fibre yield and its contributing traits *viz*., days to 50 per cent flowering, plant height (cm), base diameter (mm), green weight (kg), stick yield (g), fibre stick ratio, root content (%), defects (%), tenacity (g/tex), fibre fineness (tex) and fibre yield (g). The clustering pattern is presented in Table 1.

Among the five clusters, Cluster I was the largest comprising 46 genotypes followed by Cluster III with 10 genotypes, Cluster II with 8 genotypes, Cluster IV with 2 genotypes and Cluster V with a solitary genotype. The presence of genotypes from diverse origins in the same cluster indicated that geographical diversity was not necessarily related to genetic divergence. Similar observations were earlier reported by Kanakadurga *et al.* (1985), Anuradha *et al.* (2003), Shoba and Dharmatti (2004), Pullibai *et al.* (2005) and Satyanarayana *et al.* (2013).

The results obtained through D^2 analysis provide an opportunity for selecting genetically divergent parents for hybridization programmes aimed at improving fibre yield and quality traits. The inter and intra cluster D^2 values are presented in Table 2. The intra-cluster distance ranged from 0.00 in Cluster V to 107.8351 in Cluster III.

Among the clusters containing more than one genotype, Cluster III recorded the highest intra-cluster distance (107.8351), indicating greater heterogeneity among the genotypes within the cluster, whereas Cluster I recorded comparatively lower intra-cluster distance (59.104), suggesting close genetic similarity among its genotypes.

The maximum inter-cluster distance was observed between Cluster III and Cluster IV (407.3697) followed by Cluster IV and Cluster V (390.9171), Cluster I and Cluster IV (327.6608) and Cluster III and Cluster V (224.2705), indicating wider

Table 1. Cluster analysis of 67 genotypes by Tocher's method in roselle (*Hibiscus sabdariffa* L.)

Cluster Number	Number of genotypes	Genotypes
I	46	RIN-271, RIN-315, AHS-460, AHS-443, RIJ-3, FV-1, AHS-419, RIJ-8, RIN-230, RIN-285, RIN-302, RIJ-2, AHS-440, RIN-292, RIJ-5, RIN-222, RIN-214, RIN-245, RIN-278, RIJ-10, AMV-3, RIN-253, RIJ-9, RIN-318, HS-4288, AMV-2, RIJ-7, RIM-3, RIM-5, REX-11, AMV-7, AHS-444, RIM-2, RIN-237, RIM-1, RIN-207, RIN-219, RIM-6, AHS-429, RIN-313, AHS-454, RIJ-11, RIJ-6, AMV-1, RIN-264, AMV-9
II	8	RIN-288, RIN-297, RIN-201, AHS-420, RIM-4, AMV-5, AMV-8, AMV-11
III	10	RIN-306, RIN-311, RIN-287, REX-8, REX-6, REX-10, RIJ-15, REX-2, REX-9, REX-3
IV	2	HS-7910, RIN-304
V	1	AMV-10

Table 2. Inter and Intra cluster D² value by Tocher's method in roselle (*Hibiscus sabdariffa* L.)

Cluster	I	II	III	IV	V
I	**59.104**	117.9697	122.6768	327.6608	87.0765
II		**66.2605**	216.938	151.8591	121.9018
III			**107.8351**	407.3697	224.2705
IV				**79.2477**	390.9171
V					**0**

Table 3. The nearest and farthest clusters based on D² value in roselle (*Hibiscus sabdariffa* L.)

Cluster No.	Nearest cluster with D2 values	Farthest cluster with D2 values
I	**V** (87.0765)	**IV** (327.6608)
II	**I** (117.9697)	**III** (216.9380)
III	**I** (122.6768)	**IV** (407.3697)
IV	**II** (151.8591)	**III** (407.3697)
V	**I** (87.0765)	**IV** (390.9171)

genetic diversity among the genotypes belonging to these clusters. Wider genetic diversity was evident among genotypes belonging to different clusters than those within the same cluster. Hence, hybridization between genotypes belonging to these clusters may result in higher heterosis and wider segregation in subsequent generations. Among the cluster combinations, hybridization between genotypes belonging to Clusters III and IV may generate wider variability and higher heterosis owing to the maximum inter-cluster divergence observed between these clusters. The minimum inter-cluster distance was observed between Cluster I and Cluster V (87.0765), indicating relatively less genetic divergence between these clusters. The nearest and farthest clusters based on D² values are presented in Table 3.

Considerable variation in cluster means was observed for different characters among the five clusters and are presented in Table 4. Cluster V recorded the highest mean values for green weight (1.213), fibre stick ratio (0.357), tenacity (21.567) and fibre yield (48.433), indicating the superiority of the genotype present in this cluster for these traits. Cluster IV recorded the highest mean for plant height (245.5), whereas Cluster II exhibited higher values for basal diameter (14.641) and stick yield (137.042). Cluster I recorded the highest mean value for fibre fineness (3.266), while Cluster III recorded the highest mean values for root content (26.51) and defects (3.77).

The relative contribution of different characters towards total genetic divergence is presented in Table 5.

Table.4 Cluster means for 11 characters by Tocher's method in roselle (*Hibiscus sabdariffa* L.)

Clusters	Days to 50% flowering	Plant height (cm)	Basal diameter (mm)	Green weight (kg)	Stick yield (g)	Fibre stick ratio	Root content (%)	Defects (%)	Tenacity (g/tex)	Fibre fineness (tex)	Fibre yield (g)
Cluster I	119.522	233.775	14.587	1.092	132.145	0.353	16.738	2.989	17.333	3.266	46.605
Cluster II	110.875	240.833	14.641	1.121	137.042	0.336	16.154	2.704	17.825	3.033	45.458
Cluster III	120.9	235.6	14.557	1.131	131.717	0.351	26.51	3.77	15.9	3.21	46.25
Cluster IV	99.167	245.5	14.628	0.882	129.167	0.347	21.283	3.45	17.383	3.167	44.833
Cluster V	121	226.333	13.85	1.213	136.667	0.357	10.333	1.833	21.567	2.5	48.433

Table 5. Relative contribution of 11 characters towards divergence (D^2) in roselle (*Hibiscus sabdariffa* L.)

S. No.	Character	Contribution (%)	Times ranked
1	**Days to 50% flowering**	35.57	786
2	**Plant height (cm)**	2.11	47
3	**Basal diameter (mm)**	1.17	26
4	**Green weight (kg)**	4.04	89
5	**Stick yield (g)**	5.99	132
6	**Fibre stick ratio**	2.48	55
7	**Root content (%)**	14.19	314
8	**Defects (%)**	18.69	413
9	**Tenacity (g/tex)**	6.15	136
10	**Fibre fineness (tex)**	3.55	79
11	**Fibre yield (g)**	6.04	134

Among the eleven characters studied, days to 50 per cent flowering contributed the maximum towards genetic divergence (35.57%) followed by defects (18.69%), root content (14.19%), tenacity (6.15%), fibre yield (6.04%) and stick yield (5.99%). The remaining characters contributed comparatively less towards total divergence. The higher contribution of these traits indicated their greater role in the genetic differentiation of roselle genotypes and therefore these traits should be given due importance during parent selection in breeding programmes. Among the eleven quantitative characters studied, six characters *viz*., days to 50 per cent flowering, defects, root content, tenacity, fibre yield and stick yield together contributed major proportion towards total genetic divergence, whereas the remaining characters contributed comparatively less. Similar findings were reported by Jyothsna and Satyanarayana (2016) and Priya *et al.* (2020).

CONCLUSION

Based on cluster mean performance, AMV-10 (Cluster V) and genotypes HS-7910 and RIN-304 (Cluster IV) were identified as promising parental lines for fibre yield and fibre quality improvement. Further, hybridization between superior genotypes belonging to Clusters III and IV, which exhibited the maximum inter-cluster distance, may be useful for generating wider variability and exploiting heterosis in roselle breeding programmes.

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