

Genetic divergence studies for fibre yield traits in roselle (*Hibiscus sabdariffa* L.) In terai zone of West Bengal

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ABSTRACT

Sixty genotypes of roselle (*Hibiscus sabdariffa* L.) were evaluated for fibre yield and its contributing characters during Kharif, 2013 for eleven characters and genotypes were grouped into seven clusters. Grouping of genotypes into different clusters was not related to their geographic origin. The genotypes from different geographic locations were grouped into one cluster while genotypes of the same geographic origin showed genetic diversity. Cluster I was the largest containing 34 genotypes followed by Cluster II (fifteen), Cluster III (four), Cluster IV, V and VI with two genotypes each and mono-genotype Cluster VII. The highest inter cluster distance was observed between Cluster VI and VII followed by Cluster VI and IV and Cluster VI and I. Fibre yield per plant (42.54%) followed by dry stick weight per plant (22.48%) and petiole length (9.21%) have contributed maximum percent of contribution towards divergence. Cluster VII which consists of a single genotype has high cluster mean values for most of the characters while Cluster VI has lowest cluster mean values for most of the characters. Based on per se performance of genetic diversity and cluster means, genotypes belonging to Cluster I, IV, VI and VII may be chosen for crossing programme for roselle crop improvement.

Keywords: Cluster distance, D² analysis, genetic diversity, roselle

Roselle (*Hibiscus sabdariffa* L.) is an annual or biennial plant belonging to the large family Malvaceae and is cultivated in Tropical and Sub-Tropical regions for bast fibre, paper pulp or edible calyces, leaves and seed. In India, roselle is one of the most important bast fibre crop which occupies second place in area and production after jute and is used mainly for manufacturing of sacs, twines, carpets etc. Presence of sufficient genetic variability is a pre-requisite to formulate breeding programme aimed at improvement in yield and other characters, since the crosses made between the parents with maximum genetic divergence would more likely to yield desirable recombinants in the progeny. However, it is desirable to select suitable genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm. Further, selection of diverse parents for hybridization programme will be effective by the identification of characters responsible for the total genetic diversity among the populations (Murthy and Arunachalam, 1966).

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 as divergent parents throw heterotic crosses and also more variability could be

expected in the segregating generations. In this context Mahalanobis D² statistic is an effective tool in quantifying the degree of divergence at genetic level and it also provides quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). The present study was carried out to ascertain the nature and magnitude of genetic divergence among 60 roselle genotypes.

MATERIALS AND METHODS

Sixty roselle genotypes (consisting of eleven exotic lines; four released varieties; 28 local accessions from Andhra Pradesh and 17 local accessions from West Bengal) with diverse genetic background were evaluated at Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, West Bengal (latitude 26° 29' N and longitude 89° 20'E) during Kharif, 2013. The experimental trial was laid out in randomized complete block design with two replications under rainfed conditions. The recommended package of practices were followed to raise a good crop. Data on the basis of five randomly selected competitive plants were recorded on plant height (cm), base diameter (mm), internodal length (cm), petiole length (cm), mid diameter (mm), top diameter (mm), number of nodes plant⁻¹, bark thickness (mm), green weight plant⁻¹ (g), dry stick weight plant⁻¹ (g) and fibre yield plant⁻¹ (g). Multivariate analysis was done as per Mahalanobis D²

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statistic described by Rao (1952) and the genotypes were grouped into different clusters utilizing Tocher's method.

RESULTS AND DISCUSSION

The analysis of variance revealed significant difference among the sixty genotypes for all the characters except for mid diameter (Table-1). Plant height, base diameter, intermodal length, petiole length, number of nodes plant⁻¹, green weight plant⁻¹, dry stick weight plant⁻¹ and fibre yield plant⁻¹ were highly significant at 1% level whereas the characters top diameter and bark thickness were significant at 5% level. This indicated the existence of significant amount of variability among the sixty genotypes for the characters studied. Based on the diversity and magnitude of D² values sixty genotypes were grouped into seven clusters by Tocher's method (Table-2). Cluster I was largest with thirty four genotypes followed by Cluster II with fifteen, Cluster III with four, Cluster IV, V and VI with two each and mono-genotype Cluster VII. The variation in the composition of individual cluster with regard to the number of genotypes indicated the presence of large amount of diversity in the population. The clustering pattern indicated that there was no relationship between distribution and genetic diversity as the genotypes from different origin were grouped into the same clusters. It is an indication for the absence of relationship between genetic diversity and geographic diversity. This suggests that there are forces other than geographical separation such as natural and artificial selection, exchange of breeding materials, genetic drift and environmental variation. The results are in accordance with the findings of Anuradha (2003), Hariram Kumar *et al.* (2013), Nayak *et al.* (2009), Pulli Bai *et al.* (2005) and Roy *et al.* (2011).

On the basis of D² values the minimum intra-cluster value was observed in Cluster IV (14.06) and maximum in Cluster II (43.40) (Table-3). Similarly, the minimum inter-cluster distance for D² values was observed between Cluster IV and VII (27.32) followed by Cluster IV and V (30.68) which suggests that genotypes of these clusters were closely related. Maximum inter-cluster D² was observed between Cluster VI and VII (192.08) followed by Cluster VI and IV (139.88) and Cluster I and VI (107.14) Maximum inter-cluster values indicate that these genotypes are most diverse in the present study and crossing between genotypes of these clusters would yield good recombinants. The contribution of individual character towards the divergence (Table-4) indicated that fibre yield plant⁻¹ (42.54%) contributed the maximum followed by dry stick weight plant⁻¹,

petiole length (9.21%), bark thickness (7.63%) and green weight plant⁻¹ (7.63%). The contribution made by other characters in the study was comparatively low ranging from 0.51% for base diameter to 2.71% for plant height. These results are corroborating with the findings of Nayak *et al.* (2009), Pulli Bai *et al.* (2005) and Roy *et al.* (2011).

Cluster mean values for different characters (Table-4) indicated that the mean values for plant height, base diameter, mid diameter, top diameter, green weight plant⁻¹, dry stick weight plant⁻¹ and fibre yield plant⁻¹ were highest in Cluster VII which consists of only one genotype. Cluster IV which consists of two genotypes has high mean values for plant height, mid diameter, green weight plant⁻¹, dry stick weight plant⁻¹ and fibre yield plant⁻¹. Cluster I with thirty four genotypes has recorded high mean values for plant height, base diameter, mid diameter, bark thickness, green weight plant⁻¹, dry stick weight plant⁻¹ and fibre yield plant⁻¹. Cluster VI which comprises of two genotypes has recorded lowest mean values for most of the characters. Crosses among diverse parents are likely to yield desirable recombinants. The greater the distance between two clusters, the wider the genetic diversity among parents to be included in the hybridization programme.

The genotypes of Cluster II were highly divergent than those of Cluster I, VI indicating scope of generating high heterosis between the parents of these clusters. Maximum diversity was found between Cluster VI and VII (192.08) followed by Cluster VI and IV (139.88) and Cluster I and VI (107.14). In addition, the Clusters I, IV and VII recorded high mean values for most of the characters while Cluster VI recorded lowest for most of the characters. Selection of parents from the diverse Clusters I, IV, VI and VII for hybridization programme would help in achieving novel recombinants. Thus in the present study, roselle mesta genotypes exhibited a distinct and wide spread clustering pattern there by indicating huge amount of genetic divergence and heterogeneity. Based on the genetic distances, clustering pattern, cluster means and *per se* performance hybridization programme may be initiated involving genotypes of Clusters I, IV and VII i.e. AR-14, AR-81, R-225, ER-57, HS-4288 and AMV-4 for roselle crop improvement.

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Table 1: Analysis of variance for eleven characters in roselle

Source	df	Plant height	Base diameter	Internodal length	Petiole length	Mid diameter	Top diameter	No. of nodes plant ⁻¹	Bark thickness	Green weight plant ⁻¹	Dry stick weight plant ⁻¹	Fibre yield plant ⁻¹
Replication	1	55.49	3.60	0.67	1.43	0.006	10.82	120.00	0.32	1373.63	14.42	0.49
Genotype	59	2757.18**	6.68**	0.82**	2.73**	2.33 ^{NS}	1.36*	86.38**	0.05*	20221.74**	474.40**	62.04**
Error	59	525.34	2.93	0.40	0.74	1.56	0.80	39.36	0.03	4153.26	46.96	6.29
CD (0.05)		45.98	3.43	1.28	1.73	NS	1.79	12.59	0.35	129.28	13.75	5.03
CV %		7.57	9.73	14.15	9.08	9.92	12.06	8.70	9.78	14.07	13.59	12.24

*Significant at P = 0.05; **Significant at P = 0.01 respectively

Table 2: Distribution of sixty roselle genotypes into different clusters based on D² statistic

Cluster No.	No. of genotypes	Name of the genotypes
I	34	AR-14, AR-19, AR-42, AR-45, AR-48, AR-50, AR-55, AR-66, AR-67, AR-71, AR-79, AR-80, AR-81, AR-85, AR-88, R-16, R-29, R-30, R-37, R-48, R-67, R-68, R-77, R-86, R-134, R-180, R-225, R-243, R-271, R-284, R-318, R-322, ER-56 and ER-57
II	15	ER-60, ER-68, AS-80-6, AS-80-7, AS-80-A9, AS-80-26, AS-80-29, AS-81-1, AS-81-2, AS-81-3, AS-81-5, AS-81-9, AS-81-14, AS-81-17 and AS-81-22,
III	4	REX-6, REX-14, REX-45 and REX-52
IV	2	AMV-4 and AMV-5
V	2	REX-63 and AMV-7
VI	2	REX-34 and REX-38
VII	1	HS-4288

Table 3: Intra (in bold) and inter cluster D² values of seven clusters from sixty roselle genotypes.

Cluster	Cluster - I	Cluster - II	Cluster - III	Cluster - V	Cluster - VI	Cluster - VII
Cluster - I	40.48(6.36)	54.75(7.40)	36.67(6.06)	44.56(6.68)	107.14(10.35)	46.84(6.84)
Cluster - II	43.40(6.59)		47.71(6.91)	74.84(8.65)	57.71(7.60)	97.12(9.86)
Cluster - III			28.35(5.33)	38.41(6.20)	91.87(9.59)	41.76(6.46)
Cluster - IV			14.06(3.75)	3.0.68(5.54)	139.88(11.83)	27.32(5.23)
Cluster - V				28.91(5.38)	98.19(9.91)	43.83(6.62)
Cluster - VI					36.48(6.04)	192.08(13.86)
Cluster - VII						0.00(0.00)

*Figures in parenthesis are average cluster distances.

Table 4: Mean performance of different clusters and contribution of characters to diversity in roselle

Cluster	Plant height (cm)	Base diameter (mm)	Internodal length (cm)	Petiole length (cm)	Mid diameter (mm)	Top diameter (mm)	No. of nodes plant ⁻¹	Bark thickness (mm)	Green weight plant ⁻¹ (g)	Dry stick weight plant ⁻¹ (g)	Fibre yield plant ⁻¹ (g)
Cluster - I	313.97	18.79	4.62	9.26	12.83	7.32	72.34	1.84	489.24	56.08	22.05
Cluster - II	274.76	16.94	4.28	10.02	11.74	7.18	70.43	1.71	388.50	38.57	16.94
Cluster - III	320.53	18.13	4.38	10.29	12.93	7.99	78.13	1.71	501.10	55.28	22.45
Cluster - IV	333.35	17.74	3.76	7.98	13.18	7.61	72.50	1.58	459.20	54.70	22.61
Cluster - V	300.05	17.74	5.58	7.90	13.04	7.76	65.75	1.64	448.35	45.60	20.51
Cluster - VI	227.05	15.94	3.70	11.62	12.39	8.24	75.00	1.74	314.10	21.10	11.09
Cluster - VII	358.50	20.26	5.10	8.30	13.81	8.44	72.00	1.82	582.20	76.00	28.21
Contribution (%)	2.71	0.51	1.41	9.21	1.98	1.86	2.04	7.63	7.63	22.48	42.54

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