Electronic Journal of Plant Breeding, 6(3): 826-830 (Sep 2015)
ISSN 0975-928X

Research Note

Genetic diversity in Roselle (*Hibiscus sabdariffa* L.) for fibre yield

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(Received: 12 Dec 2014; Accepted:05 Feb 2015)

Abstract
An experiment with sixty genotypes of Roselle (*Hibiscus sabdariffa* L.) was conducted for determining the diverse genotypes based on eleven fibre yield contributing characters during *kharif*, 2013 and these genotypes were grouped into six clusters. Cluster I was the largest containing 51genotypes followed by Cluster II, Cluster III, Cluster IV and Cluster V with two genotypes each and Cluster VI was solitary. The highest inter cluster distance was observed between Cluster V and III followed by Cluster V and VI and Cluster V and Cluster I. Fibre yield plant^{-1} (53.28%) followed by dry stick weight plant^{-1}(22.99%) and fresh green weight plant^{-1}(9.89%) have contributed maximum per cent of contribution towards divergence. Cluster III which consists of two genotypes has high cluster mean values for most of the fibre yield contributing characters, followed by Cluster VI and Cluster IV while Cluster V has the lowest cluster mean values for most of the characters. Based on *per se* performance of genetic diversity and cluster means, genotypes belonging to Cluster III, IV, VI and I may be chosen for further improvement in roselle for fibre yield.

Keywords
Cluster means, Genetic diversity, Inter and Intra-cluster distance, Roselle

Roselle (H*ibiscus sabdariffa* L.) is an annual or biennial plant belonging to the 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. 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 through heterotic crosses and also more variability could be expected in the segregating generations. In this context Mahalanobis D^2 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.

Sixty roselle (*Hibiscus sabdariffa* L.) genotypes consisting of 45 indigenous accessions; eleven exotic lines and four released varieties with diverse genetic background were evaluated at

Agricultural Research Station, Ragolu, Srikakulam District which is situated in North Coastal Zone of Andhra Pradesh (latitude 18°359’ N and longitude 83° 85’E) during *Kharif*, 2013 were the crop is mostly grown. The experimental trial was laid out in randomized complete block design with two replications under rainfed conditions. The recommended packages of practices were followed to raise a good crop. Data on five randomly selected competitive plants were recorded for plant height (cm), base diameter (mm), mid diameter (mm), top diameter (mm), petiole length (cm), internodal length (cm), bark thichness (mm), fresh green weight plant^{-1} (g), dry green weight plant^{-1} (g), dry stick weight plant^{-1} (g) and fibre yield plant^{-1} (g). Multivariate analysis was done as per Mahalanobis D^2 statistic described by Rao (1952) and the genotypes were grouped into different clusters utilizing Tocher’s method.

The analysis of variance revealed significant difference among the genotypes for all the eleven characters under study. This indicated the existence of significant amount of variability among the sixty genotypes for the characters studied. Based on the diversity and magnitude of D^2 values sixty genotypes were grouped into six clusters by Tochers’ method (Table-1). Cluster I was largest with 51genotypes followed by Cluster II, III, IV and V with two each and Cluster VI consists of only one genotype. 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 Dudhane *et. al.,* (2013), Hariram Kumar *et. al.* (2013), Nayak *et. al.* (2009), Roy *et. al.* (2011) and Shaikh Md. Soyab Akhil Mohd. Ab. Mazid *et. al.* (2013).

On the basis of D^2 values the minimum intra-cluster value was observed in Cluster II (14.78) and maximum in Cluster I (82.21), while on the basis of cluster distance analysis, the minimum intra-cluster distance was observed in Cluster II (3.85) and maximum in Cluster I (9.07) (Table-2). The intra-cluster distance for Cluster I was high which may be due to the presence of highest number of genotypes with large variability within that cluster. Similarly, the minimum inter-cluster distance for D^2 values was observed between Cluster II and VI (20.87) followed by Cluster IV and II (30.39) which suggests that genotypes of these clusters were closely related. Maximum inter-cluster D^2 was observed between Cluster V and III (453.00) followed by Cluster VI and V (310.89) and Cluster I and V (207.88) while minimum inter-cluster distances was observed between Cluster II and VI (4.57) followed by Cluster IV and II (5.51) and maximum was observed between Cluster V and III (21.28) followed by Cluster VI and V (17.63) and Cluster I and V (14.42) on the basis of cluster analysis. Maximum inter-cluster values indicate that these genotypes are most diverse within the present study and crossing between genotypes of these clusters would yield good recombinants.

The contribution of individual character towards the divergence (Table-3) indicated that fibre yield plant^{-1} (53.28%) contributed the maximum followed by dry stick weight plant^{-1} (22.99) and fresh green weight plant^{-1} (9.89%). The contribution made by other characters in the study was comparatively low ranging from 0.06% for base diameter and top diameter to 4.92% for dry green weight plant^{-1}. These results are corroborate with the findings of Dudhane *et. al.* (2013) and Roy *et. al.* (2011).

Cluster mean values for different characters were indicated in Table-4. Cluster III consisting of two genotypes recorded highest mean values for mid diameter, top diameter, fresh green weight plant^{-1}, dry green weight plant^{-1}, dry stick weight plant^{-1} and fibre yield plant^{-1}; while recorded high for plant height, base diameter, petiole length, intermodal length and bark thickness. Cluster IV which consists of two genotypes recorded highest mean values for base diameter, bark thickness and high mean values for the characters plant height, mid diameter, top diameter, fresh green weight plant^{-1}, dry green weight plant^{-1}, dry stick weight plant^{-1} and fibre yield plant^{-1}. Cluster VI which is a solitary cluster recorded highest mean values for plant height; and high mean values for base diameter, mid diameter, top diameter, fresh green weight plant^{-1}, dry stick weight plant^{-1} and fibre yield plant^{-1}. Cluster I with fifty one genotypes has recorded high mean values for plant height, base diameter, top diameter, mid diameter, bark thickness, fresh green weight plant^{-1}. Cluster V 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.

Based on the cluster mean values and intra-cluster distances, genotypes belonging to Cluster III, VI and VI along with of genotypes of Cluster I having high mean values for fibre yield contributing traits may be selected for crossing which have the scope for generating heterotic seggregants for developing new high fibre yielding roselle cultivars.

Acknowledgement

The authors are highly thankful to BCKV, ANGRAU and CRIJAF (ICAR) Barrackpore, Kolkata for providing necessary help and infrastructural facilities to undertake these studies.

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Table 1. Distribution of sixty roselle (*Hibiscus sabdariffa* L.) genotypes into different clusters based on D^2 statistics

Cluster No.	No. of genotypes clustered	Name of the genotypes
I	51	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, ER-57, 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, AS-81-22, REX-6 and REX-14
II	2	REX-63 and AMV-4
III	2	REX-52 and HS-4288
IV	2	REX-45 and AMV-7
V	2	REX-34 and REX-38
VI	1	AMV-5

Table 2: Average inter and intra cluster distance with sixty roselle genotypes (*Hibiscus sabdariffa* L.)

Cluster	Cluster – I	Cluster - II	Cluster – III	Cluster - IV	Cluster – V	Cluster - VI
Cluster – I	82.21 (9.07)	56.18 (7.50)	129.87 (11.40)	59.25 (7.70)	207.88 (14.42)	74.73 (8.64)
Cluster – II		14.78 (3.85)	88.14 (9.39)	30.39 (5.51)	197.64 (14.06)	20.87 (4.57)
Cluster – III			26.00 (5.10)	105.15 (10.25)	453.00 (21.28)	49.57 (7.04)
Cluster – IV				31.71 (5.63)	191.18 (13.83)	53.10 (7.29)
Cluster – V					50.40 (7.10)	*310.89* (17.63)
Cluster – VI						0.00 (0.00)

*Figures in parenthesis are average cluster distances.
**The figures in diagonal indicate intra cluster distances

Table-3: Contribution of different characters to diversity for sixty genotypes of roselle (*Hibiscus sabdariffa* L.)

Character	Times ranked first	Contribution (%)
Plant height (cm)	76	4.29
Base diameter (mm)	1	0.06
Mid diameter (mm)	3	0.17
Top diameter (mm)	1	0.06
Petiole length (cm)	45	2.54
Internodal length (cm)	16	0.90
Bark thickness (mm)	16	0.90
Fresh green weight plant^{-1} (g)	175	9.89
Dry green weight plant^{-1} (g)	87	4.92
Dry stick weight plant^{-1} (g)	407	22.99
Dry fibre yield plant^{-1} (g)	943	53.28
TOTAL	1770	100

Table-4: Cluster means for eleven characters in roselle (*Hibiscus sabdariffa* L.)

Cluster	Plant height (cm)	Base diameter (mm)	Mid diameter (mm)	Top diameter (mm)	Petiole length (cm)	Internodal length (cm)	Bark thickness (mm)	Fresh green weight plant^{-1} (g)	Dry green weight plant^{-1} (g)	Dry stick weight plant^{-1} (g)	Dry fibre yield plant^{-1} (g)
Cluster – I	309.67	20.58	15.78	11.46	12.19	6.49	2.35	666.8	314.80	59.08	26.16
Cluster – II	306.00	19.56	15.95	11.73	9.74	6.31	2.28	592.4	258.60	58.75	26.35
Cluster – III	333.50	22.01	16.32	12.10	11.24	6.48	2.68	793.6	385.00	86.25	33.56
Cluster – IV	321.50	22.57	15.09	11.59	10.92	6.04	2.80	772.4	316.20	60.00	30.90
Cluster – V	204.25	18.84	15.16	11.21	12.78	5.72	2.62	476.2	170.00	25.00	12.75
Cluster – VI	346.00	20.87	15.64	11.97	9.40	6.34	2.09	660.00	310.00	72.50	29.57