GENETIC DIVERGENCE STUDIES IN ROSELLE (*HIBISCUS SABDARIFFA* L.) FOR FIBRE YIELD OVER SIX ENVIRONMENTS

N. Hari Satyanarayana *et al.,*

KEYWORDS

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N. HARI SATYANARAYANA*, V. VISALAKSHMI[1], BHANU PRIYA, SUBHRA MUKHERJEE[2], S. K. ROY[1] A. U. RAO AND K. K. SARKAR

Department of Genetics and Plant Breeding, BCKV, Mohanpur - 741 252, Nadia, West Bengal
*Agricultural Research Station (ANGRAU), Amadalavalasa, Srikakulam - 532 185, A. P.
[1]Agricultural Research Station (ANGRAU), Ragolu, Srikakulam - 532 484, A. P.
[2]AINP on Jute and Allied Fibres, UBKV, Pundibari, Coochbehar - 736 165, West Bengal
e-mail: haribckv@gmail.com

ABSTRACT

Sixty genotypes of roselle (*Hibiscus sabdariffa* L.) were evaluated at three different agro-climatic zones viz., North Coastal zone of Andhra Pradesh, Indo-Gangetic zone and Terai zone of West Bengal for fibre yield and its contributing characters during *Kharif*, 2013 and 2014 for twelve characters and grouped them into nine clusters based on D² analysis. Cluster I accommodated highest number of genotypes followed by Cluster III and II. Inter-cluster distance was highest between the Clusters II and IX followed by Clusters VIII and IX, whereas Intra-cluster distance was high for Cluster IV which consists of six genotypes. Cluster II recorded highest and high values for yield and its attributing characters followed by Cluster VII, whereas, Cluster IX recorded lowest and low values for yield and its attributing characters followed by Cluster IV. Dry stick weight per plant contributed high for the diversity followed by fibre yield. Based on the above genetic parameters, the diverse genotypes belonging to Cluster II, VII, VIII and IX could be utilized as parents in future Crop Improvement programmes to achieve high fibre yielding recombinants.

*Corresponding author

INTRODUCTION

Roselle (*Hibiscus sabdariffa* L.) is an annual or perennial 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 seeds (Osman et al., 2011). In India, roselle is one of the most important bast fibre crops which occupies second place in area and production after jute and is mainly used for manufacturing of sacs, twines, carpets etc. (Satyanarayana et al., 2015). In India, the major growing states of roselle crop are Andhra Pradesh, Bihar, Orissa, West Bengal and Maharastra with an area of 84 thousand ha (during 2012-13) that produced 6.16 lakh bales (1bale = 180 kg) with an average productivity of about 13.20 q/ha. (Sen and Karmakar, 2014). Raw jute, the fibre of commerce is extracted from the stem of two cultivated species of jute (tossa & white jute) and mesta (roselle & kenaf). Raw jute (jute and mesta) occupying only 0.55% of the cropped area of the country provide livelihood support to 4 million farm families, 0.25 million industrial workers and 0.50 million traders in India. India is the major grower of roselle in world (Mahapatra, 2013).

In crop improvement programme, to increase the productivity breeder needs to maintain a pool of diverse desirable donor parents (Joshi *et al.* 2013). An apparent understanding of genetic diversity is essential for the effective conservation and utilization of genetic resources. Presence of sufficient genetic diversity 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. 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). 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).

Fibre yield is quantitatively inherited and influenced by genetic factors as well as environments. To improve such important fibre crop through breeding, study on genetic diversity of important traits responsible for fibre yield is essential to identify diverse parents for hybridization programmes to evolve high yielding recombinants. The present study has been outlined to estimate genetic diversity present in a set of 60 roselle germplasm on the basis of twelve quantitative characters including fibre yield, so that desirable parents could be identified for utilization in crop improvement programme to obtain maximum fibre yield.

MATERIALS AND METHODS

Sixty roselle (*Hibiscus sabdariffa* L.) genotypes consisting of eleven exotic lines; four released varieties and 45 indigenous accessions (Table 1) were evaluated at three different agro-climatic environments viz., North Coastal zone, Andhra Pradesh

at Agricultural Research Station, Ragolu (Latitude 18⁰ 24′ N; Longitude 83. 84⁰ E at an altitude of 27m above mean sea level); Indo-Gangetic zone, West Bengal at Instructional Farm, Bidhan Chandra Krishi Vishwavidyalaya, Jaguli (Latitude 22⁰ 93′ N; Longitude 88. 59⁰ E at an altitude of 9.75m above mean sea level) for first year and at Teaching farm, Mondauri, BCKV (Latitude 22⁰ 87′ N; Longitude 88. 59⁰ E at an altitude of 9.75m above mean sea level) for second year and Terai Zone, West Bengal at University Farm, Uttar Banga Krishi Vishwavidyalaya (Latitude 26⁰ 19′ N; Longitude 89. 23⁰ E at an altitude of 43m above mean sea level). The experiments were sown during early *kharif* seasons in 2013 and 2014 at the above three zones.

The experimental trial was laid out in randomized block design with a plot size of four rows of 2m length in two replications and adapted spacing of 30 x 10cm under rainfed conditions. Recommended package of practices was 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), mid diameter (mm), top diameter (mm), internodal length (cm), petiole length (cm), nodes per plant, bark thichness (mm), green weight (g), green weight (leafless) (g), dry stick weight (g) and fibre yield (g). Genetic diversity analysis was done as per Mahalanobis D^2 statistic (Rao, 1952) and the genotypes were grouped into different clusters utilizing Tocher's method.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among sixty genotypes for all the twelve characters. This indicated the existence of significant amount of diversity among the sixty genotypes for the characters studied. On the basis of

Mahalanobis D^2 analysis, sixty genotypes were grouped into nine clusters (Table 2) based on twelve fibre yield attributing traits. The clusters were formed on the basis of average cluster distance, following Tocher's method (Rao, 1952) considering fibre yield and its attributing traits. Cluster I comprised of twenty one genotypes followed by Cluster III with eighteen genotypes, Cluster II with ten genotypes, Cluster IV with six and the remaining Clusters V, VI, VII, VIII and IX were solitary clusters with single genotype each.

There was no relationship between geographical origin and genetic diversity, as the genotypes belonging from different geographical regions were included in the same cluster of Cluster I, Cluster II, Cluster III and Cluster IV. Similarly, the genotypes belonging to the same geographic region were distributed solitarily to different clusters in Cluster VI, Cluster VII, Cluster VIII and cluster IX. Earlier, Anuradha (2003) grouped 68 roselle genotypes into eleven clusters; Shobha and Dharmatti (2004) grouped twenty six kenaf lines into five clusters; Pulli Bai *et al.* (2005) grouped 51 roselle genotypes into seven clusters; Hariram *et al.* (2013) grouped sixty genotypes of roselle into nine clusters; Asha *et al.* (2015) grouped 49 genotypes of okra into eight clusters; Kurrey *et al.* (2015) grouped twenty five chench genotypes into five groups and Satyanarayana *et al.* (2015) grouped sixty genotypes into seven clusters. The genotypes belonging to the same cluster indicated that they were more closely related than those present in separate clusters. In respect of the characters studied, grouping of the genotypes into a more number of clusters indicated presence of greater divergence among these genotypes. Cluster analysis of the sixty genotypes based on these characters had also been illustrated following dendrographic representation (Fig. 1). The results of grouping of the genotypes in different clusters obtained through D^2

Table 1a: List of sixty roselle (Hibiscus sabdariffa L.) genotypes used for the study

1	AR - 14	16	R - 16	31	R - 318	46	AS - 81 - 9
2	AR - 19	17	R - 29	32	R - 322	47	AS - 81 - 14
3	AR - 42	18	R 30	33	ER - 56	48	AS - 81 - 17
4	AR - 45	19	R - 37	34	ER - 57	49	AS - 81 - 22
5	AR - 48	20	R - 48	35	ER - 60	50	REX - 6
6	AR - 50	21	R - 67	36	ER - 68	51	REX - 14
7	AR - 55	22	R - 68	37	AS - 80 - 6	52	REX - 34
8	AR - 66	23	R - 77	38	AS - 80 - 7	53	REX - 38
9	AR - 67	24	R - 86	39	AS - 80 - 19	54	REX - 45
10	AR - 71	25	R - 134	40	AS - 80 - 26	55	REX - 52
11	AR - 79	26	R - 180	41	AS - 80 - 29	56	REX - 63
12	AR - 80	27	R - 225	42	AS - 81 - 1	57	HS - 4288
13	AR - 81	28	R - 243	43	AS - 81 - 2	58	AMV - 4
14	AR - 85	29	R - 271	44	AS - 81 - 3	59	AMV - 5
15	AR - 88	30	R - 284	45	AS - 81 - 5	60	AMV - 7

Table 1b: Grouping of sixty roselle (Hibiscus sabdariffa L.) genotypes

Type of genotype	Name of the genotypes
Indigenous (45)	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, 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-8 1-14, AS-81-17 and AS-81-22
Exotic (11)	ER-56, ER-57, ER-60, ER-68, REX-6, REX-14, REX-34, REX-38, REX-45, REX-52 and REX-63
Varieties (4)	HS-4288, AMV-4, AMV-5 and AMV-7

statistics also being confirmed with the help of dendrogram, where it clearly showed nine clusters and the number of genotypes belonging to each cluster.

The results obtained through classification of genotypes using D^2 statistics would provide a set of groups from which desirable parents may be selected for further breeding programme with respect to yield attributing characters in general and the trait fibre yield in particular. Considering the averages of inter-cluster distance (Table 3), it was noticed that the values varied from 8.76 to 37.89. Maximum inter cluster distance was observed between Cluster II and IX (37.89) followed by Cluster VIII and IX (36.40), Cluster VII and IX (32.11) and Cluster I and IX (31.11). The intra-cluster distance values ranged from 7.13 to 9.69 for the clusters having more than one genotype. Cluster IV (9.69) showed the maximum intra-cluster distance followed by Cluster II (8.11) and Cluster III (8.05). Wide genetic distance was evident among the genotypes of different group than those within same cluster. The higher inter-cluster distance between

Cluster II with Cluster IX followed by Cluster VIII, VII and I indicated that the genotype belonging to cluster IX was widely distanced genetically from those of Cluster II, VIII, VII and I. In other words, genotypic constituent of these cluster pairs might be comprised of favourable gene combination in respect of the characters which may help to breed desirable lines with high fibre yield. Minimum inter-cluster distance was observed between Cluster I and VII (8.76) followed by Cluster I and VI (9.74) which indicated that genotypes of Clusters I, VI and VII were more or less closely related.

Variations in mean values of different characters were observed in different clusters (Table 4). Among twelve characters studied Cluster II exhibited highest mean values for plant height, base diameter, petiole length and fibre yield while the lowest values for these characters were recorded from Cluster IX except for mid diameter including green weight (leafless) and dry stick weight. Cluster IX also recorded low cluster mean values for base diameter, mid diameter and green weight which indicates

Table 2: Grouping of sixty genotypes of roselle based on twelve fibre yielding traits

Sl. No.	Cluster	No. of genotypes	Name of genotypes
1.	Cluster I	21	AR-19, AR-79, AR-50, R-48, R-16, AR-48, AR-81, AMV-7, AMV-4, R-77, REX-52, AS-81-3, AR-66, R-318, AR-67, ER-56, AMV-5, AR-45, AR-88, R-225 and AR-55
2.	Cluster II	10	R-29, R-271, HS-4288, R-86, R-30, R-37, AR-71, R-180, AS-80-26 and R-284
3.	Cluster III	18	AS-81-14, REX-45, AS-80-29, AR-42, ER-68, R-243, AS-80-6, AS-81-5, AR-80, R-67, R-322, AS-81-9, R-134, AR-85, AR-14, AS-81-1, AS-81-17 and REX-63
4.	Cluster IV	6	AS-80-19, AS-81-2, REX-38, AS-80-26, AS-81-22 and ER-60
5.	Cluster V	1	R-68
6.	Cluster VI	1	REX-14
7.	Cluster VII	1	ER-57
8.	Cluster VIII	1	REX-6
9.	Cluster IX	1	REX-34

Table 3: Inter-cluster and Intra-cluster distance values for fibre yielding traits in sixty genotypes of roselle

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster - I	7.13	10.40	11.22	23.03	10.60	9.74	8.76	12.24	31.11
Cluster - II		8.11	17.21	29.71	15.74	12.04	11.06	11.10	37.89
Cluster - III			8.05	16.00	11.01	12.46	12.32	17.88	23.36
Cluster - IV				9.69	20.79	22.76	23.93	28.80	12.17
Cluster - V					0.00	14.40	13.60	14.94	27.40
Cluster - VI						0.00	11.89	10.97	30.86
Cluster - VII							0.00	15.23	32.11
Cluster - VIII								0.00	36.40
Cluster - IX									0.00

Table 4: Cluster mean values for twelve fibre yield attributing traits in sixty genotypes roselle

Cluster	Plant height @ harvest (cm)	Base diameter @ harvest (mm)	Mid diameter (mm)	Top diameter (mm)	Petiole length (cm)	Internodal length (cm)	Nodes / plant	Bark thickness (mm)	Green weight (g)	Green weight (leaf less) (g)	Dry stick weight (g)	Fibre yield (g)
Cluster - I	320.412	17.96	12.998	7.906	5.374	9.409	69.147	1.801	451.086	263.775	53.655	21.118
Cluster - II	337.858	19.048	13.53	8.041	5.603	9.159	70.358	1.89	501.945	298.792	63.051	25.454
Cluster - III	295.876	17.942	12.974	7.9	5.284	9.815	66.898	1.897	435.026	247.092	45.156	17.992
Cluster - IV	237.469	15.709	11.701	7.488	4.579	10.592	62.75	1.821	319.742	166.386	27.516	12.006
Cluster - V	312.225	18.538	13.917	7.959	4.698	10.015	74.667	1.712	489.35	297.746	56.271	16.427
Cluster - VI	317.121	18.632	13.723	8.387	5.403	11.858	68.666	1.969	484.017	282.163	52.911	23.957
Cluster - VII	320.663	18.157	13.497	8.358	5.268	7.897	66.667	1.911	494.9	300.133	55.537	23.364
Cluster - VIII	315.729	18.48	13.364	8.556	5.27	10.729	67.417	1.816	517.833	284.917	66.31	23.621
Cluster - IX	207.988	16.919	12.616	8.379	3.735	10.93	70.917	1.888	332.4	148.288	22.713	8.844

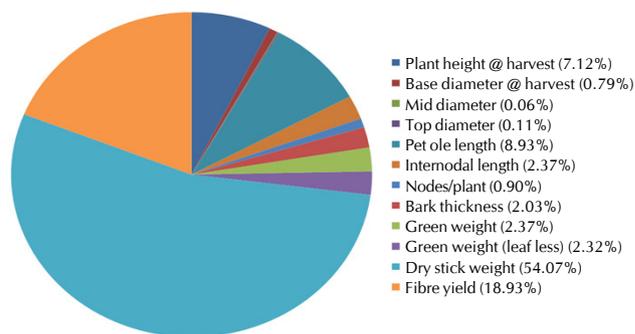**Table 5: Percent contribution of fibre yielding traits for genetic diversity in sixty roselle genotypes**

Name of the character	Times Ranked 1st	Contribution %
Plant height @ harvest (cm)	126	7.12%
Base diameter @ harvest (mm)	14	0.79%
Mid diameter (mm)	1	0.06%
Top diameter (mm)	2	0.11%
Petiole length (cm)	42	2.37%
Internodal length (cm)	158	8.93%
Nodes / plant	16	0.90%
Bark thickness (mm)	36	2.03%
Green weight (g)	42	2.37%
Green weight leaf less (g)	41	2.32%
Dry stick weight (g)	957	54.07%
Fibre yield (g)	335	18.93%
Total	1770	100.00

that the single genotype in this cluster had low values for most of the yield attributing and fibre yield trait. Cluster IV recorded lowest values for base diameter, mid diameter, top diameter, nodes per plant and green weight; low values were also recorded for plant height, internodal length, green weight (leafless), dry stick weight and fibre yield by this cluster. Cluster VII recorded highest mean values for green weight and dry stick weight and high mean values for the rest of the characters. In addition to these clusters, Cluster I and III have recorded above average to high values for most of the fibre yield attributing characters.

Cluster II appeared to be most important since it showed highest mean value for a number of important desirable characters including fibre yield and from which improved genotypes could be directly selected or they could be considered as parents to complement the deficit of other parents, present in distant group. Interestingly, most of the minimum and maximum mean values were distributed in relatively distant clusters. Therefore, hybridization between genotypes falling in different clusters may provide ample scope for development of desirable lines. The results of the present study suggested that hybridization between genotypes in Cluster II could provide a wide spectrum of variation in the segregating generation which could provide opportunity for isolation of elite lines as some cluster comprised of genotypes contributing positively towards some specific character and in some clusters genotypes showed both high and low cluster mean values for some other characters and some clusters revealed very low mean clusters for many characters. Cluster II was found with genotypes showing highest and high mean for four and seven characters respectively and most of them were related to yield and on the contrary, Cluster IV comprised the genotypes which resulted into lowest mean for as many as five characters and lower mean values for five other characters which includes fibre yield and other yield attributes. Internodal length and bark thickness were highest within genotypes in Cluster VI with second best fibre yield. Green weight (leafless) and top diameter highest in Cluster VII and Cluster VIII respectively. Minimum number of nodes and dry stick weight were observed within genotypes of Cluster IV and IX. Cluster IX also comprised of genotypes with lowest and lower mean values for five and three characters respectively. Parents within these clusters
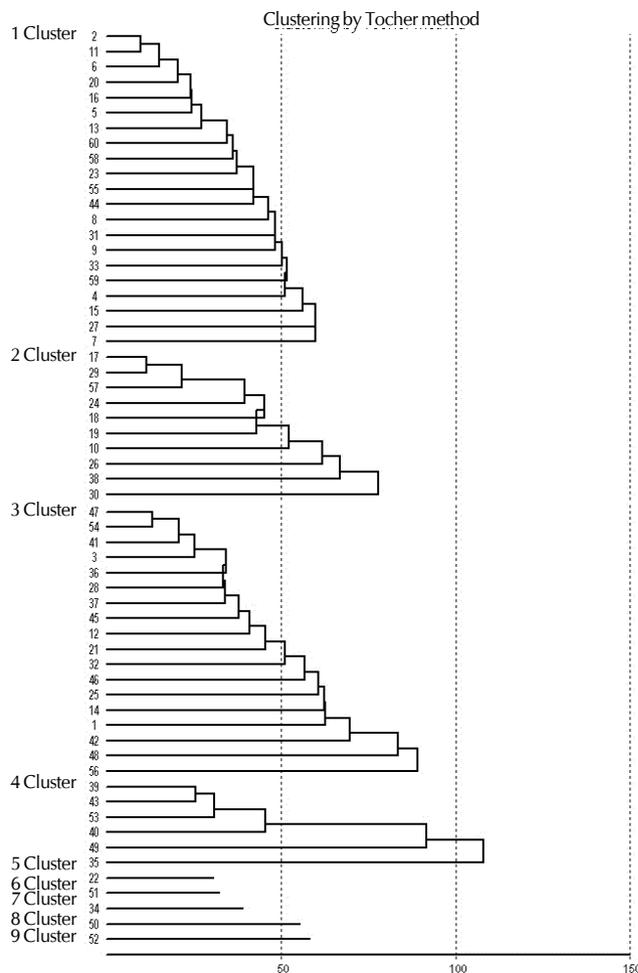
Figure 1: Grouping of sixty genotypes of roselle based on twelve fibre yield attributing characters

Figure 2: Percent contribution of fibre characters towards diversity in roselle

could be considered in breeding for development of elite lines desirable yield and its attributing characters. Thus, on the basis of cluster mean and also on the basis of mean performances and *per se* performance of individual genotypes it could be suggested that selection of the genotypes belonging from Cluster II could be proposed for plant height, base diameter and high fibre yield; Cluster VIII for green weight and dry stick weight may be fruitful to develop desirable lines.

Per cent contribution of individual characters (Table 5 and Fig. 2) towards total genotypic divergence in sixty genotypes under study was found highest by dry stick weight (54.07%) to total divergence and it was followed by fibre yield (18.93%), internodal length (8.93%), plant height (7.12%), green weight and petiole length (2.37%), green weight (leafless) (2.32%), bark thickness (2.03%) and the other characters contributed less than 1% towards total divergence. The results of the present study were in close agreement with the findings of Hariram *et al.* (2013) in roselle, Asha *et al.* (2015) in okra, Kurrey *et al.* (2015) in chench genotypes, Sandhya *et al.* (2015) in rice, Kumari and Singh (2015) in finger millet and Satyanarayana *et al.* (2015) in roselle.

Based on all the above, the genotypes belonging to Cluster, II, VII, VIII and IX viz., R-29, R-271, HS-4288, R-86, R-30, R-37, AR-71, R-180, AS-80-26, R-284, ER-57, REX-6 and REX-34 could be selected as parents in future breeding programme.

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