



Multivariate Analysis of Quantitative Characters for Fiber Yield in Roselle (*Hibiscus Sabdariffa* L.) Over Six Environments

Satyanarayana NH^{2*}, Visalakshmi V³, Bhanu Priya¹, Subhra Mukherjee¹, Roy SK³, Rao AU⁴ and Sarkar KK¹

Abstract

Sixty genotypes of roselle (*Hibiscus sabdariffa* L.) were evaluated at three different agro-climatic zones in India viz., North Coastal zone of Andhra Pradesh, Indo-Gangetic zone and Terai zone of West Bengal for fiber yield and its contributing characters during *Kharif*, 2013 and 2014 for twelve characters. Principal component analysis (PCA) indicated that three components (PC₁ to PC₃) with eigen values more than one accounted for about 88% of the total variation among twelve quantitative characters in roselle genotypes. The principal components PC₁, PC₂ and PC₃ contributed about 74.56%, 8.24% and 5.04% respectively to the total variation. The first principal component had high positive loading for dry stick weight, plant height, fiber yield and green weight (leafless) which contributed more to the diversity. The second principal component had high loading for petiole length, dry stick weight and fiber yield. The genotypes viz., ER-60, REX-34, AS-81-22, REX-6, R-284, AR-71, R-30, R-37, ER-57 and AS-80-7 were identified as the most diverse genotypes, based on component scores for use as parents in hybridization programme. High degree of variability existing within the accessions and the characters will help for further improvement of the rosella crop by evolving high fiber yielding cultivars.

Keywords

Multivariate analysis; Principal components; Roselle

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 best fiber, paper pulp or edible calyces, leaves and seeds [1]. In Asia, roselle is grown mostly for its fibers in countries such as Thailand, India and China. In Africa the roselle plant is grown for its flower and calyx [2]. In India, Roselle is one of the most important bast fiber crops which occupies second place in area and production after jute [3]. The world is now looking for eco-friendly alternatives to plastic; attention is drawn towards improving the fiber yields of jute and mesta [4].

Fiber yield is quantitatively inherited and influenced by genetic factors as well as environments. 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 [5]. Adequate analysis of genetic diversity is essential for understanding and utilization of genetic variability among accessions and their characters. Selection is likely to be effective for traits viz., green weight, dry stick weight and fiber yield along with traits like plant height and base diameter based on the studies of heritability and genetic advance. Based on character association and path analysis studies fiber yield may be improved by selection of tall plants coupled with high base diameter, mid diameter, more green weight and dry stick weight [6].

Principal component analysis helps researchers to distinguish significant relationship between traits. This is a multivariate analysis method that aims to explain the correlation between a large set of variables in terms of a small number of underlying independent factors [7]. The cluster analysis is also an appropriate method for determining family relationships but the main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only [8]. Therefore, the present investigation was undertaken with main objective to assess the potential genetic diversity among sixty genotypes of Roselle through principal component analysis based on twelve yield attributing traits for selection of parents in hybridization programme to obtain desirable segregants in advanced generation.

Materials and Methods

Sixty roselle (*Hibiscus sabdariffa* L.) genotypes (consisting of eleven exotic lines; four released varieties and 45 indigenous accessions) were evaluated at three different agro-climatic environments viz., North Coastal Zone, Andhra Pradesh at Agricultural Research Station, Ragolu (Latitude 18° 24' N; Longitude 83.84° E at an altitude of 27 m above mean sea level); Indo-Gangetic Zone, West Bengal at Instructional Farm, Bidhan Chandra Krishi Vishwavidyalaya, Jaguli (Latitude 22° 93' N; Longitude 88.59° E at an altitude of 9.75 m above mean sea level) for first year and at Teaching farm, Mondauri, BCKV (Latitude 22° 87' N; Longitude 88.59° E at an altitude of 9.75 m above mean sea level) for second year and Terai Zone, West Bengal at University Farm, Uttar Banga Krishi Vishwavidyalaya (Latitude 26° 19' N; Longitude 89.23° E at an altitude of 43 m 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 2 m length in two replications and adapted spacing of 30x10cm under rain fed conditions. The recommended package of practices was followed to raise a good crop. Data on the basis of five randomly selected competitive plants were

*Corresponding author: N Hari Satyanarayana, Agricultural Research Station (ANGRAU), Amadalavalasa, Srikakulam, AP, India-532 185, Tel: 09440518085; E-mail: namburihari@gmail.com

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recorded on plant height (cm), base diameter (mm), mid diameter (mm), top diameter (mm), internodal length (cm), petiole length (cm), nodes per plant, bark thickness (mm), green weight (g), green weight (leafless) (g), dry stick weight (g) and fiber yield (g). The principal component analysis method explained by Harman [9] was followed in the extraction of the components. Principal Component Analysis was performed using Minitab 14 software.

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 variability among the sixty genotypes for the characters studied. Three principal components were identified through Principal Component Analysis (PCA) with eigen values more than one having contributed about 88% of total variance (Table 1).

The first principal component (PC₁) contributed maximum towards variability (74.565%) with significant loading of dry stick weight (0.701), plant height (0.481), fiber yield (0.413) and green weight (leafless) (0.215) which were positively correlated (Tables 2 and 3). The second principal component (PC₂) accounted for 8.24 percent of total variance and it reflected significant loading of petiole length (-0.615) and dry stick weight (-0.578) which were negatively correlated and fiber yield (0.425) was positively correlated. The third principal component (PC₃) accounted for 5.04 percent of cumulative variance and it was characterized by conspicuously high loading for fiber yield (-0.720), bark thickness (-0.399) and petiole length (-0.372) which were negatively correlated and nodes per plant (0.232), green weight leafless (0.216) and plant height (0.205) which were positively correlated.

The characters dry stick weight (0.701), plant height (0.481), fiber yield (0.413) and green weight (leafless) (0.215) contributed maximum to the diversity in PC₁. To the diversity in the PC₂, fiber yield (0.425), nodes per plant (0.181), green weight (leafless) (0.148) and plant height (0.115) contributed maximum. In PC₃, nodes per plant (0.232), green weight (leafless) (0.216) and plant height (0.205) contributed maximum to the diversity.

Balogun et al. [10] studied fifty one genotypes of kenaf and reported three principal components with eigen value more than one, contributed for a cumulative variation of 66.23 percent. Nargis et al. [11] depicted two vectors while studying diversity for fiber and seed yield characters in tossa jute with twenty nine breeding lines. Similarly, Faruq et al. [12] reported three principal components contributing to 86.73 percent of total variation in kenaf by studying thirty two genotypes. Likewise, Denton and Nwangbaruka [13] reported three principal components contributing to 80.45 percent of total variation in tossa jute by studying fifteen genotypes. Four principal components contributed for 82.31 percent of total variation in roselle by studying sixty genotypes was reported by Hariram and Appalaswamy [3].

Cluster analysis

Seven group patterns were observed in three dimensional (3D) PCA score plot by the first two principal components which accounted for 82.80% of total variation (Figure 1). Hence, based on PCA analysis, sixty genotypes of roselle (originating from different sources) were grouped into seven clusters based on twelve quantitative characters component scores. Out of seven clusters three were monogenic, with the genotypes, AS-81-22, REX-6 and R-284. One cluster had two genotypes, ER-60 and REX-34 and the other

cluster had five genotypes, viz., AR-71, R-30, R-37, ER-57 and AS-80-7. All the above five clusters were diverse in nature in the scatter plot and the rest of the clusters were included with twelve and thirty eight genotypes and were closely related. Crosses between the genotypes of the diverse clusters will help to produce high fiber yielding segregants for the crop improvement.

Conclusion

Under the present investigation, out of sixty genotypes studied, the genotypes viz., ER-60, REX-34, AS-81-22, REX-6, R-284, AR-71, R-30, R-37, ER-57 and AS-80-7 were identified as the most diverse genotypes, based on component scores through Principal Component Analysis which ultimately showed the amount of variability present in the genotypes which could be used for improvement of roselle crop. These genotypes can be utilized as parents in hybridization programme for roselle crop improvement to develop high fiber yielding varieties which will fetch higher margins to the poor roselle farmers of India, thereby improving their livelihood standards. Moreover, growing this crop in larger areas will help the nation and mother earth to

Table 1: List of sixty roselle (*Hibiscus sabdariffa* L.) genotypes.

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 2: Eigen values, percent and cumulative variance for three principal components in roselle (*Hibiscus sabdariffa* L.).

Principal Component	PC ₁	PC ₂	PC ₃
Eigen value	69.57	23.13	18.09
Total variance (%)	74.5646	8.2377	5.0415
Cumulative variance (%)	74.5646	82.8023	87.8438

Table 3: Character loading of three principal components for sixty genotypes of roselle (*Hibiscus sabdariffa* L.) for twelve quantitative characters.

Characters	PC ₁	PC ₂	PC ₃
Plant height (cm)	0.4807	0.1147	0.2045
Base diameter (mm)	-0.0165	-0.1383	-0.1536
Mid diameter (mm)	-0.0588	-0.0527	0.0537
Top diameter (mm)	0.0028	-0.0724	-0.1001
Petiole length (cm)	0.0599	0.0774	-0.0616
Internodal length (cm)	-0.1971	-0.6149	-0.3717
Nodes/plant	0.0942	0.1812	0.2317
Bark thickness (mm)	-0.0669	0.0318	-0.3991
Green weight (g/plant)	0.0370	-0.0767	-0.0049
Green weight leaf less (g/plant)	0.2146	0.1481	0.2157
Dry stick weight (g/plant)	0.7013	-0.5777	0.0502
Fibre yield (g/plant)	0.4125	0.4245	-0.7196

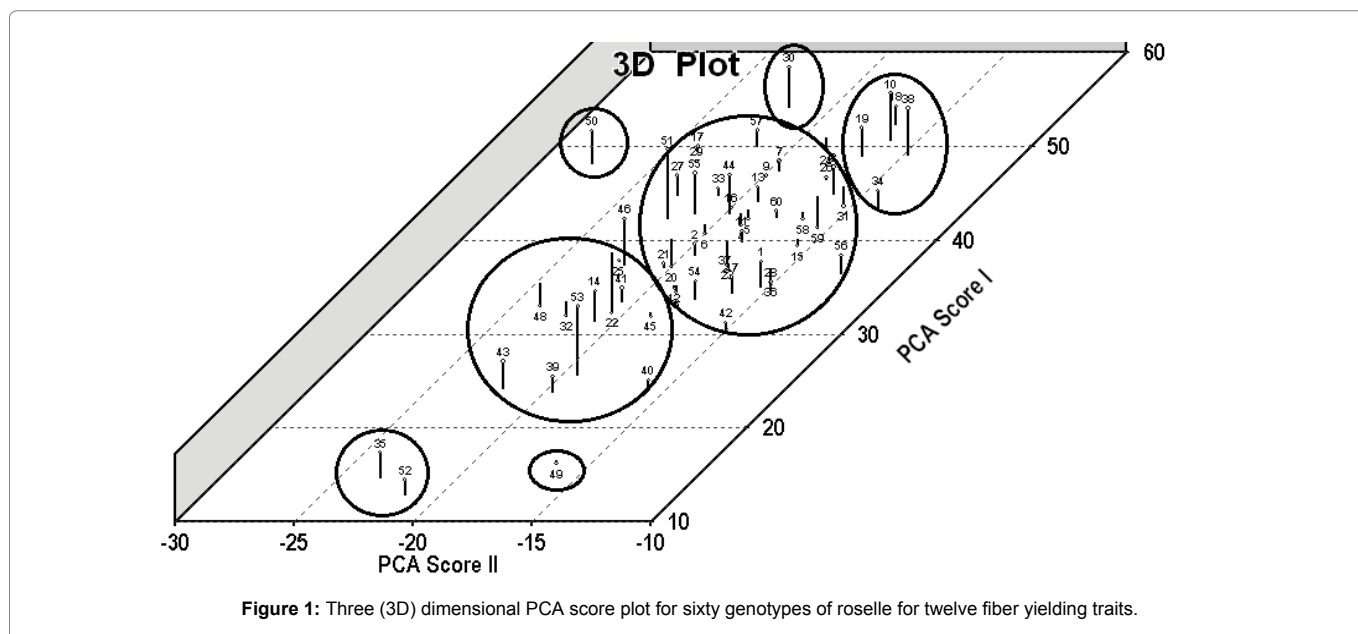


Figure 1: Three (3D) dimensional PCA score plot for sixty genotypes of roselle for twelve fiber yielding traits.

reduce pollution as the products made utilizing natural fibers are biodegradable and eco-friendly unlike plastics.

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Author Affiliations

Top

¹Department of Genetics and Plant Breeding, BCKV, Mohanpur, Nadia, West Bengal, India

²Agricultural Research Station (ANGRAU), Amadalavalasa, Srikakulam District, AP, India

³Agricultural Research Station (ANGRAU), Ragolu, Srikakulam District, A.P, India

⁴AINP on Jute and Allied fibers, UBKV, Pundibari, Coochbehar, West Bengal, India

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