

GENETIC DIVERSITY ANALYSIS FOR DIFFERENT AGRO-MORPHOLOGICAL CHARACTERS OF TOSSA JUTE

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ABSTRACT

The genetic diversity was studied for eleven growth and yield related characters in fifty three genotypes of tossa jute which were collected from the Gene Bank of Bangladesh Jute Research Institute (BJRI), Dhaka. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The highest intra-cluster distance was estimated for cluster IV (0.338) which consisted of fourteen genotypes followed by cluster III (0.330) for eighteen genotypes, cluster V (0.297) for seven genotypes and cluster II (0.284) for eleven genotypes. Cluster III contained the largest number of genotypes (eighteen) followed by cluster IV (fourteen) and cluster II (eleven), respectively. The inter cluster distance was maximum between cluster I and V (20.616) followed by the distance between clusters I and IV (18.405), I and III (14.857), II and V (10.984), I and II (10.277) indicating that the genotypes grouped within these cluster were highly divergent from each other. The least genetic distance at inter-cluster level was observed between cluster IV and V (2.871), followed by the distance between clusters III and IV (4.296), and between II and III (4.584) indicating that the genotypes of these clusters were genetically closely related. The maximum contribution was paid by the character, base diameter (0.5335) followed by green wt. without leaves (0.4790), green bark thickness (0.4672) and plant height (0.3858).

Key words: Genetic diversity, clustering, tossa jute.

Introduction

Information on genetic divergence among the parental materials is vital to plant breeder for an efficient choice of parents for hybridization. More diverse parents are the chances for high heterotic F_1 S and broad spectrum of variability in segregating generation (Murty and Arunachalam, 1966). However, evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm (Tomooka, 1991). In the past, very few researches have been carried out related to morpho-agronomic diversity and relationships in jute with diverse geographical origins. Plave and Sinha (2005) used 6 accessions of *C. capsularis* L. and 7 accessions of *C. olitorius* L. for their study. Recently, Benor *et al.* (2012) used only *C. olitorius* L. species to study genetic diversity and relationships inferred from molecular and morphological data. Moreover, multivariate methods particularly principal component analysis (PCA) have proven to be useful for characterizing, evaluating and classifying germplasm when a large number of accessions are assessed for several characteristics of agronomic importance (Badenes *et al.*, 2000). Rapid genetic improvement of crop depends on the availability of sufficient genetic diversity, which could be selected and combined in various forms to produce reasonable improvement (Wani, 2011). Hence in the present study the genetic diversity was studied for eleven growth and yield related characters in fifty three genotypes for further development and creation of higher diversity in tossa jute.

Materials and Methods

Fifty three genotypes consisting of 50 accessions and three cultivated varieties of tossa jute with different origin were included for the study from the Gene Bank of Bangladesh Jute Research Institute (BJRI), Dhaka. The list of genotypes including their origin was given in Table 1. The experiment was conducted during the period from April to August, 2017. The seeds of the experimental materials were sown in well-prepared land in randomized complete block design with three replications. The seeds were sown on

06 April, 2017 and each genotype was allotted in 3 rows of 3m long. The rows were 30 cm apart with planting space of 5-7 cm. The replications (blocks) were interspaced with 60 cm. The genotypes were assigned randomly to each plot within each block. The agronomic practices with fertilizer application were in accordance with standard recommendation. The data on fibre yield and its attributes were recorded from five randomly selected plants of each genotype from each replication after harvest (120 days crop age). The data were recorded on : plant height (m), base diameter (mm), green bark thickness (mm), leaf length (cm), leaf width (cm), leaf angle ($^{\circ}$), petiole length (cm), green weight with leaves (kg), green weight without leaves (kg), fibre yield (g) and stick yield (g).

Multivariate analysis is a potent tool in divulging the divergence among the genotypes based on multiple characters. Genetic divergence was estimated following Mahalanobis (1936) generalized distance (D^2) extended by Rao (1952). Tocher's method (Rao, 1952) was followed for determining the group constellations. Canonical analysis was also done according to Rao (1952) to confirm the results of cluster and D^2 analysis. Mean data for each character were subjected to multivariate analysis techniques for Principal component analysis (PCA), Principal co-ordinate analysis (PCoA), Canonical vector analysis (CVA) and Cluster analysis (CLSA) by computer using GENSTST 5.13 software program. Mahalanobis's (1936) D^2 -statistic analysis was used for assessing the genetic divergence among the test entries for a rational choice of potential parent in a breeding program.

Table 1. Sources and stem colours of tossa jute genotypes used in this study

Sl.No.	Genotypes	Country/Dist. Name	Stem Pigmentation
01.	Acc.-1148	Faridpur, Bangladesh	Red
02.	Acc.-2381	Sirajgonj, Bangladesh	Light Red
03.	Acc.-2541	Bagerhat, Bangladesh	Green
04.	Acc.-2666	Jessore, Bangladesh	Green
05.	Acc.-2667	„	Green
06.	Acc.-2670	„	Green
07.	Acc.-3031	Jenaidha, Bangladesh	Green
08.	Acc.-3032	„	Green
09.	Acc.-3033	„	Green
10.	Acc.-3035	„	Green
11.	Acc.-3038	„	Green
12.	Acc.-3339	Rangamati, Bangladesh	Green
13.	Acc.-3340	„	Green
14.	Acc.-3341	„	Green
15.	Acc.-3342	„	Green
16.	Acc.-3343	„	Green
17.	Acc.-3423	Faridpur, Bangladesh	Green
18.	Acc.-3424	„	Green
19.	Acc.-3425	„	Green
20.	Acc.-3426	„	Green
21.	Acc.-3429	„	Green
22.	Acc.-3430	„	Green
23.	Acc.-3432	„	Green
24.	Acc.-3433	„	Green
25.	Acc.-3435	„	Green
26.	Acc.-3438	„	Red
27.	Acc.-3439	„	Green
28.	Acc.-3533	Madaripur, Bangladesh	Green
29.	Acc.-3535	Shoriotpur, Bangladesh	Green
30.	Acc.-3536	„	Red
31.	Acc.-3538	Gopalganj, Bangladesh	Green
32.	Acc.-3542	Shoriotpur, Bangladesh	Green
33.	Acc.-3543	„	Green

Sl.No.	Genotypes	Country/Dist. Name	Stem Pigmentation
34.	Acc.-3731	Kenya	Green
35.	Acc.-3733	Kenya	Green
36.	Acc.-3856	Chittagong, Bangladesh	Green
37.	Acc.-3857	Feni, Bangladesh	Green
38.	Acc.-3860	Chittagong, Bangladesh	Red
39.	Acc.-3985	Syria	Red
40.	Acc.-3986	Syria	Red
41.	Acc.-3987	Syria	Red
42.	Acc.-4674	Moudabag	Green
43.	Acc.-4756	Tanzania	Red
44.	Acc.-4785	Kenya	Red
45.	Acc.-4828	Kenya	Green
46.	Acc.-4848	Guinea	Red
47.	Acc.-4851	-	Red
48.	Acc.-4892	-	Red
49.	Acc.-5103	Tanzania	Red
50.	Acc.-5138	Ivorycost	Green
51.	O-9897	BJRI, Bangladesh	Green
52.	O-795	BJRI, Bangladesh	Red
53.	JRO-524	India	Green

Results and Discussion

Principal component analysis (PCA): The Principal component analysis gave eigen values of each principal component axes of coordination of genotypes with the first axes totally accounting for the variation among the genotypes, whereas two of these eigen values above unity accounted for 66.46% (PCA I is 51.03 and PCA II is 15.43) (Table 2). The scatter diagram showed five arbitrary clusters. The genotypes were distantly located from each other (Fig. 1).

Principal coordinate analysis (PCoA): Principal coordinate analysis was performed on auxiliary of principal component analysis. Intra-cluster distance were estimated using the inter genotypic distance, as quoted in Singh and Chaudhary (1985). The highest intra-cluster distance (Table 5) was estimated for cluster IV (0.338) which consisted of fourteen genotypes and, this was followed by cluster III (0.330) for eighteen genotypes, cluster V (0.297) for seven genotypes and cluster II (0.284) foreleven genotypes. The cluster I showed the lowest intra-cluster distance (0.184) composed of three genotypes. Yahiya (2007) reported that clusters with lesser magnitude of divergence showed instability, while widely divergent clusters remained distance in different environments. These results revealed that the genotypes in cluster IV were distantly related with the genotypes of other clusters. On the other hand the genotypes in cluster I were closely related.

Clustering of 53 genotypes of tossa jute: In respect of D^2 analysis 53 genotypes were grouped into five clusters. These results confirmed the clustering pattern of the genotypes according to the principal component analysis. Cluster III contained the largest number of genotypes (eighteen) followed by cluster IV (fourteen) and cluster II (eleven). The remaining ten genotypes were distributed in two clusters of which seven in cluster V and three in cluster I. It was observed from the distribution pattern that the geographic divergence did not influence the clustering pattern as the varieties/ genotypes within the same cluster originated from different districts/countries; rather, those were distributed in random (Table 3).

The eighteen genotypes included in the cluster III originated from Bangladesh, Kenya and Tanzania. Similarly the cluster I, II, IV and V consisted of three, eleven, fourteen and seven genotypes respectively, which were from Bangladesh, Kenya, Tanzania, Syria, Guinea, Ivory Coast and India. Hence, the same cluster included genotypes from different eco-geographical regions. This geographical distribution was in agreement with Devi *et al.* (2004), who reported that the pattern of clustering had no general association

between ecological distribution of genotypes and its genetic divergence. This might be due to differential adaptation, genetic drift, selection pressure and environment. The grouping of genotypes of same origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin or vice-versa. Table 4 shows the comparison of cluster means for different characters. Cluster I had the highest mean values for plant height (3.68), base diameter (17.54), leaf length (16.87), green bark thickness (2.47), green weight with leaves (6.0), green weight without leaves (4.18), fibre weight (427.33) and stick weight (889.67). Cluster II ranked 1st for petiole length (6.42). Cluster V ranked 1st for leaf width (6.53) and leaf angle (58.57). None of the eleven characters had high mean values under clusters III and IV.

Table 2. Eigen values and percentages of variation in respect of eleven characters in 53 genotypes of tossa jute

Principal component characters	Eigen values	Percentage of total variation	Cumulative percentage
PC1	5.613	51.03	51.03
PC2	1.697	15.43	66.46
PC3	0.872	7.93	74.39
PC4	0.776	7.06	81.45
PC5	0.525	4.78	86.23
PC6	0.494	4.49	90.72
PC7	0.059	0.54	91.26
PC8	0.351	3.20	94.46
PC9	0.304	2.77	97.23
PC10	0.221	2.02	99.25
PC11	0.082	0.75	100.00

Table 3. Distribution of 53 genotypes of tossa jute in five clusters

Clusters	No. of genotypes	Name of genotypes	Accession No.
I	3	G ₅ , G ₄₈ , G ₅₁	2667, 4892, O-9897.
II	11	G ₃ , G ₇ , G ₈ , G ₉ , G ₁₈ , G ₂₂ , G ₂₃ , G ₂₅ , G ₃₈ , G ₄₇ , G ₄₉	2541, 3031, 3032, 3033, 3424, 3430, 3432, 3433, 3435, 3860, 5103.
III	18	G ₁ , G ₆ , G ₁₀ , G ₁₁ , G ₁₃ , G ₁₅ , G ₁₆ , G ₁₇ , G ₂₆ , G ₂₈ , G ₃₁ , G ₃₃ , G ₃₄ , G ₃₅ , G ₃₇ , G ₄₂ , G ₄₃ , G ₄₅	1148, 2670, 3035, 3038, 3340, 3342, 3343, 3423, 3438, 3533, 3538, 3543, 3731, 3733, 3857, 4674, 4756, 4828.
IV	14	G ₂ , G ₄ , G ₁₂ , G ₁₉ , G ₂₀ , G ₂₁ , G ₂₄ , G ₃₀ , G ₃₂ , G ₃₆ , G ₃₉ , G ₄₄ , G ₄₆ , G ₅₂	2381, 2666, 3339, 3425, 3426, 3429, 3536, 3542, 3856, 3985, 4785, 4848, 4851, O-795.
V	7	G ₁₄ , G ₂₇ , G ₂₉ , G ₄₀ , G ₄₁ , G ₅₀ , G ₅₃	3341, 3439, 3535, 3986, 3987, 5138, JRO-524.

Canonical vector analysis (CVA): To compute the inter-cluster Mahalanobis's (D^2) values canonical variate analysis was used. Table 4 presents the intra and inter-clusters distance (D^2) values. The inter cluster distance was maximum between cluster I and V (20.616) followed by the distance between clusters I and IV (18.405), I and III (14.857), II and V (10.984), I and II (10.277) indicating that the genotypes grouped within these cluster were highly divergent from each other. Choosing of parents belonging to the maximum divergent clusters is expected to manifest maximum heterosis in crossing and also wide variability in genetic architecture. The least genetic distance at inter-cluster level was observed between cluster IV and V (2.871), followed by the distance between clusters III and IV (4.296), and between II and III (4.584) indicating that the genotypes of these clusters were genetically closely related. The clustering pattern of D^2 analysis (Table 5) followed the similar trend of distribution of genotypes in PCA (Fig 1). The D^2 and PCA were found to be alternative methods to yield information regarding the clustering pattern presented in Fig. 2. Moreover, the PCA provided information on contribution of the characters towards divergence.

Contribution of the characters towards divergence of the genotypes: The contributions of 11 characters on genetic diversity pertained in 53 genotypes of tossa jute are presented in Table 6. The maximum contribution was paid by the character, base diameter (0.5335) followed by green wt. without leaves (0.4790), green bark thickness (0.4672) and plant height (0.3858). The summations of both the vectors for 11 characters were considered to describe relative contributions on genetic diversity. Interestingly it is noted that higher contributions of the four characters were measured due to positive values obtained in both the vectors. On the contrary, the minimum contribution toward genetic diversity was waged by the character, petiole length (-0.6142) because both the vectors yielded negative magnitudes. Other characters contributed medium to lower contributions on genetic diversity as projected by summations of both the vector values against the characters under consideration. Therefore, base diameter, green wt. with leaves, green bark thickness and stick weight appeared as the important characters in tossa jute to assess genetic diversity based on morphological features.

Table 4. Cluster means value for yield and yield contributing characters of tossa jute

Characters	Cluster				
	I	II	III	IV	V
Plant height (m)	3.68	3.40	3.30	3.30	3.13
Base diameter (mm)	17.54	15.98	15.91	16.12	15.70
Leaf length (cm)	16.87	15.81	15.26	15.19	15.41
Leaf width (cm)	5.89	6.40	6.41	6.43	6.58
Green bark thickness (mm)	2.47	2.19	1.70	1.75	1.63
Petiole length (cm)	6.40	6.42	6.17	6.20	5.99
Leaf angle (dg)	51.11	54.39	57.04	57.86	58.57
Green wt. with leaves (kg)	6.00	4.56	3.70	3.19	3.18
Green wt. without leaves (kg)	4.18	3.49	2.98	2.65	2.69
Fibre weight (g)	427.33	300.64	247.32	221.07	212.90
Stick weight (g)	889.67	688.94	591.04	489.76	412.43

Table 5. Inter and intra-cluster (bold) distance (D^2) of fifty three genotypes of tossa jute

Cluster	I	II	III	IV	V
I	0.184				
II	10.277	0.284			
III	14.857	4.584	0.330		
IV	18.405	8.425	4.296	0.338	
V	20.616	10.984	7.129	2.871	0.297

Table 6. Contribution of different characters towards genetic diversity of tossa jute

Characters	Vector-I	Vector-II	Total
Plant height (m)	0.3394	0.0464	0.3858
Base diameter (mm)	0.1795	0.4540	0.5335
Leaf length (cm)	0.2268	0.0724	0.2992
Leaf width (cm)	0.1222	-0.6302	-0.5080
Green bark thickness (mm)	0.2849	0.1823	0.4672
Petiole length (cm)	-0.1222	-0.4920	-0.6142
Leaf angle (dg)	0.3068	-0.1958	0.1110
Green wt. with leaves (kg)	0.3778	0.0070	0.3848
Green wt. without leaves (kg)	0.3976	0.0814	0.4790
Fibre weight (g)	-0.3860	0.0565	-0.3295
Stick weight (g)	0.3723	0.0105	0.3828

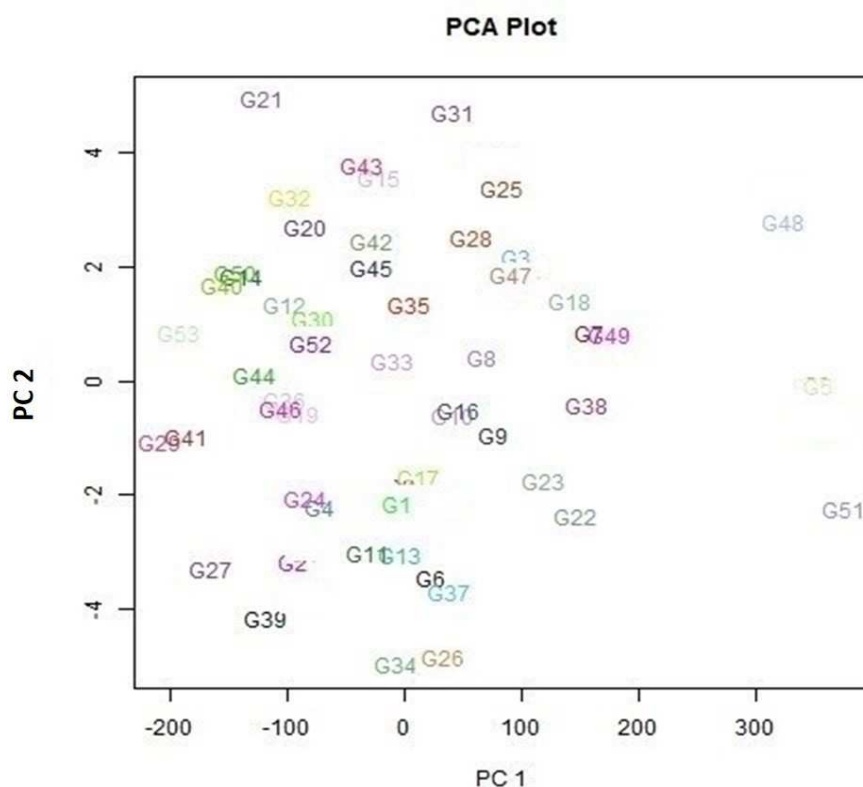


Fig. 1 Scattered diagram of fifty three genotypes of tossa jute based on their principal component scores

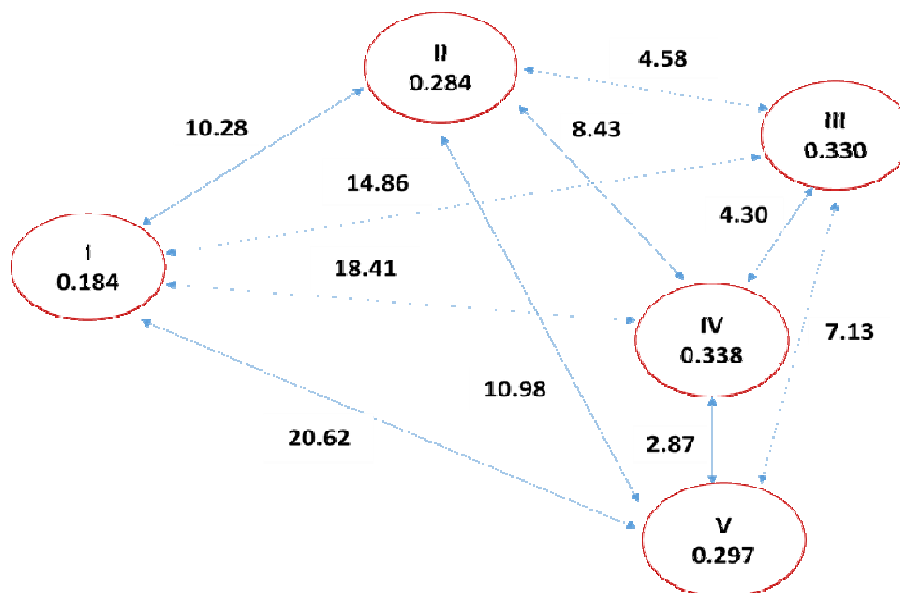


Fig. 2 Graphical representation of Intra and Inter cluster distances in tossa jute genotypes

Conclusion

The variations existed among the genotypes were accounted through principal component analysis (PCA) and principal coordinate analysis (PCoA). Fifty three genotypes were grouped into five clusters. The cluster I comprised with 3, cluster II with 11, cluster III with 18, cluster IV with 14 and cluster V with 7 genotypes. It was observed the distribution patterns of the genotypes were not correlated with geographical divergence, because the genotypes originated from our country were distributed into different clusters, and moreover, the Indian genotype was included in the same cluster with our locally developed genotypes. The maximum inter cluster distance (20.616) between the cluster I and cluster V. and the minimum (2.871) between the clusters IV and V. The highest as well as positive vector I and vector II specified the higher contribution toward genetic divergence; accordingly the character, base diameter of the plant appeared as the greatest contributor followed by green bark thickness, green wt. without leaves and plant height in creating genetic divergence among the studied genotypes. The cluster mean for a particular character was estimated to determine its potentiality for selection of parents in hybridization. A breeder might select the genotypes from cluster having high mean for the concerned character.

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