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GENETIC VARIABILITY IN YIELD CONTRIBUTING CHARACTERS OF TOSSA JUTE (*Corchorus capsularis* L.)

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Abstract

Fifty-six hybrids of Tossa jute (*Corchorus olitorius* L.) were raised at Hajee Mohammad Danesh Science and Technology University, Dinajpur from the parental lines O-9897, O-795, JRO-524, Acc.-2381, Acc.-3423, Acc.-3438, Acc.-3533 and Acc.-3860 and studied. Maximum 24 genotypes were in cluster II followed by 11 in I, 9 in IV, 6 in VI, 4 in V and only 2 in cluster IV and the minimum (2.871) was between the clusters IV and V. Cluster VI produced the highest mean values for all the characters indicated the higher potential. Intra-cluster distances were lower than inter-cluster distances, suggested less diversity within a cluster. Mahalanobis D^2-statistics for genetic divergent classified those 56 genotypes into six clusters. Cluster VI showed the highest intercluster distance (23.565) with cluster I. Therefore, jute breeders may consider the hybrids having desirable trait of cluster I and VI for further improvement of Tossa jute.

Keywords: Tossa jute (*Corchorus capsularis*), inter-cluster distance, Eigen values, Yield Contributing Character, Mahalanobis D^2.

Introduction

Jute is a natural fibre popularly known as the golden fibre of Bangladesh. It is an important traditional cash crop of the country. In fact, jute is the second most important natural fibre in terms of global consumption after cotton. The global awareness for the environmental protection creates the opportunity of exploring jute (Chowdhury and Rashed, 2015). Jute has the priority over the synthetic fiber as this contains quality of biodegradability and recycling (Islam and Ahmed, 2012). Considering the impacts that it creates to the environment and recycling nature, jute is considered as 'sustainable'. Still there is potential prospect to revive jute industry. By this time, with the help of technology, jute gets new dimension. The future of jute fiber is very greatly depending on its quality. The breeders gather deep knowledge on the genetic diversity and variability, genetic architecture for fiber yield, and yield-related anatomical traits of jute germplasm for varietal improvement of jute (Ngomuo *et al.*, 2017). The plants are sometimes selected on the basis of some morphological traits which is actually unable to give any accurate

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information on fiber quality. So, the breeders need to do anatomical studies of jute plants for accurate information on fiber improvements (Majumdar, 2002). Correlations between jute fiber quality and other yield attributing anatomical characters are helpful to improve desired characters as well as to select good germplasm for breeding purpose (Kumar *et. al.*, 2007; Mati and Satya, 2009). Multivariate methods such as cluster analysis and principal component analysis (PCA) have proven to be useful for characterizing, evaluating, and classifying germplasm for diversity when a large number of accessions or genotypes to be assessed for several characteristics of anatomical importance (Badenes *et al*., 2000).

Improvement of varieties is required to have more productivity from the cultivation. Generally, the success of any crop improvement program largely depends on the magnitude of genetic variability, genetic advance, character association, direct and indirect effects on yield and its attributes. The selected sergeants can be used in advancing the generation to develop diverse genotypes in segregating generations. In this context, the present investigation was undertaken to assess and also to explain the nature and magnitude of genetic variability of 56 hybrids of Tossa Jute of O-9897, O-795, JRO-524, Acc.-2381, Acc.-3423 Acc.-3438, Acc.-3533, and Acc.-3860 parents.

Materials and Methods

A set of 56 experimental hybrid of the Tossa jute generated and maintained by the Department of Genetics and Plant Breeding of Hajee Mohammad Danesh Science and Technology University, Dinajpur were used in this study. The experiment was laid out in Randomized Complete Block Design with three replications. The seeds of each genotype were sown in 3 rows of 3 meter long plot. The rows were 30 cm apart with planting space of 5-7 cm. The replication blocks were interspaced with 60 cm. Manures and fertilizers were applied as per recommended dose. Seeds were sown on 30 April 2018. After 120 days of sowing, the sample plants of individual plots were harvested for fibre yield. The data on fibre yield and its attributes as plant height (m), base diameter (mm), green bark thickness (mm), green wight without leaves (g), fibre weight (g), stick weight (g), fibre strength (MPa), days to flowering and days to maturity were recorded from 5 randomly selected plant of each genotype from each replication. The data obtained for different characters were recorded first on MS excel sheet. Afterwards, the data were analyzed using the software package R of version 3.4.2 and Statistical Tool for Agricultural Research (STAR) Version: 2.0.1. Genetic divergence analysis was concurrently performed by using Mahalanobis D^2-statistics and based on the unique D^2- values 56 hybrids were classified purposefully into 6 groups. Multivariate analysis named clustering analysis and Principal Component Analysis (PCA) were performed with the help of GENSTAT 5 program in computer.

Table 1. Characteristics of eight selected genotypes of Tossa jute

Sl. No.	Accessions/ Varieties	Origin	Parental symbol	Other characteristics
01.	O-9897	O-5 x BZ-5	P1	Plant full green, leaves ovate lanceolate, fruit indehiscence in nature, seed bluish green in colour, less photosensitive and late maturing.
02.	O-795	Uganda red x O-4	P2	Plant reddish, leaves ovate lanceolate, fruit indehiscence in nature, seed bluish green in colour, less photosensitive and late maturing
03.	JRO-524	Indian origin	P3	Plant full green, leaves ovate lanceolate, fruit indehiscence and sticky in nature, seed bluish green in colour, less photosensitive and late maturing.
04.	Acc. 2381	Local collection	P4	Plant reddish, leaves ovate lanceolate, seed bluish green in colour.
05.	Acc. 3423	Local collection	P5	Plant full green, leaves ovate lanceolate, seed bluish green in colour.
06.	Acc. 3438	Local collection	P6	Plant reddish, leaves ovate lanceolate seed bluish green in colour.
07.	Acc. 3533	Local collection	P7	Plant full green, leaves ovate lanceolate, seed bluish green in colour.
08.	Acc. 3860	Local collection	P8	Plant reddish, leaves ovate lanceolate, seed bluish green in colour.

Results and discussion

Principal Component Analysis (PCA)

The first two principal components having eigen values for plant height (5.798) and base diameter (1.753) accounted for 69% of the total variation among ten characters of Tossa jute for 56 genotypes studied. Similar kind of results were reported by Ghosh *et al*., (2014) in jute. Sawarkar *et al.*, (2015) reported the highest contribution (12.63%) was exerted by plant height of total divergence, which supports the current findings. Alam *et al.*, (2016) calculated Eigen values and percentage of variation in respect of eleven characters in white jute (*C. capsularis* L.) germplasm and found four of these Eigen values above unity accounted for 90.81%.

Table 2. Eigen values and percentages of variation in respect of ten characters in 56 hybrids of Tossa jute

Parameters	Eigen values	Percentage of total variation accounted for individual characters	Cumulative percentage
Plant Height (m)	5.798	52.74	52.74
Base Diameter (mm)	1.753	15.94	68.68
Green Bark Thickness (mm)	0.901	8.19	76.88
Green Wight Without Leaves (g)	0.802	7.29	84.17
Fibre Weigh (g)	0.542	4.93	89.10
Stick Weight (g)	0.510	4.64	93.74
Fibre Strength (MPa)	0.314	2.86	96.60
Days to Flowering	0.228	2.08	98.68
Days to Maturity	0.085	0.77	99.45
Fibre Weight/ Stick Weight	0.061	0.55	100.00

Cluster analysis

On the basis of Mahalanobis D^2 analysis 56 genotypes were grouped into 6 clusters. The grouping of materials of same origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin or vice-versa. All members of cluster VI were from P8 origin. Table 3 represent the composition of different clusters with their corresponding genotypes. Maximum 24 genotypes were in cluster II followed by 11 in I, 9 in III, 6 in VI, 4 in V and only 2 in cluster IV.

Table 3. Distribution of 56 hybrids of Tossa jute in 6 clusters

Cluster	Number of hybrids	Hybrids
I	11	P1 x P2, P1 x P5, P3 x P4, P4 x P6, P2 x P1, P3 x P1, P3 x P2, P6 x P3, P7 x P1, P8 x P1, P5 x P7
II	24	P1 x P3, P1 x P7, P1 x P8, P2 x P3, P2 x P5, P2 x P6, P2 x P7, P3 x P5, P3 x P6, P3 x P7, P3 x P8, P4 x P7, P4 x P8, P5 x P6, P5 x P8, P6 x P7, P7 x P8, P4 x P2, P4 x P3, P5 x P1, P5 x P3, P5 x P4, P7 x P2, P7 x P6
III	9	P1 x P4, P1 x P6, P2 x P4, P2 x P8, P4 x P5, P4 x P1, P5 x P2, P6 x P4, P7 x P4
IV	2	P6 x P8, P7 x P5
V	4	P6 x P1, P6 x P2, P6 x P5, P7 x P3
VI	6	P8 x P2, P8 x P3, P8 x P4, P8 x P5, P8 x P6, P8 x P7

The Inter and intra-cluster distance (D^2) of 56 genotypes of Tossa jute were shown in Table 4. The maximum inter-cluster distance (23.565) between the cluster I and cluster VI followed by cluster I and cluster V (20.616), cluster I and cluster IV (18.405), cluster I and cluster III (14.857), cluster II and cluster V (10.984) clearly indicating the presence of high genetic diversity between the clusters. Similar kind of results in Tossa jute were found by Akter *et al*., (2005), Roy *et al*., (2011), Jatothu *et al*., (2018) and Biswas *et al*., (2018). Selecting tossa jute genotypes from high inter cluster distances with high mean values for fibre yielding characters will help in developing high heterotic hybrids and also useful in selecting better recombinants in the segregating generations for higher fibre yield (Jatothu *et al*., 2018).

Table 4. Inter and intra-cluster distance of 56 genotypes of Tossa jute

Cluster	Cluster Distance					
	I	II	III	IV	V	VI
I	**0.1837**					
II	10.277	**0.2843**				
III	14.857	4.5840	**0.3297**			
IV	18.405	8.4250	4.2960	**0.3376**		
V	20.616	10.984	7.1290	2.8710	**0.2971**	
VI	23.565	14.05	10.72	5.4220	3.37051	**0.37051**

In the present study, the maximum intra cluster distance was found in cluster VI (0.37051) revealing high genetic diversity and minimum in cluster I (0.1837) revealing less variation among genotypes in this cluster. In general, intra cluster distances were lower than inter cluster distances suggesting less diversity within a cluster but the genotypes under a cluster were far away from the genotypes of other clusters.

Cluster mean analysis

Table 4 shows the comparison of cluster means for different characters. Cluster VI produced the highest mean values for total plant height, base diameter, green bark thickness, green wight without leaves, fibre weigh, stick weight, fibre strength and days to maturity compared to the rest of the cluster indicated the higher potentials of the genotypes in the population. The cluster means for the selected characters determined the potential of a cluster for a character that might help in selection of genotypes for further breeding programme for amelioration of this important cash and fiber crop.

Table 5. Cluster mean value for yield and yield contributing characters of Tossa jute

Characters	Cluster mean					
	I	II	III	IV	V	VI
Plant Height (m)	3.36	3.36	3.36	3.21	3.07	3.42
Base Diameter (mm)	15.89	15.88	15.88	15.97	16.31	17.35
Green Bark Thickness (mm)	15.22	15.23	15.18	15.05	14.34	16.99
Green Wight Without Leaves (g)	2.94	2.95	2.93	2.80	2.56	4.17
Fibre Weigh (g)	555.92	558.17	555.67	508.47	486.27	851.29
Stick Weight (g)	247.78	247.97	245.87	233.41	224.50	407.59
Fibre Strength (MPa)	590.10	591.68	592.78	589.61	576.29	617.22
Days to Flowering	77.05	76.98	76.96	77.15	77.13	76.61
Days to Maturity	112.31	112.44	112.43	112.06	111.67	113.06
Fibre Weight/ Stick Weight	2.24	2.25	2.26	2.18	2.17	2.09

Conclusion

The selected 10 characters showed wide range of variability among 56 hybrids of Tossa jute. Plant height, base diameter, green bark thickness and green weight without leaves, fibre weight and fibre weight/stick weight are the fibre yield enhancing characters. Therefore, jute breeders might exploit these characters for improving fibre yield in Tossa jute. Genetically distant parents have the potential to develop useful recombinants for obtaining heteroblastic programming. Considering the inter and intra-cluster distance, the inter genotypic crosses between the genotypes from cluster I (P1 x P2, P1 x P5, P3 x P4, P4 x P6, P2 x

P1, P3 x P1, P3 x P2, P6 x P3, P7 x P1, P8 x P1, P5 x P7) and cluster VI (P8 x P2, P8 x P3, P8 x P4, P8 x P5, P8 x P6, P8 x P7) may be suggested to proceed further selection.

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