

Genetic Divergence Among the Genotypes of Tossa Jute (*Corchorus olitorius* L.)

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Abstract

Based on 12 characters of yield and yield components 35 genotypes of tossa jute were grouped into 8 clusters using genetic divergence (D^2) values following Tocher's method. These clusters showed various magnitude of characters where stick weight per plant contributed maximum to divergence. Maximum inter cluster average D^2 was observed between cluster IV and cluster VII followed by between clusters IV and V. TRO-4/ARO-11 from cluster IV may produce potential segregates when it would be crossed with JRO-7835/TJ-40 from clusters VII and V respectively in hybridization breeding program.

Key words : Tossa jute, Genetic divergence, Inter cluster, Intra cluster.

Jute is an important fiber crop producing about 78.56 lakh bales (1 bale = 180 kg) of jute fiber per annum in India. But, very limited success has been attained by breeders to break yield plateau in this crop. It may be attributed to the narrow genetic base in the material available with the breeder. Genetic diversity of the parental line is a good indicator of performance of the progenies (1). Therefore, the selection of parents on the basis of genetic divergence is important because more diverse the parents, the greater are the chances of obtaining broad spectrum of variability in segregating generations. Success through hybridization and subsequent selection depends primarily on the selection of parents having high genetic variability for various agronomic traits (2). In jute, reports on genetic divergence using D^2 statistic is rather limited. So attempt was made to classify 35 genotypes based on 12 characters in tossa jute (*Corchorus olitorius* L.) following D^2 statistic.

Methods

A set of 35 genotypes of tossa jute (*Corchorus olitorius* L.) including five exotic, six national and state released varieties and 24 collections from different states of the country were sown in a randomized complete block design with four replications having a plot size of 3.5 m × 1.8 m for each genotype at Jute Research Station, Kendrapara, Orissa. A row spac-

ing of 30 cm was given and after final thinning about 50 plants were maintained in each row. Chemical fertilizers at 40 kg N, 20 kg P_2O_5 and 20 kg K_2O and FYM at 3 tons/ha were applied to the crop.

Except days to flowering, which was studied on plot basis, observations on other eight quantitative characters were recorded on 10 randomly selected competitive plants of each genotype in each replication. In addition, three derived characters were also studied, namely internode length, TD/BD and fiber/wood.

Multivariate test of significance of differences among the genotypes mean for pooled effect of all the characters was performed using Wilk's criterion and V statistics (3).

Genetic divergence among the 35 genotypes was estimated by using Mahalanobis D^2 statistic following Rao (3) with data of error variance-covariance matrix and mean values of 12 traits. All possible D^2 s among the 35 genotypes were grouped into clusters following Tocher's method as described by Rao (3).

Results and Discussion

Analysis of variance and *F* tests revealed highly significant differences among the genotypes for all

Table 1. Clustering pattern of 35 genotypes of tossa jute.

Clu- sters	No. of geno- types	Name of genotypes	Place of origin
I	15	Wild Olitorius Red, AP5A, AP 10A, MP 50 D, UP 17C, UP 43A, 0-10A, 0-15A, D-20B, JBO 9, JBO 11, Chinsura Green, JRO 878, JRO 632, JRO 524	Exotic, AP, MP, UP, Orissa, WB
II	8	Russian 1, Bangkok, Tanganyika, Wild Olitorius Dwarf, MGO 1, MGO 2, MNO 1, ARO 17	Exotic, Meghalaya, Manipur, Arunanchal Pradesh
III	6	TRO 2, ASO 8, ASO 12, D4A, CHNP 4A, CHNP 12A	Tripura, Assam, Orissa, Bihar
IV	2	TRO 4, ARO 11	Tripura, Arunanchal Pradesh
V	1	TJ 40	Trorabay
VI	1	KOM 62	Orissa
VII	1	JRO 7835	West Bengal
VIII	1	MP 59E	MP

12 characters. Multivariate test by Wilk's criterion also revealed highly significant differences among the genotypes indicating a wide genetic diversity among them.

All the 35 genotypes of tossa jute based on D² values of 595 combinations were grouped into eight clusters (Table 1). The cluster-1 was the largest containing three national varieties and 12 genotypes

collected from five states of India and abroad. This cluster was characterized by medium values for 50% flowering, top diameter, fiber wood, and plant height and high values for basal diameter, green weight, stick weight and fiber yield per plant (Table 2). The cluster II included eight genotypes each of four exotic and four state collections. Early flowering, medium height and low values for nodes per plant, basal diameter, green weight, stick weight and fiber yield per plant were the characteristic of this group. In cluster III, there were six genotypes, all being different state collections and characterized by early flowering, tall plants height, medium values for top diameter, D/BD and fiber yield per plant. Earliest flowering, shortest plant height, lowest values for nodes per plant, basal diameter, green weight, stick weight and fiber yield per plant were the characteristics of cluster IV having two genotypes one each from Tripura and Arunanchal Pradesh. Clusters V, VI and VII each having one released variety showed highest value for plant height and nodes per plant, basal diameter, bark thickness, green weight, stick weight and fiber yield and days to 50% flowering respectively. Cluster VIII having only one genotype from MP collection showed combination of characters having lower and higher values but none of the extreme character was included in this group. This showed that the genotypes were not only classified into different groups on the basis of genetic diversity (D²) but also grouped pertaining to different potentialities of the characters evolved. The present study as judged by relative contribution of different characters revealed that stick weight had

Table 2. Cluster means of 35 genotypes for 12 characters in tossa jute. Bold figures are highest values and italic figures are lowest values.

Character	Average cluster means								Per cent of average D ²
	I	II	III	IV	V	VI	VII	VIII	
1. Days to 50% flowering	101.1	95.2	97.6	<i>91.6</i>	112.5	114.0	114.5	92.2	2.98
2. Plant height (cm)	289.5	234.3	277.5	<i>169.8</i>	315.0	307.7	308.9	225.9	14.96
3. Nodes / plant	61.7	45.2	50.1	<i>36.6</i>	64.5	64.1	59.8	45.7	4.22
4. Internode length (cm)	4.8	5.0	4.8	<i>4.6</i>	4.9	4.8	<i>4.6</i>	4.9	2.35
5. Basal diameter (mm)	12.2	10.8	11.4	<i>9.5</i>	11.7	13.8	11.1	10.9	3.68
6. Top diameter (mm)	4.2	5.0	3.5	5.4	2.9	4.6	2.5	4.8	8.38
7. TD / BD	0.3	0.5	0.3	0.6	0.3	0.3	<i>0.2</i>	0.4	4.09
8. Bark thickness (mm)	1.4	1.24	1.2	1.4	<i>0.9</i>	1.7	1.51	1.3	7.01
9. Green weight (g / plant)	142.6	75.1	109.9	<i>49.5</i>	136.5	192.5	148.7	95.5	6.80
10. stick weight (g / plant)	33.8	12.3	30.4	<i>7.7</i>	33.3	38.7	35.8	10.8	30.75
11. Fiber yield (g / plant)	12.2	4.1	7.8	<i>3.0</i>	13.7	16.6	12.6	4.2	11.95
12. Fiber / wood	0.4	0.4	<i>0.3</i>	0.4	0.4	0.4	0.4	0.4	2.83

Table 3. Average inter-cluster (off diagonal) and intra-cluster (diagonal) distance (D^2) in 35 genotypes of tossa jute. Figures in parentheses indicate the number of genotypes in the respective clusters.

Cluster	I (15)	II (8)	III (6)	IV (2)	V (1)	VI (1)	VII (1)	VIII (1)
I	24.8	104.1	41.3	153.9	55.0	49.8	49.8	130.9
II		17.0	97.2	40.7	156.1	167.4	204.8	40.8
III			17.5	151.8	72.3	117.8	69.2	141.3
IV				9.3	236.0	207.5	261.8	72.2
V					0	103.8	93.6	184.6
VI						0	56.5	180.7
VII							0	224.7
VIII								0

the highest (30.7%) contribution to divergence followed by plant height (15.0%), fiber yield (12.0%), TD (8.4%) and bark thickness (7.0%).

The average intra and inter-cluster distance (Table 3) revealed that cluster I consisting of maximum (15) genotypes and had the highest intracluster distance (D^2 of 24.8). This indicated that it was the most heterogeneous group. But it exhibits low divergence, on an average, from most of the clusters. On the other hand cluster IV containing only two genotypes possessed maximum divergence from almost all the clusters except from clusters II and VIII. Highest average inter-cluster distance was observed between clusters IV and VII followed by IV and V indicating maximum genetic divergence among the genotypes between the clusters. It is generally suggested that genetic diversity must form the sound base for selecting parental stocks (1, 2 & 4) and the usefulness of this technique has also been experimentally demonstrated

in wheat by Bhatt (5). Accordingly, it is believed that parental combination of TR04/ARO-11 with TJ-40/JRO-7835 may produce a wide spectrum of variation among the progenies in segregating generations.

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