SHORT COMMUNICATION

Genetic Divergence of Tossa Jute (*Corchorus olitorius* L.) for Fibre Yield and its Related Component Characters Under Moisture Stress Condition

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The present investigation studied genetic divergence of 60 genotypes of tossa jute (*Corchorus olitorius* L.) which included sixteen standard varieties to identify the most diverged genotypes under moisture stress condition. On the basis of Mahalanobis D^2 analysis, genotypes were grouped into five clusters. Maximum inter-cluster distance was observed between cluster IV and V while cluster III showed the maximum intra-cluster distance. Cluster V exhibited highest means for days to 50% flowering, plant height, number of node, internode length, base diameter, mid diameter, top diameter, bark thickness and fibre weight. The highest contribution (12.63%) was exerted by plant height of total divergence. The results of the present study suggested that hybridization between genotypes in cluster V and IV could provide a wide spectrum of variation in the segregating generation which could provide opportunity for isolation of drought tolerant with high fibre yielding lines.

Jute, adorably called as "Golden Fibre" is obtained from bark of the two cultivated species of the genus *Corchorus,* viz., *C. capsularis* L. and *C. olitorius* L. of the family, Malvaceae (formerly, it was placed in Tiliaceae family) having chromosome number 2n=14. According to Kundu (1951), primary centre of origin of *C. olitorius* is Africa and its secondary centre of origin may be India or the Indo-Burma region, while the origin of *C. capsularis* is Indo-Burma region. Commercially, tossa jute covers 90 percent of the area and *C. capsularis* covers 10% of the total jute in India (Karmakar *et al.,* 2008). In West Bengal, jute is sown within first fortnight of April often accompanied by unpredictable and very low rainfall which exposes jute crop to moisture stress condition. Therefore, timely sowing and seedling establishment of jute mostly depends on availability of assured irrigation. Moreover, total precipitation during the jute growing season is decreasing day-by-day due to changed climatic conditions. Owing to erratic nature of rainfall over space, time and quantity, the crop is often subjected to phasic spell of moisture stress during early growth stage. There is limited scope for further improvement of cultivated varieties of jute against moistures stress in the absence of requisite variability and genetic diversity due to its narrow genetic base. Therefore, the present investigation was carried out to identify the most diverged genotypes under moisture stress condition from the existing germplasm so that it would help in planning hybridization programme to develop moisture-stress tolerant hybrids.

The experimental material consisted of 60 genotypes of *C. olitorius* of which sixteen were standard varieties collected from BCKV, All India Network Project on Jute and Allied Fibres, Kalyani, in collaboration with ICAR-CRIJAF, Barrackpore, Kolkata. The experiment was laid out in randomized block design with three replications. In each replication each genotype was grown in a plot of five rows of three meter length maintaining 30 cm space between the rows. The size of each plot was 3 m x 1.5 m and plot-to-plot distance was 0.5 m. Sowing was done under fully moisture stress condition on 5th April 2012 and 29th March 2013. The moisture stress condition was maintained when the plants showed symptoms of permanent wilting point (*viz.* failed to recover from wilting next morning), the plots were watered to half the field capacity. Recommended doses of major nutrient (40 kg N, 20 kg P_2O_5 and 20 kg K_2O) and FYM at 3 tons/ha were applied. Except days to 50% flowering, which was studied on plot basis, observations on other ten quantitative characters, namely, plant height (cm/plant), node number/plant, internode length (cm/plant),

base diameter (cm/plant), mid diameter (cm/plant), top diameter (cm/plant), bark thickness (mm/plant), green weight (g/plant), stick weight (g/plant) and fibre weight (g/plant) were recorded from ten plants randomly selected from each genotype from each replication. From pooled data, genetic divergence was estimated by multivariate analysis using Mahalanobis D^2 statistic described by Rao (1952) and the genotypes were grouped into different clusters by employing Ward method.

On the basis of Mahalanobis D^2 analysis, 60 genotypes were grouped into five clusters. (Table 1). Cluster I comprised of maximum number i.e. 23 genotypes (JRO 3690,S 19, TJ 40, JRO 878, JRO 7835,CO 58, OIN 259,OIN 409,OIJ 266,OIN 427,OIN 975,OIJ 213,OIN 986, OIJ 054,OIN 981, OIN 082,OEX 014,OIJ 264, OIN 915,OIN 666,OIN 926, OIN 581 and OIN 378). Cluster II was comprising of 14 genotypes (JRO 204, JR0 128, OEX 039, OIJ 104, OIN 714, OIN 309, OIN 515, OIN 959, OIN 623, OIJ 937,OIN 533,OIJ 168, OEX 019, OIJ 257), Cluster III and V with 8 genotypes each and cluster IV with 7 genotypes. Earlier Roy *et al.* (2011) grouped 52 genotypes into twenty clusters, Das and Kumar (2012) grouped fourteen varieties of white jute into three clusters, Das *et al.* (2012) grouped twenty eight genotypes of *C. olitorius* jute into five clusters, Majumdar *et al.* (2012) studied 27 genotypes of tossa jute and grouped them in 11 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 more number of clusters indicated presence of greater divergence among these genotypes. Cluster analysis of the 60 genotypes based on these characters had also been illustrated by the dendrogram (Fig.1). The results of grouping of the genotypes in different clusters obtained through D^2 statistic were also confirmed with the help of dendrogram where it clearly showed five clusters and the number of

genotypes belonging to each cluster. The results obtained through classification of germplasm using D^2 statistic would provide a set of groups from which desirable parents may be selected for further breeding programme with respect to yield in particular.

Considering the averages of inter-cluster distance (Table 2), it was noticed that the values varied from 4.118-7.167. Maximum inter-cluster distance was observed between clusters IV and V followed by between clusters II and V, clusters I and V, and clusters III and V. Cluster III showed the maximum intra-cluster distance followed by cluster V and II. Wide genetic distance was evident among the genotypes of different group than those within the same cluster. The higher inter-cluster distance between cluster IV with cluster V followed by between cluster II and cluster I indicated that the genotypes belonging to cluster V was widely distanced genetically from those of cluster IV, II and I. Minimum inter-cluster distance was observed between clusters II and IV followed by clusters I and IV and clusters II and III which indicated that genotypes of clusters II and IV, clusters I and IV and clusters II and III were more or less closely related. It could be predicted that the genotypes belonging to different clusters separated by high estimated statistical distance could be used in hybridization programme to develop moisture stress tolerant line in jute which can successfully overcome water stress at early phase of growth.

Variations in mean values of different characters were observed in different clusters (Table 3). Among 11 characters studied cluster V exhibited highest means for days to 50% flowering, plant height, number of node, internode length, base diameter, mid diameter, top diameter, bark thickness and fibre weight, while the lowest values for these characters were recorded for cluster IV except for internode length which was observed in cluster I. Lowest value for top diameter,

Table 1. Grouping of sixty genotypes of *C. olitorius* in different clusters under moisture stress condition from pooled data of 2012 and 2013

S.No.	Cluster no.	Total no. of genotypes	Name of genotypes
1	I	23	JRO 3690, S 19, TJ 40, JRO 878, JRO 7835,CO 58, OIN 259, OIN 409, OIJ 266, OIN 427, OIN 975, OIJ 213, OIN 986, OIJ 054, OIN 981, OIN 082, OEX 014, OIJ 264, OIN 915, OIN 666, OIN 926, OIN 581, OIN 378
2	II	14	JRO 204, JRO 128, OEX 039, OIJ 104, OIN 714, OIN 309, OIN 515, OIN 959, OIN 623, OIJ 937, OIN 533, OIJ 168, OEX 019,OIJ 257
3	III	8	JRO 66, JRO2407,IRA, JRO 632, OIJ 218, OIJ 214, OIN 990, OEX 05
4	IV	7	JRO 524, JRO 8432, Bidhan Rupali, KOM 62, OIN 976, OIN 937, OIN 970
5	V	8	OIJ 263, OIJ 284, OIN 124, OIJ 216, OIN 196, OIN 791, OIJ 177, OEX 29

Cluster Dendrogram

dist(ab)
hclust (*, "ward")
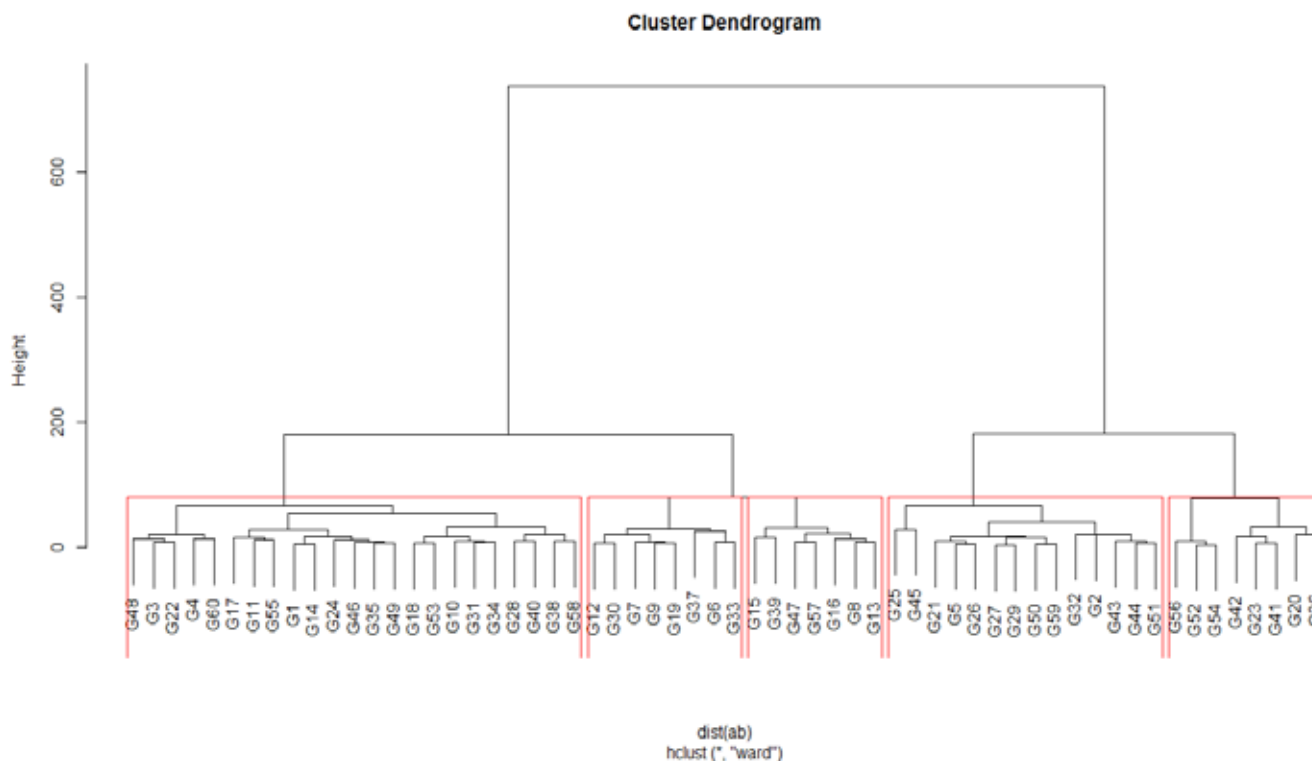
G1=JRO3690; G2=JRO204; G3=S19; G4=TJ40; G5=JRO128; G6=JRO66; G7=JRO2407; G8=JRO524; G9=IRA; G10= JRO878; G11=JRO7835; G12=JRO632;G13=JRO8432; G14=CO58; G15=BIDHAN RUPALI, G16=KOM62; G17-OIN259; G18=OIN409; G19=OIJ218; G20=OIJ263; G21=OEX039; G22=OIJ266; G23=OIJ284; G24=OIN427; G25=OIJ104, G26=OIJ714; G27=OIN309; G28=OIN975; G29=OIN515; G30=OIJ214; G31=OIJ213; G32=OIN959; G33=OIN990; G34=OIN986; G35=OIJ054; G36=OIN124; G37=OEX05; G38=OIN981; G39=OIN976; G40=OIN082; G41=OIJ216; G42=OIN196; G43=OIN623; G44=OIJ937; G45=OIN533; G46=OEX014; G47=OIN937; G48=OIJ264; G49=OIN915; G50=OIJ168; G51=OEX019; G52=OIN791; G53=OIN66; G54=OIJ177; G55=OIN926; G56=OEX29; G57=OIN970; G58=OIN581; G59=OIJ257; G60=OIN378.

Fig 1. Cluster analysis of sixty *C. olitorius* genotypes represented by dendrogram

Table 2. Intra and inter-cluster distances of *C. olitorius* under moisture stress condition from pooled data of 2012 and 2013

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	2.511	4.400	4.217	4.140	6.179
Cluster II		3.530	4.169	4.118	6.293
Cluster III			4.078	4.614	6.107
Cluster IV				3.504	7.167
Cluster V					3.697

Table 3. Cluster mean of *C. olitorius* under moisture stress condition from pooled data of 2012 and 2013

Cluster	Days to 50% flowering	Plant height (cm)	No. of node	Internode length (cm)	Base diameter (cm)	Mid diameter (cm)	Top diameter (cm)	Bark thickness (mm)	Green weight (g)	Dry stick weight (g)	Fibre weight (g)
Cluster I	102.102	257.419	74.942	4.163	1.147	0.893	0.629	0.782	140.582	23.787	6.464
Cluster II	102.509	260.796	74.905	4.210	1.136	0.919	0.637	0.741	179.267	29.350	6.503
Cluster III	102.027	272.148	76.229	4.439	1.174	0.843	0.580	0.815	123.655	21.550	6.969
Cluster IV	99.936	254.260	73.167	4.358	1.102	0.805	0.584	0.760	115.681	24.643	6.028
Cluster V	105.292	290.875	79.292	4.778	1.305	0.929	0.653	0.872	172.940	28.375	8.344

dry stick weight was recorded in cluster III, for bark thickness in cluster II and for green weight and days to 50% flowering in cluster IV. Cluster V appeared to be most important since it showed highest mean value for a number of important desirable characters including fibre yield and from this cluster improved genotypes could be directly selected or could be considered 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 V could provide a wide spectrum of variation in the segregating generation which might provide an opportunity for isolation of elite lines. Cluster V was found with genotypes showing highest mean for as many as nine characters and most of them were related to yield. On the contrary, cluster IV comprised of the genotypes which resulted into lowest mean for as many as seven characters among eleven characters studied. Further, in case of cluster I, II and III some characters produced higher mean while for others were very low mean. Highest contribution towards total genetic divergence (12.63%) was exerted by plant height followed by bark thickness (12.42%), green weight (12.12%), dry stick weight (10.12%), top diameter (9.24%%), internode length (8.48%), mid diameter (8.02%), node number (7.84%), fibre weight (7.68%), base diameter (5.81%) and days to 50% flowering (5.59%) (Table 4).

Thus, on the basis of cluster mean and also on the basis of mean performance and *per se* performance of individual genotypes, it could be suggested that selection of the genotypes from clusters V and IV could be proposed for earliness and high fibre yield and clusters V and II containing genotypes for base diameter, mid diameter and green weight may be fruitful to develop desirable lines. Noticeably, genotypes OIJ 263, OIJ 284, OIN 124, OIJ 216, OIN 196, OIN 791, OIJ 177, OEX 29 belonging to the cluster V and JRO 524, JRO 8432,

Table 4. Contribution of individual characters towards total genotypic divergence in sixty genotypes of *C. olitorius* under moisture stress condition from pooled data of 2012 and 2013

S. No.	Characters	Per cent contribution towards divergence D2 statistics
1	Days to 50% flowering	5.591%
2	Plant height(cm)	12.635%
3	Node No.	7.878%
4	Internode length(cm)	8.482%
5	Base diameter (cm)	5.809%
6	Mid diameter(cm)	8.024%
7	Top diameter (cm)	9.238%
8	Bark thickness (mm)	12.422%
9	Green weight (g)	12.124%
10	Dry stick weight(g)	10.123%
11	Fibre weight (g)	7.674%

Bidhan Rupali, KOM 62, OIN 976, OIN 937, OIN 970 from cluster IV may be used as parents for hybridization programme to evolve a line with drought tolerance and high fibre yielding.

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