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Research Article

PRINCIPAL COMPONENT ANALYSIS, EUCLIDEAN CLUSTERING OF TOSSA JUTE (*CORCHORUS OLITORIUS* L.) GENOTYPES FOR THE DROUGHT STRESS TOLERANCE

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Abstract: Jute is adorably called as "Golden Fibre". Two species namely *Corchorus capsularis* and *Corchorus olitorius* are commercially cultivated in India. It is the second-largest natural bast fiber in the world after cotton. Because of climatic change, low and erratic nature of rainfall over space and time the crop is often subjected to phasic spell of drought during early growth stage which frequently leads to crop failure or poor fibre yield. 60 genotypes of olitorius jute were assess for the drought tolerant genotypes, raised in randomised block design in three replications in two regimes *i.e.*, Control and Drought. All the characters were observed low to high reduction in dry matter. Based on the genetic distance, eight and seven clusters were formed in control and drought environment using agglomerative cluster analysis. In drought condition, cluster VII includes genotypes like OIN791, OIJ177 and OEX29 with the highest number of relative mean values of plant height, bark thickness and lower number of days to 50% flowering while in control conditions, five standard varieties were found highest mean values for plant height, base diameter and fibre weight. The principal component analysis studied showed first three component maximum variation *i.e.*,79.86%. The biplot analysis indicated nine genotypes were in maximum proximity with the plant height, base diameter, bark thickness and fibre weight. Various drought tolerant indices like Drought Susceptible Index(DSI), Stress tolerance (TOL), Stress tolerance index (STI), Yield index (YI) and Yield stability index (YSI) values showed superiority in OIN791, OIJ177, S19, OEX29, JRO2407 and OEX039.

Keywords: *Drought, Abiotic stress, Cluster analysis and PCA, Tossa jute, Drought tolerance index*

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Introduction

Jute, adorably called as "Golden Fibre". Among more than 100 species of this genus, only two species namely white jute (*Corchorus capsularis* L.) and Tossa jute (*Corchorus olitorius* L.) are commercially cultivated. Jute belonged to the family Malvaceae (formerly, it was placed in Tiliaceae family) having chromosome number (2n)=14. (Jute 6). A few tetraploid (2n)=28 are also identified. Around 215 species, subspecies, varieties and land races are contributed in the genus *corchorus*, where 60 species are more important and shows some extent of variability [1]. The cultivated white jute and tossa jute has been evolved through conventional breeding and pure line selection based on their yield and other yield attributing characters[2]. The white jute was evolved in the Indo-Burma region and tossa jute evolved in Tropical Africa [3]. Jute fibre is called as bast fibre. The taste of *Corchorus capsularisleaves* is unpleasant due to the presence of bitter glucoside-'Corchorin' and taste bitter on chewing. Hence it is often known as 'Tita'(bitter) pat, while *Corchorus olitorius is* 'Mitha' (sweet) pat. *Corchorus urticifolius*, has been identified as the common ancestor of the both cultivated species through phylogenetic analysis with the help of 38 polymorphic nuclear microsatellites. The nuclear progenitor of *C. olitorius* was found the *C. urticifolius* but not identified for C. Capsularis [4]. The quality of tossa jute fibre yield is finer, softer, stronger and more lustrous than that of whitish, reddish or greyish fibre in colour in white jute depending upon the nature of retting of water.

In case of jute area, production and productivity, India ranked first which is followed by Bangladesh, China, Uzbekisthan etc. During 2020-21 year, India produced raw jute fibre of 43.18 million bales from 0.38 million hectare of area with an average productivity of 20.51 q/ha(www.jutecomm.gov.in).

Both cultivated species is self-pollinated, however 15% natural outcrossing is occurred in tossa jute and 5% in white jute [5, 6]. The wild species of jute are the potential source for abiotic and biotic stress tolerant genes as well as important genetic resources for the improvement jute varieties. It has been reported thattossa jute is higher yielder than white jute except in inundated regime. It cannot tolerate in the abiotic stress. There is strong sexual incompatibility barrier exist between the two cultivated species.

Indeed, they are distantly related and their maternal origin are different but the genetic variability present at the intraspecific level is low [7]. Earlier research work was mainly focused on the development pure line varieties, where plant height and quality of fibre were main concern. As a result, the genetic diversity is narrowed down in both cultivated species. For example, the average genetic diversity of *Corchorus olitorius* and *Corchorus capsularis* was 7.2% (range 2.8–12.3%) and 7.6% (range 2.2–13.1%), respectively. Therefore, there is an urgent need in genetic improvement and development high yielding varieties in jute.

Currently, in global climate change is disturbing the balance between the ecosystem and other living entities, especially crop species. It induces several abiotic stresses like which are considered as the significant constraints for crop productivity, namely, drought, waterlogging/flooding, salinity, extreme temperature (high and low), toxic metals/metalloids, etc. [8]. Drought is not only hampering different morpho-physiological and biochemical features of plants, but leads to a considerable decrease in plant growth and productivity. In jute production temperature and rainfall is the most crucial factors. In the beginning phase of jute seedling the erratic rainfall and the high temperature results in the reduced in fibre quality and 20- 30% loss of fibre yield. Therefore, there is space for the integrated approach from Plant Breeder, Plant Physiologist, Agronomist and other related experts to mitigate the effect of drought on jute crops. Recently, several genetic and molecular approaches have been used to develop the drought tolerance varieties in jute. The genome sequence of jute created a new avenue for molecular breeding [9].

In search for heterosis and transgressive segregation, the genetic diversity is an important tool and has wide applicability in the correction of defect in commercial varieties and development of novel varieties [10, 7]. Hence, the identification of diverse line (if it is available) or creations of diverse line (if it is not available or limited) are the major goals of any crop improvement programme [10]. Therefore, the available valuable genetic variability in the diverse germplasm can be explored at intra specific and interspecific level and be utilized for breeding purpose.

For any crop improvement programme the diversity and genetic variability are the pre-requisites for the new high yielding, climate resilient and stable variety. Breeder should have knowledge and ability to understand evolutionary relationships among the germplasmon the basis of their variation in different morphological traits like plant height, diameter of the stem,fresh weight of the green plant with or without leaves, dry fibre weight and dry stick weight [11]. The desired trait offers itself for selection for the breeder when it shows the high heritability associated with the high genetic advance. The proper assessment of relationships between yield and yield attributing characters in jute plants helps in identification of contribution of traits towards fibre yield.

The breeder should be familiar with the knowledge of diversity of the genotypes, different methods of studying the genetic diversity, factors affecting the genetic diversity. He must be explored different software of the genetic diversity and their effective utilization. Through identification of diverse germplasm of jute using conventional breeding methods by hybridization and combined with molecular assisted selection would be helpful for the jute breeders [12].Multivariate methods such as cluster analysis and principal component analysis (PCA) have recognised to be useful for characterization, evaluation, and classifying germplasm for diversity when a large number of germplasm or genotypes to be assessed for several characteristics of anatomical importance. The principal component analysis is an effective way to represent the enormous experimental datasets to interpret similarities and dissimilarities among the experimental genotypes based on their desirable traits. [13]

Keeping these notions in mind, 60 pre-released tossa jute varieties were evaluated in drought regime for the identification of potential diverse drought tolerant genotypes, their nature and degree of genetic diversity which will be helpful for the selection of promising parents to develop transgressive segregants, which is ultimately used for developing new jute variety.

Materials and Methods

The geographical location of the experimental site

The experiment was carried out in consecutive two season at the Instructional Farm, Bidhan Chandra Krishi Vishwavidyalaya, Jaguli, West Bengal. (22057'N 88.200E) having gangetic alluvial sandy loam soil and located 9.75 m above sea level. The experiment site comes under subtropical humid region with an average temperature range from 250C -36.50C and 1500 mm rainfall.

Plant/seed materials

The experimental materials consisted of sixty genotypes [Table-1] of *Corchorus olitorius* of which 25 were indigenous, 16 genotypes were standard varieties, 14 were accessions of International Jute Organization (IJO) and 5 exotic varieties were from All India Network Project on Jute and Allied Fibres, Kalyani Centre, BCKV (in collaboration with CRIJAF, ICAR).

Field preparation, experimental design, seeding and plant growing

To conduct the experiment, drought condition was created by watering the field upto 50% field capacity (half of the field capacity of the field). The experimental plots were prepared by ploughing, weeding, and levelling. Fertilizers (Urea, TSP, MoP, Gypsum, and zinc sulphate) were applied at 100, 50, 60, 95, and 11 kg ha-1, respectively. The seeds were treated with fungicide (Bavistin at 0.25% of seed weight) to remove seed borne pathogens and sun dried to break the dormancy. The experiment was laid out by randomized block design with three replications in a plot of 5 rows of 3-meter length maintaining 30 cm space between the rows (3 m × 1.5 m).

Data collection

After attaining the physiological maturity for the fibre production, around 110-120 days of sowing, the jute plants were harvested and the fibre yield and other yield attributing characters [Table-2] were recorded. Except days 50% flowering, which was studied on plot basis, plant height (cm), base diameter (cm), bark thickness (mm), green weight (g), dry stick weight (g) and fibre weight (g) were recorded from ten plants randomly selected from each genotype from each replication and averaged it. The harvested plants were submerged in clean water and retted properly after 20–25 days of inundation [14]. Then the fibres were collected, washed clearly, sun dried by hanging from bamboo stick manually [15]. Then dry fibre and stick yields were recorded carefully.

The various drought tolerance indices were also calculated using the formulas given by the researchers.

Drought Susceptibility Index (DSI)=A=[1-(Ys/Yp)]/ [1- ($\overline{Ys}$/ $\overline{Yp}$))] ..... [16]

Stress tolerance (TOL)= Yp-Ys ..... [17]

Lesser values of TOL indicates the genotypes being stable in two different environments

Stress tolerance index STI= (Yp+Ys)/ ($\overline{Yp}^2$) ..... [18]

High STI values indicates genotypes being drought tolerant.

Yield index (YI)= Ys/ $\overline{Ys}$ ..... [19]

Higher the value of YI categorized genotypes as stable genotypes over two environments

Yield stability index (YSI)= Ys/Yp ..... [20]

Higher values of YSI categorized the genotypes as stable ones in contrasting environments.

Where, Ys= fibre yield of the genotype under drought environment, Yp= fibre yield of the genotype under normal environment, $\overline{Ys}$ and $\overline{Yp}$ = mean yields of all genotypes under drought and normal environments, respectively.

Statistical parameters and data analyses

After taking carefully the data, it was feed into the Microsoft office excel programme. The descriptive data like mean and maximum and minimum values, were calculated followed by analysis of variance (ANOVA) in R software for the estimation of significant differences among all genotypes.

Genetic divergence analysis was carried to measure the distance between two populations for a number of traits. Various clusters are formed in order to increasing magnitude of D^2 value from each individual population, following the method suggested by Tocher [21] and Euclidean squared distances (D^2) described by Joe [22, 23].

The D^2 values of genotypes were arranged in order of relative distances from each other, while the method suggested by [24] was used for cluster formation.

Average Intra- and Intercluster distances were calculated by the following formula:

Average intracluster: $D^2=\sum D^2 n$

Where, $\sum Di^2$is the sum of distance between all possible combinations (n) of the populations included in the cluster and „n" is the total number of all possible combinations.

Average intercluster: $D^2=\sum D^2_{ij} / n_i \times n_j$.

$\sum D^2$ is the sum of distance between the populations of i^{th} and j^{th} cluster. n= Number of populations in cluster i and n_j= Number of populations in cluster j.

Table-1 List of sixty germplasm along with their source.

Genotype No.	*Corchorus olitorius* germplasm	Types of germplasm	Source	Genotype No.	*Corchorus olitorius* germplasm	Types of germplasm	Source
1	JRO 3690	Pre-released standard variety	CRIJAF, Barrackpore, INDIA	31	OIJ 213	Accession	CRIJAF, Barrackpore, INDIA
2	JRO 204	Pre-released standard variety		32	OIN 959	Indigenous	
3	S 19	Pre-released standard variety		33	OIN 990	Indigenous	
4	TJ 40	Pre-released standard variety		34	OIN 986	Indigenous	
5	JR0 128	Pre-released standard variety		35	OIJ 054	Accession	
6	JRO 66	Pre-released standard variety		36	OIN 124	Indigenous	
7	JRO 2407	Pre-released standard variety		37	OEX 05	Exotic	
8	JRO 524	Pre-released standard variety		38	OIN 981	Indigenous	
9	IRA	Pre-released standard variety		39	OIN 976	Indigenous	
10	JRO 878	Pre-released standard variety		40	OIN 082	Indigenous	
11	JRO 7835	Pre-released standard variety		41	OIJ 216	Accession	
12	JRO 632	Pre-released standard variety		42	OIN 196	Indigenous	
13	JRO 8432	Pre-released standard variety		43	OIN 623	Indigenous	
14	CO 58	Pre-released standard variety		44	OIJ 937	Accession	
15	BidhanRupali	Pre-released standard variety		45	OIN 533	Indigenous	
16	KOM 62	Pre-released standard variety		46	OEX 014	Exotic	
17	OIN 259	Indigenous		47	OIN 937	Indigenous	
18	OIN 409	Indigenous		48	OIJ 264	Accession	
19	OIJ 218	Accession		49	OIN 915	Indigenous	
20	OIJ 263	Accession		50	OIJ 168	Accession	
21	OEX 039	Indigenous		51	OEX 019	Exotic	
22	OIJ 266	Accession		52	OIN 791	Indigenous	
23	OIJ 284	Accession		53	OIN 666	Indigenous	
24	OIN 427	Indigenous		54	OIJ 177	Accession	
25	OIJ 104	Accession		55	OIN 926	Indigenous	
26	OIN 714	Indigenous		56	OEX 29	Exotic	
27	OIN 309	Indigenous		57	OIN 970	Indigenous	
28	OIN 975	Indigenous		58	OIN 581	Indigenous	
29	OIN 515	Indigenous		59	OIJ 257	Accession	
30	OIJ 214	Accession		60	OIN 378	Indigenous	

Table-3 Pooled analysis of variance of different yield attributing characters of C. olitorius under normal condition in field

Sources of Variations	d.f.	Mean sum of squares						
		Days to 50% flowering	Plant Height (cm)	Base diameter (cm)	Bark thickness (mm)	Green weight (g)	Dry stick weight (g)	Fibre weight (g)
Replication	2	0.1954	0.9847	0.00001	3E-06	2.4178	0.0708	0.0017
Genotypes	59	77.1143***	1090.8070***	0.0374***	0.0436***	3771.1831***	175.6954***	7.6084***
Environments	1	0.0019	0.0162	0.0003	0.0001	0.0688	0.0028	0.0029
Interactions	2	130.9124***	873.8416***	0.0168***	0.0074***	242.2491***	7.4369***	0.5717***
Error	295	4.5057	30.2642	0.0007	0.0003	10.4442	0.3158	0.0215

Table-4 Pooled analysis of variance of different yield attributing characters of C. olitorius under drought condition in field

Sources of Variations	d.f.	Mean sum of squares						
		Days to 50% flowering	Plant height (cm)	Base diameter (cm)	Bark thickness (mm)	Green weight (g)	Dry stick weight (g)	Fibre weight (g)
Replication	2	0.1603	0.8482	0.00001	1.4E-06	2.515	0.0282	0.001
Genotypes	59	70.7535***	2264.5044***	0.0434***	0.0935***	4918.5425***	50.8640***	6.9542***
Environments	1	0.3176	0.3932	0.0039	0.0006	0.3247	0.872	0.0074
Interactions	2	143.8140***	1031.9904***	0.0199***	0.0095***	397.9741***	2.6027***	1.1374***
Error	295	4.9613	37.8349	0.0017	0.0004	16.0924	0.1534	0.0513

Principal Component Analysis (PCA) is a multivariate technique that analyses an observation which is represented by several inter-correlated quantitative dependent variables. The main aim is to extract the important information into new orthogonal variables called principal components. 'Proper values' measure the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The higher the coefficients, regardless of the direction (positive or negative), the more effective they will be in discriminating between accessions [25]. D^2 statistics, cluster mean analysis, and principal component analysis were carried out by using statistical software package R.

Table-2 List of yield attributing characters and their methods of measurement

Characters	Method of collection the data per replication
Days 50% flowering	Period from planting to 50% flowering
Plant height (cm)	From base of the stem to the uppermost leaf at maturity
Base diameter (cm)	From basal portion of the plant by Vernier Calliper.
Bark thickness (mm)	Measured by using Vernier Calliper very close to base of the stem.
Green weight (g)	After maturity, whole plant was weighed except root
Dry stick weight (g)	After retting, stick was dried and weighed
Fibre weight (g)	After retting, extracted fibre was weighed

Results and Discussion

The successful of any breeding programme primarily depends on the presence of genetic variation in the genotypes. [Table-3] and [Table-4] showed the analysis of variances of the 11 yield attributing characters of jute in normal and drought condition. In both regimes, it was found that significant differences were observed among the genotypes, between the genotypes and genotype x environment effect for all the characters. *i.e.*, Days 50% flowering, Plant height (cm), Base diameter (cm), Bark thickness (mm), Green weight (g), Dry stick weight (g) and Fibre weight (g). This is clearly indicating that there is presence of variability among the genotypes for the mentioned traits.

The degree of water stress is increased gradually in the field, it significantly affects the growth and development of the jute plant. It disturbs the morphological and physiological processes which results drastically reduced in the fibre yield. Four physiological stages *viz.*, mid-vegetative, flowering, pod formation and pod filling, has been identified where the jute showed reduction in fibre yield [26, 8]. Though every stage of the jute plant drought stress decreased the growth and yield. According to [27] study, highest yield reduction (64%) was found in flowering stage marked as most critical stage, followed by the pod filling stage (47%). In our study, we compared the performance of various yield components in normal and drought conditions. All the characters were greatly hampered in drought condition, for examples, plant height, base diameter, bark thickness, green weight and fibre weight except dry stick weight. The significant effect of drought stress was found in the plant height, base diameter and fibre weight per plant which is main contributors to the yield while the marginal difference was observed in the day to50% flowering, bark thickness and green weight. This indicates that these characters are least affected by the stress and could be important in making some genotypes drought tolerant. Similar results were found by [28] in olitorius jute and in rice by [29]. Box plots showing comparison between drought and control water regime over various yield contributing traits [Fig-1].

Table-5 Mean values of the different clusters for yield attributing characters in under control and drought stress conditions (higher and lower values shows in bold)

Characters		Clust.'	Clust	Clus'	Clus'	Clus'	Clus'	Clus'	Clus
DTF	C	108.12	109.67	109.35	108.79	104.72	103.54	105.75	104.94
	D	101.22	103.33	102.60	100.52	101.71	100.45	111.51	-
PH	C	302.89	313.25	281.94	336.06	293.32	285.37	277.09	272.38
	D	258.61	271.41	261.73	251.24	290.99	247.51	298.66	-
BD	C	1.34	1.36	1.26	1.47	1.30	1.25	1.24	1.19
	D	1.16	1.19	1.15	1.07	1.33	0.94	1.30	-
BTHK	C	0.84	1.09	0.88	0.91	0.94	0.74	0.78	0.85
	D	0.81	0.85	0.74	0.67	0.89	0.58	0.91	-
GW	C	205.33	205.19	157.32	191.46	175.18	152.02	200.99	220.54
	D	130.17	145.10	173.31	130.61	165.88	196.22	187.95	-
DSW	C	17.95	17.65	16.04	16.58	16.44	11.43	20.14	14.79
	D	22.21	26.80	28.20	22.25	28.86	40.00	30.86	-
FW	C	10.38	10.77	9.00	11.48	9.94	9.29	8.73	7.93
	D	6.16	7.55	6.58	6.05	8.18	4.69	9.10	-

Table-6 Clusters on the basis of D^2 values in control environment

Clusters	No. of Genotypes	Genotypes in clusters
I	9	JRO 3690, JRO 128, JRO 878, OIJ 263, OIJ 937, OIJ 168, OIN 427, OIN 714, OIN 196
II	9	JRO 204, S 19, JRO 8432, OEX 039, OEX 29, OIN 124, OIN 791, OIJ 177, OIJ 216
III	9	TJ 40, JRO 66, JRO 7835, OIN 259, OIN 409, OIN 082, OIN 666, OIN 926, OIN 581
IV	5	JRO 2407, JRO 524, JRO 632, OIJ 284, OIJ 214
V	13	JRO 3690, CO 58, IRA, OIJ 218, OIJ 266, OIJ 264, OIN 309, OIN 975, OIN 515, OIN 990, OIN 981, OIN 970, OIN378
VI	4	BIDHANRUPALI, OIJ 213, OIN986, OIN 976
VII	7	KOM 62, OIN 959, OIN 937, OIN 915, OEX 019, OIJ 257,OIJ 104
VIII	4	OIJ 054, OIN 623, OIN 533, OEX 014

Table-7 Clusters on the basis of D^2 values in drought environment

Clusters	No. of genotypes	Genotypes in clusters
I	20	JRO 3690, JRO 66, JRO 524, JRO 7835, JRO 8432, OIJ 218, OIJ 054, OEX 05, OEX 014, OIN 259, OIN 409, OIN 975, OIN 990, OIN 981, OIN 976, OIN 082, OIN 915, OIN 666, OIN 926, OIN 970.
II	11	JRO 204, S 19, TJ 40, JRO 2407, IRA, JRO 632, OEX 039, OIJ 266, OIJ 214, OIJ 264, OIN 124
III	14	JRO 128, CO 58, OIJ 104, OIN 714, OIN 309, OIN 515, OIN 959, OIN 196, OIN 623, OIN 378, OIJ 937, OIJ 168, OIJ 257, OEX 019
IV	8	JRO 878, BIDHANRUPALI, KOM 62, OIN 427, OIN 986, OIN 937, OIN 581, OIJ 213
V	3	OIJ 263, OIJ 284, OIJ 216
VI	1	OIN 533
VII	3	OIN 791, OIJ177, OEX 29

Table-8 Eigenvalues, proportion of variability and yield attributing traits that contributed to the first three principal components of jute genotypes

Characters	Control			Drought		
	PC1	PC2	PC3	PC1	PC2	PC3
DTF	0.021	0.059	0.942	0.2969	-0.2388	0.8349
PH	0.184	0.98	-0.06	0.4894	0.1249	0.0433
BD	0	0.004	0	0.4589	0.2755	-0.0745
BTHK	0	0.003	0.006	0.3725	0.3935	-0.2427
GW	0.982	-0.186	-0.015	0.2637	-0.5954	-0.0549
DSW	0.018	0.002	0.331	0.2158	-0.5833	-0.4798
FW	0.007	0.051	-0.008	0.4548	0.0433	-0.0583
Eigen values	843.61	357.262	10.5819	3.3841	1.4371	0.7692
Proportion of variance (%)	69.1	29.29	0.87	48.34	20.53	10.99
Cumulative proportion (%)	69.1	98.47	99.33	48.34	68.87	79.86

Agglomerative Cluster Analysis

The Agglomerative cluster analysis grouped the 60 experimental genotypes into 8 and 7 major clusters in control and drought conditions respectively using yield attributing traits. The jute germplasm was shown in the same cluster indicates the similar agro-morphological traits, also shown in Agglomerative dendrogram. The genotypes which were belonged to different clusters depicted the genetic divergence. Under control condition, cluster V was larger with 22% genotypes including 3 pre-released varieties (JRO 3690, CO 58, IRA), 3 accessions(OIJ 218, OIJ 266, OIJ 264), 7 indigenous (OIN 309, OIN 975, OIN 515, OIN 990, OIN 981, OIN 970, OIN378) germplasm.

It was followed by cluster I, II and III, each containing 9 germplasm (15%). The cluster I included 3 pre-released varieties (JRO 3690, JRO 128, JRO 878), 3 accessions (OIJ 263, OIJ 937, OIJ 168) and 3 indigenous germplasm (OIN 427, OIN 714, OIN 196). The cluster II was occupied 3 pre-released (JRO 204, S 19, JRO 8432), 2 exotics (OEX 039, OEX 29), 2 indigenous (OIN 124, OIN 791) and 2 accessions (OIJ 177, OIJ 216) with the highest relative mean for bark thickness. The cluster III contained 3 pre-released varieties (TJ 40, JRO 66, JRO 7835) and 6 indigenous germplasm (OIN 259, OIN 409, OIN 082, OIN 666, OIN 926, OIN 581) contributing highest relative mean for days to 50% flowering.The cluster VII occupied (12%) 1 pre-released variety(KOM 62), 3 indigenous varieties (OIN 959, OIN 937, OIN 915), 1 exotic (OEX 019) and 2 accessions (OIJ 257, OIJ 104) with highest mean value of dry stick weight. The cluster IV included(8%) 3pre-released varieties (JRO 2407, JRO 524, JRO 632) and 2 accessions (OIJ 284, OIJ 214) with highest relative mean for plant height, base diameter and fibre weight. The remaining two clusters, VI and VIII each contained 4 germplasm. *i.e.*, Cluster VI included 1 pre-released variety (BIDHANRUPALI), one exotic(OIJ 213) and 2 indigenous germplasm(OIN986, OIN 976).This cluster has been contributed for the lowest relative mean values for days to 50% flowering; bark thickness, green weight and dry stick weight. The cluster VIII occupied 1 accession(OIJ 054), 2 indigenous (OIN 623, OIN 533) and 1 exotic (OEX 014) germplasm with lowest relative mean values for plant height, base diameter and fibre weight and highest for green weight.

Under drought condition, cluster I occupied the maximum number of germplasm(34%). Out of 20, 5 pre-released varieties (JRO 3690, JRO 66, JRO 524, JRO 7835, JRO 8432), 2 accessions (OIJ 218, OIJ 054),2 exotics (OEX 05, OEX 014,) and 11 indigenous (OIN 259, OIN 409, OIN 975, OIN 990,OIN 981,

Table-9 Mean values of Fibre yield, percentage (%) of reduction in yield and drought tolerant indices like DSI (Drought Salinity Index), TOL (Stress Tolerance), STI (Stress Tolerance Index), YI (Yield Index) and YSI (Yield Stability Index).

SN	Genotypes	Y_S	Y_P	% reduction in yield	DSI	TOL	STI	YI	YSI
1	JRO3690	6.323	10.750	41.19	1.32	4.428	0.178	0.938	0.588
2	JRO204	7.699	11.025	30.17	0.30	3.326	0.195	1.143	0.698
3	S19	9.048	11.150	18.86	0.19	2.103	0.210	1.343	0.811
4	TJ 40	6.399	9.950	35.69	0.36	3.551	0.170	0.950	0.643
5	JR0128	7.199	10.599	32.08	0.32	3.400	0.185	1.068	0.679
6	JRO66	6.298	10.198	38.25	0.38	3.901	0.172	0.935	0.618
7	JRO2407	8.998	11.519	21.89	0.22	2.522	0.214	1.335	0.781
8	JRO524	6.599	11.199	41.08	0.41	4.600	0.185	0.979	0.589
9	IRA	6.474	10.578	38.80	0.39	4.104	0.177	0.961	0.612
10	JRO878	6.069	9.598	36.77	0.37	3.529	0.163	0.901	0.632
11	JRO7835	5.298	9.643	45.06	0.45	4.346	0.156	0.786	0.549
12	JRO632	6.253	11.245	44.40	0.44	4.993	0.182	0.928	0.556
13	JRO8432	6.200	10.940	43.33	0.43	4.741	0.178	0.920	0.567
14	CO58	6.800	10.200	33.34	0.33	3.401	0.177	1.009	0.667
15	BIDHAN RUPALI	5.050	9.105	44.54	0.45	4.055	0.147	0.749	0.555
16	KOM62	6.199	8.950	30.74	0.31	2.752	0.158	0.920	0.693
17	OIN259	6.298	8.795	28.40	0.28	2.498	0.157	0.935	0.716
18	OIN409	5.300	7.885	32.79	0.33	2.586	0.137	0.787	0.672
19	OIJ218	6.899	8.933	22.77	0.23	2.034	0.165	1.024	0.772
20	OIJ263	8.299	10.825	23.33	0.23	2.526	0.199	1.232	0.767
21	OEX039	8.199	10.415	21.28	0.21	2.217	0.194	1.217	0.787
22	OIJ266	8.099	10.467	22.62	0.23	2.368	0.193	1.202	0.774
23	OIJ284	8.341	11.558	27.84	0.28	3.217	0.207	1.238	0.722
24	OIN427	7.205	10.735	32.88	0.33	3.530	0.187	1.069	0.671
25	OIJ104	6.445	8.892	27.52	0.28	2.447	0.160	0.957	0.725
26	OIN714	6.305	10.125	37.73	0.38	3.820	0.171	0.936	0.623
27	OIN309	6.795	9.809	30.73	0.31	3.014	0.173	1.008	0.693
28	OIN975	7.690	10.295	25.30	0.25	2.605	0.187	1.141	0.747
29	OIN515	5.905	10.495	43.74	0.44	4.590	0.171	0.876	0.563
30	OIJ214	7.600	11.860	35.92	0.36	4.261	0.203	1.128	0.641
31	OIJ213	6.099	9.799	37.76	0.38	3.700	0.165	0.905	0.622
32	OIN959	5.810	8.529	31.88	0.32	2.719	0.149	0.862	0.681
33	OIN990	5.905	9.850	40.05	0.40	3.945	0.164	0.876	0.599
34	OIN986	5.399	8.660	37.66	0.38	3.261	0.146	0.801	0.623
35	OIJ054	5.600	7.901	29.13	0.29	2.302	0.141	0.831	0.709
36	OIN124	7.298	10.600	31.16	0.31	3.303	0.186	1.083	0.688
37	OEX05	7.298	10.420	29.97	0.30	3.123	0.184	1.083	0.700
38	OIN981	6.398	8.689	26.37	0.26	2.292	0.157	0.949	0.736
39	OIN976	6.135	9.602	36.11	0.36	3.467	0.164	0.911	0.639
40	OIN082	6.005	9.154	34.40	0.34	3.149	0.158	0.891	0.656
41	OIJ216	7.898	10.657	25.89	0.26	2.759	0.193	1.172	0.741
42	OIN196	7.645	10.210	25.12	0.25	2.565	0.186	1.135	0.749
43	OIN623	5.499	8.275	33.55	0.34	2.776	0.143	0.816	0.665
44	OIJ937	7.301	10.275	28.94	0.29	2.974	0.183	1.084	0.711
45	OIN533	4.690	7.482	37.32	0.37	2.792	0.127	0.696	0.627
46	OEX014	6.075	8.050	24.53	0.25	1.975	0.147	0.902	0.755
47	OIN937	5.300	8.895	40.42	0.40	3.596	0.148	0.787	0.596
48	OIJ264	7.795	10.290	24.25	0.24	2.496	0.188	1.157	0.757
49	OIN915	5.701	8.490	32.85	0.33	2.789	0.148	0.846	0.671
50	OIJ168	7.075	10.290	31.24	0.31	3.215	0.181	1.050	0.688
51	OEX019	6.499	8.750	25.73	0.26	2.251	0.159	0.965	0.743
52	OIN791	9.093	10.821	15.97	0.16	1.729	0.207	1.349	0.840
53	OIN666	5.083	8.199	38.01	0.38	3.117	0.138	0.754	0.620
54	OIJ177	8.899	10.592	15.98	0.16	1.693	0.203	1.321	0.840
55	OIN926	5.574	8.029	30.58	0.31	2.455	0.142	0.827	0.694
56	OEX29	9.299	10.845	14.26	0.14	1.546	0.210	1.380	0.857
57	OIN970	6.659	9.177	27.44	0.27	2.519	0.165	0.988	0.726
58	OIN581	7.048	9.315	24.34	0.24	2.268	0.170	1.046	0.757
59	OIJ257	5.601	8.586	34.77	0.35	2.985	0.148	0.831	0.652
60	OIN378	7.300	9.955	26.68	0.27	2.656	0.180	1.083	0.733

OIN 976, OIN 082, OIN 915, OIN 666, OIN 926, OIN 970) with the minimum relative mean values for green weight and dry stick weight. The cluster III contained 2 pre-released varieties(JRO 128, CO 58), 8 indigenous varieties (OIJ 104, OIN 714, OIN 309, OIN 515, OIN 959, OIN 196, OIN 623, OIN 378), 3 accessions (OIJ 937, OIJ 168, OIJ 257) and 1 exotic (OEX 019). The cluster II grouped into 11 genotypes, which contain 6 pre-released varieties (JRO 204, S 19,TJ 40, JRO 2407, IRA, JRO 632),1 exotic (OEX 039), 3 accessions(OIJ 266, OIJ 214, OIJ 264) and 1 indigenous (OIN 124) contributing the highest number of relative means for fibre yield. The cluster IV occupied 3 pre-released varieties (JRO 878, BIDHANRUPALI, KOM 62), 4 indigenous (OIN 427, OIN 986, OIN 937, OIN 581) and 1 accession (OIJ 213,) with minimum relative mean values for base diameter. The remaining three cluster, cluster V contributed 3 accessions (OIJ 263, OIJ 284, OIJ 216) with highest average values for base diameter, cluster VI only 1 indigenous(OIN 533) with lowest relative mean values for days to 50% flowering, plant height, bark thickness, green weight and fibre weight and highest for dry stick weight and cluster VII contained 1 indigenous(OIN 791), 1 accessions(OIJ177) and 1 exotic(OEX 29) contributing the highest average values for days to 50% flowering, plant height and bark thickness.

The cluster VI in both environments showed the extreme values for most of the studied characters like days to 50% flowering, bark thickness, green weight and dry stick weight. Therefore, genotypes were contributed this cluster could be selected directly for the further improvement or as parents for the future hybridization programme for drought tolerance.

Principal component analysis (PCA)

In the present study, the visualization of the total variance by different variables and components of 60 genotypes under control and drought conditions were presented in [Table-8]. According to [30] and later by supported by [31], the first three principal components are very important in most cases to visualise the pattern of variations exist in the genotypes and the traits linked with these are more beneficial in differentiating the genotypes. The principal component analysis under control condition, first three principal components explained the cumulative variance 99.33% with more than unity in eigen values. Among these, first two PCs *i.e.*, PC1 and PC2 explained 69.1% and 29.29% of phenotypic variation respectively. The measurement of the cut-off limit for the coefficients was given by [32]. According to him, component matrix coefficients greater than 0.3 indicated an ample component effect and have importance of that component for a particular trait. In this study, PCA revealed that green weight per plant (g) had greater influence (>0.3) on PC 1, plant height (cm) for PC2 and days to 50% flowering and dry stick weight for PC3. In case of drought condition, the first three components explained the 79.86% of the cumulative total variance. Out of three PCs, the PC1 explained the 48.34% and 20.53% by PC2.

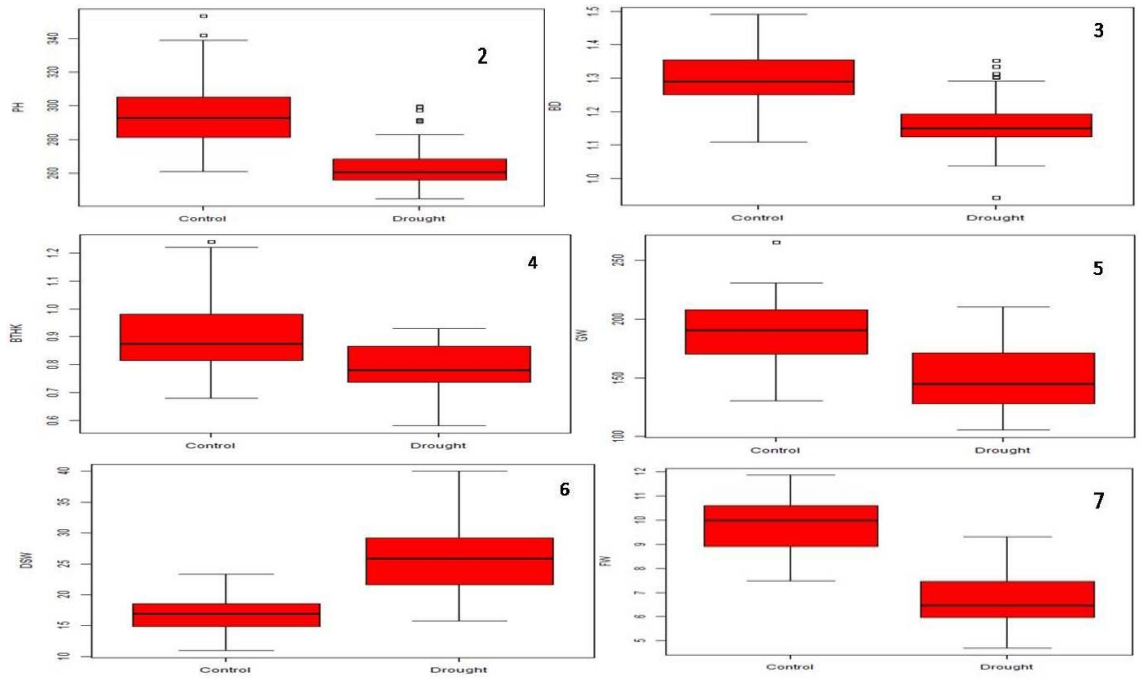

Fig-1 Box plots showing comparison between drought and control water regime over various yield contributing traits 2. Plant height (cm) 3. Base diameter (cm) 4. Bark thickness (mm) 5. Green weight (g) 6. Dry stick weight (g) and 7. fibre weight (g).

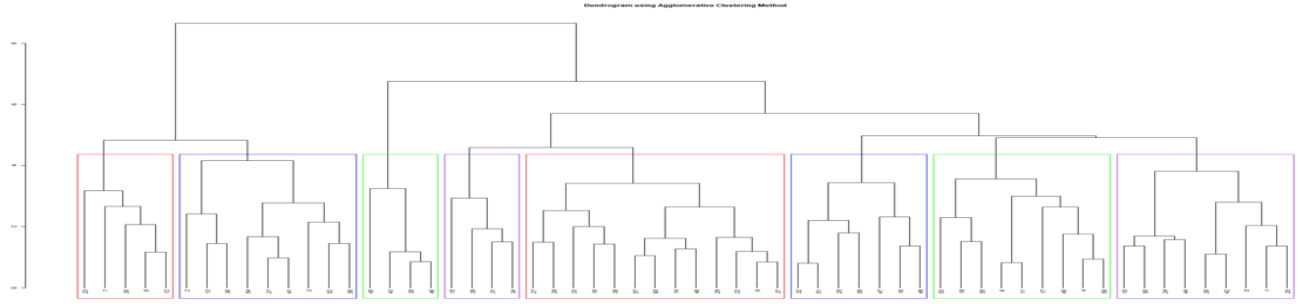

Fig-2 Dendrogram showing the genetic diversity using yield attributing characters for 60 genotypes in control condition. (Note: The numbers shown in dendrogram is represented by Genotype no. see in Table1).

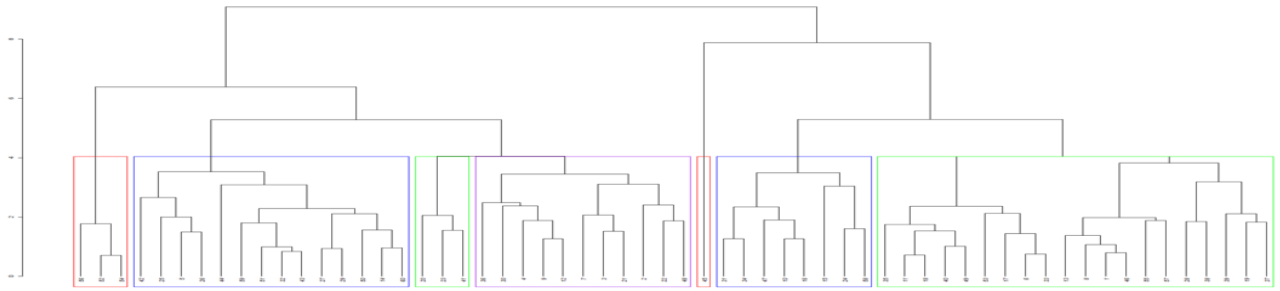

Fig-3 Dendrogram showing the genetic diversity using yield attributing characters for 60 genotypes in drought condition (Note: The numbers shown in dendrogram is represented by Genotype no. see in Table1)

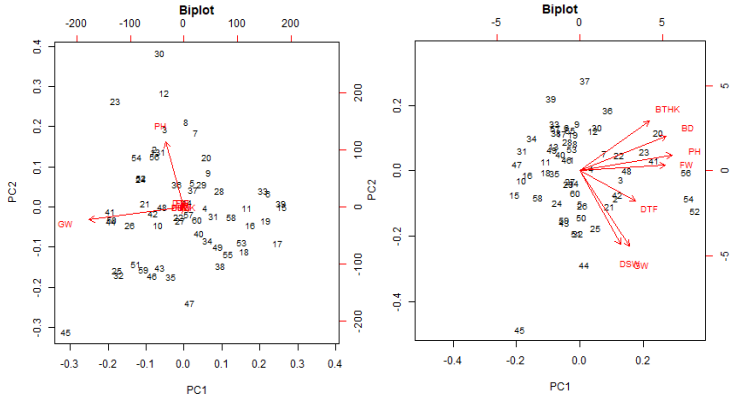

Fig-4 Biplot analysis genotypic x characters under control and drought conditions plotting PC1 against PC2. (Note: The numbers shown in Biplot are represented by Genotype no. see in Table1).

The yield attributing characters like Plant height, base diameter and fibre weight influence on PC1, bark thickness on PC2 and days to 50% flowering on PC3. Therefore, these characters should be given importance for the selection. [23] found about 85% of the total variation of the first two principal components and suggested that fibre weight, stick weight, plant height, green weight and bark thickness were the prime characters for the discrimination.

PCA Biplot analysis

A genotype x characters was created from a two-way matrix of 7 characters and 60 genotypes of jute for both control and drought condition. The association among different characters and genotypes with respective principal components were described by the principal component biplots for both control and drought stress represented by [Fig-4]. In the graph, the narrow angles between two adjacent vectors in same direction showed strong correlation of a character in terms of discerning genotypes. In control conditions, the first two component of a PCA biplot summarizing the relationships between the characters and the genotypes explained 69.1% of the total variance by PC1 and 29.29% of the variance by PC2. The several genotypes were scattered in all axes. Except plant height and green weight, all the characters *viz*., days to 50% flowering, base diameter, bark thickness, dry stick weight and fibre weight were located near the origin of both the components. This indicates, these traits were in close association between them. The genotype 3=S19, 8=JRO524, 7=JRO2407, 2=JRO204, 31=OIJ213 and 56=OEX29 were clogged near the vicinity of plant height trait. In drought conditions, the first two axes of a PCA biplot summarizing the relationships between the characters and the genotypes explained 48.34% of the total variance by PC1 and 20.53% of the variance by PC2. Under drought conditions, the genotypes 4 =TJ40, 7=JRO2407, 12=JRO632, 20=OIJ263, 22= OIJ266, 23= OIJ284, 30= OIJ214, 36= OIN124 and 41=OIJ216 have PC1 score > 0 and positive for PCA2. These genotypes have highest load and proximity with the characters like plant height, base diameter, bark thickness and fibre weight. For days to 50% flowering 2=JRO204, 42=OIN196, 52=OIN791, 54=OIJ177 had higher positive PC1 score but negative for PC2 while for green weight and dry stick weight 44=OIJ937 had nearly zero for PC1 and negative for PC2.

Drought tolerant indices

For the further to ascertain the selection of drought tolerant genotypes from the study, some drought tolerant indices like Drought Susceptibility Index(DSI), Stress tolerance (TOL), Stress tolerance index (STI), Yield index (YI) and Yield stability index (YSI) were calculated and represented in the [Table-9]. From the table, OEX29, OIN791, OIJ177, S19, OEX039, OIJ218, and OIN 581 were had minimum DSI and TOL values and were categorized has drought tolerant genotypes. JRO3690, JRO7835, JRO8432, BIDHAN RUPALI, JRO524, JRO632, OIN515, OIN990 and IRA were found maximum DSI and TOL values and were categorized as drought susceptible genotypes. Most of genotypes having high values for DSI and TOL were found high yielder in normal conditions. The maximum percentage in reduction of fibre yield was found in drought condition in the genotypes which had highest values for TOL. Another drought tolerant indices, stress tolerant index (STI) which classified the genotypes into most drought tolerant and least tolerant or susceptible one. JRO2407, S19, OEX29, OIN791, OIJ284, OIJ177, OIJ214 were classified as drought tolerant due to their high STI values and OIN533, OIN409, OIN666, OIJ054, OIN926, OIN623, OIN986, OEX014, B. RUPALI were classified as least tolerant or susceptible genotypes due to their low STI values.

The drought tolerant genotypes with the stability in wide environment are an important criterion for the true identification desirable genotypes for the drought condition. Therefore, further two drought tolerant indices were used e.g., Yield Index (YI) and Yield Stability Index (YSI). The YI ranked the genotypes on the basis of yield performance in drought condition. The maximum value for YI was identified in OEX29, OIN791, S19, JRO2407, OIJ177, OIJ284, OIJ263, OEX039 and OIJ 266 and least YI was found in OIN533, BIDHAN RUPALI, OIN666, JRO7835, OIN937, OIN409 and OIN986. The least yield stability index in drought condition is an indicator of stable genotypes. The maximum YSI exhibited as genetic stability over normal and drought conditions and recorded by OEX29 followed by OIN791, OIJ177, S19, OEX039, JRO2407, OIJ266 and OIJ218. Similar drought tolerant indices were used by [33] in wheat.

The results of different drought tolerant indices highlighted some common genotypes which showed the minimum DSI, TOL but maximum STI, YI and YSI. It indicates that studied drought tolerant indices were in harmony to each other for the identification of drought tolerant genotypes. These common genotypes are OEX29, OIN791, OIJ177, S19 and OEX039 identified as drought tolerant genotypes with stable performance in drought environment.

Discussion

One of the major abiotic stress, drought is greatly affected in crop production in the form of reduction in yield. Gradually it has now become severe problem wherever there is uncontrolled population growth, global scarcity of water resources and climate abnormalities. In current investigation, to address such abiotic stress *i.e*., drought, genotypes were exposed in artificially created dry condition upto wilting point where plants possess genotypically strong, physiological, biochemical sturdy metabolism were retained. Similar kind of investigation were also done by [34]. They studied the effects of water deficit stress on 6 olitorius genotypes in terms of phenotypic traits, leaf gas exchange, water relations, secondary metabolite profile and fibre properties. Moreover, [35, 36], [37], [38], [39] were found significantly reduction in phenotypic and yield attributing traits in jute crop. From principal component analysis and biplot analysis indicated that selection would be effective in drought for days to 50% flowering, plant height, base diameter, bark thickness and fibre weight. Similar findings were reported by [13] in earlier. These characters were also had higher mean values in the cluster mean data against the control condition. The cluster analysis classified genotypes into eight and seven clusters in drought and control environment respectively. The genotypes were in the same cluster also found the higher drought tolerant indices. These genotypes were OEX29, OIN791, OIJ177, S19 and OEX039 with little percentage of reduction in drought environment.

Conclusion

From the above investigation it was found all the germplasm showed more or less tolerant in sudden increase/decrease drought situation. The plant metabolism and genetic combination of the genotypes play an important role during drought situation. From the divergence analysis, cluster mean analysis, principal component analysis and drought tolerant indices it was identified that OEX29, OIN791, OIJ177, S19, JRO2407 and OEX039 to be drought tolerant while JRO524, JRO632, JRO3690, JRO3690, OIJ214 and OIN970 were found the most susceptible genotypes. These genotypes could be used in jute hybridization programme for the development of drought tolerant variety and in studying the inheritance pattern of stress tolerance.

Application of research: The present research is about the screening for drought stress tolerant genotypes. The identified superior genotypes could be used for drought stress breeding programme.

Research Category: Genetics and Plant Breeding

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Cultivar / Variety / Breed name: Jute

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