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Trait Variability and Association Revealed by Multivariate Analysis in Tossa Jute (*Corchorus olitorius* L.)

S. K. Roy, S. Vishnupriya, L. Hijam, M. Chakraborty, B. Maying, B. Thapa, D. T. Surje

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ABSTRACT

The present study was carried out to investigate fiber yield and quality traits in 52 tossa jute (*C. olitorius* L.) accessions, in order to generate information regarding the extent of genetic variability influencing fiber yield. The experiment was laid out over two years during 2006 and 2007. Parameters like plant height (cm), basal diameter (cm), green weight (g/plant) and fiber yield (g/plant) were recorded. The analysis of variance revealed the presence of significant variability among the 52 tossa jute genotypes. Diversity analysis revealed four clusters and it showed that average inter cluster distance was higher than the average intra-cluster distance. The magnitude of PCV was slightly higher than the GCV for all the traits. High estimates of heritability and genetic gain were observed for green weight (0.84 and 33.58%) and fiber yield (0.85 and 34.23%), suggesting that straight selection for these traits may bring worthwhile improvement and help in identifying superior genotypes of tossa jute. All the three yield attributing traits revealed a significant positive correlation with fiber yield. According to rescaled index value, the accessions OIJ-218, OIN-915 and OIN-975 secured the first, second and third rank respectively on the basis of all the four traits in the present study. In the principal component analysis four principal components were generated out of which only PC1 exhibited eigen value more than one. All the components of PC1 revealed a high degree of variability indicating the genotypes can be used as a good parental stock for the further tossa jute improvement program.

Keywords Diversity analysis, Heritability, Correlation, Principal component analysis, Tossa jute.

S.K. Roy[1*], S. Vishnupriya[2], L. Hijam[3], M. Chakraborty[4], B. Maying[5]
Department of Genetics and Plant Breeding, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar 736165, West Bengal, India

B. Thapa[6]
[6]Regional Research Station, Hill Zone, Uttar Banga Krishi Viswavidyalaya, Kalimpong, West Bengal, India

D. T. Surje[7]
[7]Kewalramji Harde College of Agriculture, Chamorshi, Maharashtra, India

Email: suvendukumarroy@gmail.com
*Corresponding author

INTRODUCTION

Jute is a self-pollinated crop belonging to the family *Tiliaceae* under *Corchorus* genus (Zhang *et al*. 2019). Jute is mostly diploid bearing the chromosome number 2n = 2x = 14, but sometimes few tetraploids are also reported (Bhaduri and Bairagi 1968). Two species of jute are mainly cultivated in India namely, *Corchorus capsularis* L. (White jute) and *Corchorus olitorius* L. (Tossa jute). Jute is one of the major cash crops in India and the average land area under

the cultivation of jute and mesta is nearly 800 thousand hectares. Approximately 4 million farmers are involved in the raw jute production and nearly 3.50 lakh workers are dependent on forward and backward linkages of jute industry (IJMA 2022). Therefore, to elevate the jute industry it is mandatory to explore the various jute genotypes for the improvement of quality as well as quantity of fiber yield content. Since jute is a self-pollinated crop, the presence of genetic variation is very limited (La Farge *et al*.1997). Hence, it is need for the breeders to study the available variability among the jute genotypes for the further improvement program.

Fiber yield and its attributing parameters are the most widely targeted traits for jute improvement program worldwide. The improvement of a crop is largely dependent on the degree of available genetic variability and its heritability of desired characters into its next generation. The success of any breeding program can be improved when the available variability within the existing germplasm is more which helps the plant breeder to produce new varieties or to improve the already existing genotypes. Therefore, the knowledge of genetic parameters is important for any crop improvement program. The objective of this study was to explore the genetic parameters of jute which includes genotypic, phenotypic and environmental variations, genotypic correlation, broad sense heritability along with genetic advance for the further improvement of jute.

MATERIALS AND METHODS

The experiment was conducted at the Agricultural Instructional Farm, Uttar Banga Krishi Vishwavidhyalaya (UBKV), Cooch Behar, West Bengal. Fifty-two tossa jute (*C. olitorius* L.) accessions were obtained from ICAR - Central Research institute for Jute and Allied Fibers (ICAR-CRIJAF), Barrackpore, West Bengal. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The data was recorded on five randomly selected plants from each accession in each replication leaving the border rows to avoid the sampling error. All the observations were recorded using standard methodology. Readings from five plants were averaged in the three replications and the mean data was subjected to statistical analysis for yield and its attributing traits. The parameters observed were plant height (cm), basal diameter (cm), green weight (g/plant) and fiber yield (g/plant). The means of the traits over the replications were used for statistical analysis. Genetic diversity was studied using Mahalanobis (1936) generalized distance (D^2) extended by Rao (1952). Based on D^2 values, the jute accessions were grouped into clusters following the method suggested by Tocher (Rao 1952). Intra and inter cluster distances were calculated using the method suggested by Singh and Chaudury (1985) and the statistical analysis was carried out using the IRRI software STAR (Version 2.0.1), January 2014. The genotypic and phenotypic variances as well as heritability were estimated according to the formula given by Johnson *et al*. (1955). Genotypic and phenotypic coefficient of variance was estimated according to the formula suggested by Burton and Singh *et al*. (1997) and categorized according to Siva subramanian and Menon (1973). Estimation of genetic advance was calculated following Robinson *et al*. (1949) and GA% was calculated by the formula suggested by Johnson *et al*. (1955).

Computation of rescaled index value

According to Iyengar and Sudharshan (1982), rescaling index approach was formulated for 52 white jute accessions for four traits.

$$Y_{id} = (X_{id} - \text{Min } X_{id})/(\text{Max } X_{id} - \text{Min } X_{id})$$

Where X_{id} = mean of the character, Min X_{id} and Max X_{id} are the minimum and maximum of ($Xi1$, X_{i2}……X_{in}) respectively. The above formula for fiber yield was used for charcters that are moves towards positive direction ie., character which on enhancement is not expected to reduce fiber yield like plant height, basal diameter, green weight and fiber yield. In these characters the genotypes with the highest value would have one (1) and the one with the lowest rescaled index value zero (0). In case of characters which were considered negative like the disease and insect pest incidence the genotypes with the lowest value scored the highest rescaled index value of 1 and the genotypes with the highest value

Table 1. ANOVA for fiber yield components in tossa jute (*C. olitorius* L.) germplasm combined over two years (2006 and 2007). * Significant at 5% probability level, ** Significant at 1% probability level.

Sources of variation	df	Mean sum of squares			
		Plant height (cm)	Basal diameter (cm)	Green weight (g/plant)	Fiber yield (g/plant)
Year	1	1974675.143**	2.028**	100378.253**	634.895**
Error	4	836.081	0.091	1341.398	5.751
Genotypes	51	2484.66**	0.050**	4969.178**	17.776**
Year × Genotypes	51	4398.832**	0.064**	8365.665**	28.335**
Error	204	515.506	0.021	248.656	0.804

scored the lowest rescaled index value. At the end, all the rescaled index values were added up and then the genotypes were ranked accordingly. The rescaled index values were unitless and were summed up to a total value and there after the ranking of the genotypes was done on the basis of this total index.

RESULTS AND DISCUSSION

The analysis of variance of all the 52 tossa jute germplasm accessions (Table 1) showed significant variation among the years, genotypes and the year × genotype interaction, for all the four characters under present study. This indicated the presence of considerable variability and genetic worth of the genotypes which provides an adequate scope for the selection of superior genotypes, that provides us the variability for the improvement of genetic yield potential of tossa jute.

According to Arunachalam (1981), genetic variability among the available germplasm is an important information for plant breeders for an efficient selection of parents for hybridization program, since diverse parents contribute to desirable segregants. Therefore, the selection of parents through divergence analysis would be more efficient for any hybridization program. Based on Mahalanobis (1936) D^2 analysis, 52 tossa jute germplasms were grouped in four different clusters (Table 2). The highest number of accessions (30) were grouped into cluster I followed by cluster IV (18), and cluster II (2) and Cluster III (2). Maximum inter-cluster distance was observed between cluster I and cluster IV (20.441), followed by cluster II and cluster IV (15.908), cluster I and cluster II (18.605), Cluster III and cluster IV (13.607), cluster II and cluster III (11.478) and between cluster I and cluster III (10.222) (Table 3). The maximum intra-cluster distance was observed in cluster IV (22.518) followed by cluster I (17.437), cluster III (0.597) and cluster II (0.429). The maximum inter-cluster distance between cluster I and cluster IV followed by cluster I and cluster II (18.605), indicated that the genetic variation is very distinct among the groups and if the genotypes from these groups are used for hybridization, they may produce a wide spectrum of segregating population. The lowest inter-cluster distance was expressed by

Table 2. Distribution of 52 tossa jute germplasm accessions in 5 clusters.

Cluster No.	Total no. of germplasm accessions	Source	Name of germplasm accessions
I	30	ICAR-CRIJAF, Barrackpore, Kolkata, West Bengal	OIN-901, OIN-907, OIN-911, OIN-913, OIN-915, OIN-916, OIN-921, OIN-926, OIN-936, OIN-937, OIN-941, OIN-955, OIN-959, OIN-962, OIN-970, OIN-975, OIN-976, OIN-977, OIN-981, OIN-984, OIN-986, OIN-990, OIN-993, OIN-994, OIJ-168, OIJ-172, OIJ-213, OIJ-214, OIJ-216 and OIJ-266.
II	2	-do-	OIJ-233 and OIJ-253
III	2	-do-	OIJ-227 and OEX-019
IV	18	-do-	OIJ-218, OIJ-228, OIJ-239, OIJ-246, OIJ-257, OIJ-263, OIJ-264, OIJ-282, OIJ-284, OIJ-299, OEX-008, OEX-025, OEX- 041, JRO-524 and JRO-8432

Table 3. Average intra (diagonal) and inter-cluster (off-diagonal) D values in tossa jute.

Cluster	I	II	III	IV
I	17.437	18.605	10.222	20.441
II		0.429	11.478	15.908
III			0.597	13.607
IV				22.518

Cluster I and cluster III (10.222) followed by cluster II and cluster III (11.478), suggesting a close relationship among these three clusters and the genotypes belonging to these clusters cannot be selected as parents for hybridization program. It is to be noted that the average intra-cluster distances were lower than the average inter-cluster distances indicating the presence of wide genetic variability among the genotypes of different clusters than the genotypes present on the same cluster. Similar results were also found by Jatothu *et al*. (2018) and Islam *et al*. (2021). The intra-cluster distances were very low in case of Cluster I, II and III indicating the homogeneity of the jute genotypes within the clusters.

Three cluster combinations were computed by using the four clusters (Table 4). The first cluster combination comprised of cluster I and cluster IV with a inter cluster distance of 20.422. Two genotypes OIJ-941 and OIJ-218 with distance of 160 were selected in this cluster combination. The second cluster combination comprised of cluster I and cluster IV with inter cluster distance of 20.441. Two genotypes namely OIN-926 and OIJ-282 with a distance of 137 were selected from the clusters. The third cluster combination comprised of cluster I and cluster II with an inter-cluster distance of 18.605. From this cluster combination, two genotypes (OIJ-216 and OIJ-218) were selected with a distance of 153. Hence, it can be concluded that, the genotypes OIJ-941 and OIJ-218 from cluster I and IV represented the most diverge genotypes which may be selected as parents for crossing program followed by OIJ – 216 and OIJ-218 form cluster I and II at a distance of 153.

Table 4. Distribution of genetically divergent clusters and distance between the tossa jute genotypes selected.

Cluster combination	Inter-cluster distance (D^2 value)	Genotype selected from the cluster	Distance between the selected genotypes (D^2 value)
I and IV	20.441	11 and 30 (OIJ-941 and OIJ-218)	160
I and IV	20.441	8 and 41 (OIN-926 and OIJ-282)	137
I and II	18.605	29 and 30 (OIJ-216 and OIJ-218)	153

Table 5. Cluster mean for the four characters in tossa jute.

Cluster	Plant height (cm)	Basal diameter (cm)	Green weight (g/plant)	Fiber yield (g/plant)
I	288.103	1.157	158.376	9.296
II	302.150	1.218	156.747	9.832
III	284.125	1.175	146.942	8.623
IV	283.511	1.154	156.219	9.404
Population mean	217.03	1.96	157.127	9.328
Percent contribution	9.05	5.81	31.15	54.00

The cluster mean for all the four characters are given in the Table 5. For the trait plant height cluster II possess the highest mean value of plant height (302.15 cm), basal diameter (1.21 cm) and for fiber yield (9.832 g/plant). Cluster I possessed the highest mean value for green weight (158.376). Fiber yield exhibited the highest percent contribution (54%), followed by green weight (31.15%), plant height (9.5%) and basal diameter (5.81%) towards total divergence.

The mean performance and the total rescaled index value for all the 52 tossa jute accessions including two checks over two years (Table 6) revealed that the highest mean was exhibited by OIN-975 (340.77 cm) for plant height. For the basal diameter, the jute accession OIJ-218 attained the highest mean value of 1.41 cm. In case of green weight and fiber yield, OIN-956 expressed the highest mean value of 226.68 g/plant and 13.25 g/plant respectively. On the basis of total rescaled index value, the accession OIJ-218 (Total RI = 4.193) attained rank 1 followed by OIN-915 (Total RI = 3.532) at rank 2, OIN-975 (Total RI = 3.420) at rank 3, OIN-926 (Total RI =3.273) at rank 4 and OEX-025 (Total RI =3.050) at rank 5.

The basic knowledge of genetic variability is an important tool for any crop improvement program. Commonly, the variability that is already present in the population is measured by genotypic coefficient of variation (GCV) and phenotypic coefficient of

Table 6. Mean performance and ranking of the 52 tossa jute accessions along with two checks, over two years 2006 and 2007 on the basis of rescaled index value of each germplasm accession.

Sl. No.	Germplasm accession	Plant height (cm)	Rescaled index Value (A)	Basal diameter (cm)	Rescaled index value (B)	Green weight (g/plant)	Rescaled index value (C)	Fiber yield (g/plant)	Rescaled index value (D)	Total rescaled index value (A+B+C+D)	Ranks on the basis of total rescaled index value
1	OIN-901	277.77	0.33	1.06	0.26	130.43	0.24	7.58	0.23	1.0663	46
2	OIN-907	295.58	0.52	1.17	0.49	159.63	0.47	9.23	0.46	1.9354	21
3	OIN-911	293.60	0.50	1.20	0.55	183.45	0.66	10.95	0.69	2.3969	10
4	OIN-913	310.17	0.67	1.32	0.80	192.03	0.73	11.25	0.73	2.9285	6
5	OIN-915	328.17	0.87	1.32	0.80	218.04	0.93	12.78	0.94	3.5322	2
6	OIN-916	316.22	0.74	1.16	0.46	155.95	0.44	9.12	0.44	2.0838	14
7	OIN-921	272.93	0.28	1.14	0.43	147.21	0.37	8.71	0.39	1.4684	36
8	OIN-926	306.05	0.63	1.24	0.64	226.68	1.00	13.25	1.00	3.2730	4
9	OIN-936	291.63	0.48	1.16	0.47	164.24	0.51	9.66	0.52	1.9667	17
10	OIN-937	290.07	0.46	1.16	0.46	166.21	0.52	9.67	0.52	1.9607	18
11	OIN-941	271.78	0.26	1.06	0.26	112.25	0.10	6.49	0.09	0.7116	49
12	OIN-955	257.05	0.11	1.12	0.38	140.74	0.32	8.26	0.33	1.1321	45
13	OIN-959	288.43	0.44	1.15	0.45	148.88	0.39	8.65	0.38	1.6535	31
14	OIN-962	276.28	0.31	1.12	0.38	136.69	0.29	7.95	0.28	1.2634	42
15	OIN-970	306.22	0.63	1.18	0.50	162.68	0.49	9.48	0.49	2.1206	13
16	OIN-975	340.77	1.00	1.27	0.70	207.97	0.85	12.28	0.87	3.4207	3
17	OIN-976	285.75	0.41	1.08	0.31	135.93	0.28	8.09	0.30	1.3062	41
18	OIN-977	277.33	0.32	1.14	0.42	160.23	0.48	9.70	0.52	1.7393	25
19	OIN-981	259.90	0.14	1.19	0.53	159.18	0.47	9.20	0.45	1.5822	34
20	OIN-984	272.00	0.27	1.19	0.53	139.77	0.31	7.95	0.28	1.3898	38
21	OIN-986	304.23	0.61	1.24	0.63	163.47	0.50	9.30	0.47	2.2074	12
22	OIN-990	294.65	0.51	1.10	0.34	157.76	0.46	9.08	0.44	1.7370	26
23	OIN-993	268.95	0.23	1.19	0.53	171.56	0.56	10.39	0.61	1.9376	20
24	OIN-994	284.60	0.40	1.16	0.46	163.11	0.50	9.28	0.46	1.8244	23
25	OIJ-168	287.63	0.43	1.14	0.43	133.68	0.27	7.91	0.28	1.4102	37
26	OIJ-172	284.15	0.40	1.17	0.49	160.07	0.47	9.56	0.50	1.8611	22
27	OIJ-213	268.35	0.23	1.01	0.16	123.61	0.19	7.60	0.24	0.8101	47
28	OIJ-214	306.07	0.63	1.20	0.56	189.28	0.70	11.29	0.74	2.6290	8
29	OIJ-216	247.00	0.00	0.94	0.00	105.26	0.04	6.34	0.07	0.1080	52
30	OIJ-218	329.33	0.88	1.41	1.00	241.69	1.12	14.71	1.20	4.1938	1
31	OIJ-227	282.03	0.37	1.19	0.53	145.84	0.36	8.51	0.36	1.6196	32
32	OIJ-228	277.73	0.33	1.11	0.36	128.29	0.22	7.57	0.23	1.1464	44
33	OIJ-233	297.33	0.54	1.20	0.55	153.71	0.42	9.68	0.52	2.0312	15
34	OIJ-239	288.73	0.45	1.20	0.55	139.86	0.31	8.69	0.38	1.6963	27
35	OIJ-246	279.93	0.35	1.19	0.53	161.89	0.49	10.05	0.57	1.9388	19
36	OIJ-253	306.97	0.64	1.24	0.63	159.78	0.47	9.98	0.56	2.2997	11
37	OIJ-257	278.78	0.34	1.07	0.28	142.87	0.34	9.05	0.43	1.3891	39
38	OIJ-263	295.67	0.52	1.11	0.36	143.81	0.35	8.53	0.36	1.5904	33
39	OIJ-264	260.68	0.15	1.09	0.33	145.85	0.36	8.33	0.33	1.1702	43
40	OIJ-266	279.77	0.35	1.15	0.44	135.32	0.28	7.87	0.27	1.3423	40
41	OIJ-282	248.33	0.01	1.05	0.24	100.02	0.00	5.85	0.00	0.2520	51
42	OIJ-284	259.72	0.14	1.03	0.20	125.45	0.20	7.71	0.25	0.7831	48
43	OIJ-299	249.87	0.03	0.95	0.03	125.88	0.20	7.67	0.25	0.5076	50
44	OEX-008	285.78	0.41	1.16	0.47	148.14	0.38	8.99	0.42	1.6867	28
45	OEX-014	308.05	0.65	1.28	0.71	193.06	0.73	11.68	0.79	2.8873	7
46	OEX-019	286.22	0.42	1.16	0.47	148.05	0.38	8.74	0.39	1.6627	30
47	OEX-024	269.48	0.24	1.21	0.57	163.24	0.50	9.47	0.49	1.8012	24
48	OEX-025	301.05	0.58	1.31	0.78	206.45	0.84	12.14	0.85	3.0507	5
49	OEX-039	312.10	0.69	1.30	0.76	167.52	0.53	9.91	0.55	2.5380	9
50	OEX-041	291.55	0.48	1.07	0.27	146.17	0.36	8.96	0.42	1.5324	35

Table 6. Continued.

Sl. No.	Germplasm accession	Plant height (cm)	Rescaled index Value (A)	Basal diameter (cm)	Rescaled index value (B)	Green weight (g/plant)	Rescaled index value (C)	Fiber yield (g/plant)	Rescaled index value (D)	Total rescaled index value (A+B+C+D)	Ranks on the basis of total rescaled index value
51	JRO-524	276.95	0.32	1.08	0.29	163.84	0.50	9.91	0.55	1.6664	29
52	JRO-8432	289.45	0.45	1.16	0.46	167.92	0.54	10.06	0.57	2.0203	16
	Mean	286.90		1.159		157.127		9.328			
	CV (%)	7.91		12.47		10.04		9.62			
	Sem (±)	9.27		0.0589		6.4376		0.3661			
	CD (P=0.05)	25.8		0.164		17.945		1.021			

variation (PCV). The estimates of different statistical parameters mean, range, standard deviation, GCV and PCV, heritability (broad sense), genetic advance as percentage of mean are presented in Table 7. Plant height and basal diameter revealed a low GCV whereas, green weight and fiber yield expressed moderate GCV and PCV. The magnitude of PCV was higher than that of GCV for all the traits indicating the influence of the environment in the phenotypic expression of these traits. Also, none of the characters exhibited high GCV and PCV whereas, green weight and fiber yield showed a moderate GCV and PCV. Plant height and basal diameter exhibited a moderate heritability whereas, green weight and fiber yield expressed high heritability. Low genetic advance was noticed for plant height and basal diameter and high genetic advance was observed for green weight and fiber yield. Green weight and fiber yield exhibited a high heritability of 0.84 and 0.85 respectively, coupled with high genetic advance as percentage of mean (33% and 34% respectively). Similar findings were reported by Ghosh *et al*. (2020) in tossa jute. Therefore, green weight and fiber yield can be considered as reliable selection criteria for crop improvement in terms of fiber yield and its attributing traits in tossa jute.

Statistically, correlation coefficient is used to know about the kind of association of characters. It helps the breeders to select the component traits that are useful in the process of selection. The correlation study between fiber yield and its components provides us the information regarding the involvement of those characters in enhancing the yield that eventually is useful to implement the crop improvement program. In the present investigation, all the four traits such as plant height, basal diameter, green weight and fiber yield exhibited high level of positive significance (Table 8) and result indicated that the higher magnitude of genotypic coefficient of variation for these characters provide us a better opportunity for the improvement through selection. Similar findings were also reported by Sardana *et al*. (1990), Ghosh *et al*. (2021) and Islam *et al*. (2001).

Path coefficient is a ratio of standard deviation of the effect due to a given cause (independent variable) to the total standard deviation of effect (dependent variable). Usually, simple correlation study does not provide us the exact information on the role of direct and indirect effects of each of the component characters towards yield. Path coefficient analysis is used to overcome this drawback by separating the correlation coefficient into direct and indirect effects. From Table 9, it is observed that all the three characters such as

Table 7. Genetic parameters for the different characters of 77 genotypes of white jute (*C. capsularis* L.).

Characters	Mean	Range	Standard deviation	GCV	PCV	Heritability (broad sense)	GA as percentage of mean
Plant height (cm)	286.90	247.10-340.77	20.35	6.263	8.513	0.541	9.491
Basal diameter (cm)	1.159	0.94-1.41	0.09	5.953	10.727	0.308	6.806
Green weight (g/plant)	157.127	100.02-241.69	28.78	17.767	19.365	0.842	33.581
Fiber yield (g/plant)	9.328	5.85-14.71	1.72	17.957	19.404	0.856	34.231

Table 8. Genotypic correlation between fiber yield components in tossa jute. * Significant at 5% probability level, ** Significant at 1% probability level.

Characters	Basal diameter (cm)	Green weight (g/plant)	Fiber yield (g/plant)
Plant height (cm)	0.838*	0.819*	0.817*
Basal diameter (cm)		0.993*	0.917*
Green weight (g/plant)			0.992*

plant height, basal diameter and green weight have highly significant positive effect on fiber yield, indicating the direct effect of all above mentioned traits on fiber yield which favours the improvement of yield through selection. Similar findings were reported by Mandel *et al*. (1980) and Akter *et al*. (2005).

Principal component analysis (PCA) is a multivariate statistical technique which is used in several studies to access the relationship between the various characters and clustering the genotypes. In the present study PCA was used to depict the correlation between the morphological traits. A matrix of mean values of two years was used to draw the correlation between the traits under study. The PCA revealed four principal components which are presented in Table 10. Estimation of relative contribution of characters towards the variation in the accession's PC1, PC2, PC3 and PC4 respectively explained 86.91%, 7.71%, 5.14% and 0.24% of the total variability. Out of the four principal components, only PC1 exhibited eigen value more than one and therefore PC1 can be given

Table 9. Direct (diagonal) and indirect (off-diagonal) effects of different yield components on fiber yield in tossa jute. * Significant at 5% probability level, ** Significant at 1% probability level. Residual effect = 0.124.

Characters	Plant height (cm)	Basal diameter (cm)	Green weight (g/plant)	Correlation with fiber yield (g/plant)
Plant height (cm)	0.01146	-0.01984	0.82511	0.817*
Basal diameter (cm)	0.00960	-0.02367	1.03059	0.917*
Green weight (g/plant)	0.00939	-0.02422	1.00713	0.992*

Table 10. Summary of the contribution of the principal components to variability.

Components	Eigen value	Percent of cumulative variance	Total variance
PC1	3.4764	86.91	86.91
PC2	0.3083	7.71	94.62
PC3	0.2056	5.14	99.76
PC4	0.0097	0.24	100.00

more importance for further explanation. There is no standard test to prove the significance of eigen values and coefficients (Jolliffe 2002). Therefore, it is concluded that selecting genotypes from PC1 will initiate the selection process for a successful hybridization program as it would contribute maximum diversity with high eigen value. Four principal components along with their factor loadings (Table 11) show that each trait contributing equally to the total variation in 52 jute accessions would make a good parental source for hybridization. Similar finding was also reported by Sawarkar (2015).

According to Chakravorty *et al*. (2013), the characters which are coming together in different principal components explains the variability, showing the tendency to remain together and it should be taken into consideration during the study of these characters in the further breeding program. The PCA plot generated

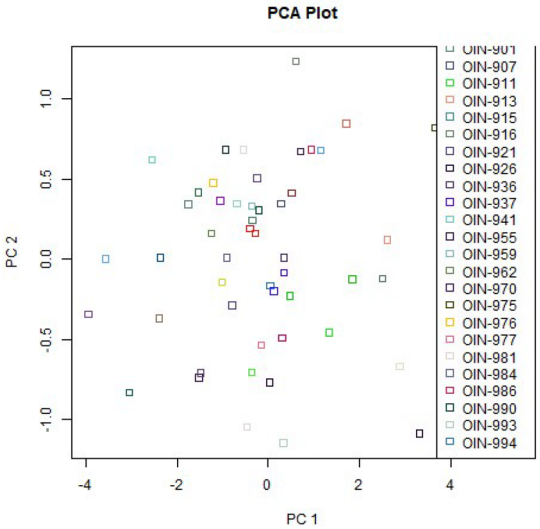

Fig. 1. PCA plot for PC 1 and PC 2.

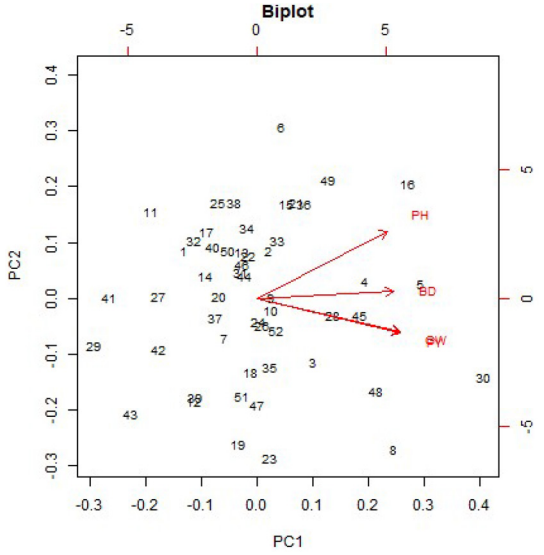

Fig. 2. Biplot for PC 1 and PC 2.

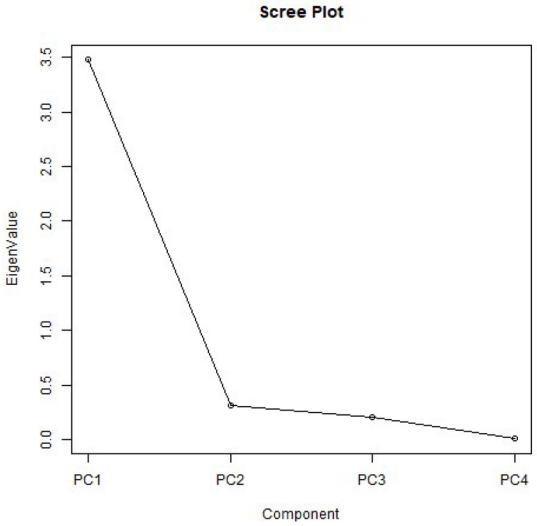

Fig. 4. Scree plot for the different principal components.

for PC1 and PC2 showed a moderate correlation between the jute genotypes (Fig. 1). The biplot analysis between PC1 and PC2 indicated that the accession OIN-975 possessed a positive correlation and it was mainly determined by plant height (cm). Similarly OIN-915 was highly influenced by basal diameter and OIJ-218 was influenced by green weight (Fig. 2). It is to be noted that the accessions OIJ-218, OIN-915 and OIN-975 which are highly influenced by green weight, basal diameter and plant height respectively, have secured the first, second and third rank in the rescaled index. Already, it is proved in the present study that these three traits are significantly correlated with yield. Hence, by selecting these three accessions for further breeding process will definitely help in the improvement of fibre yield in tossa jute.

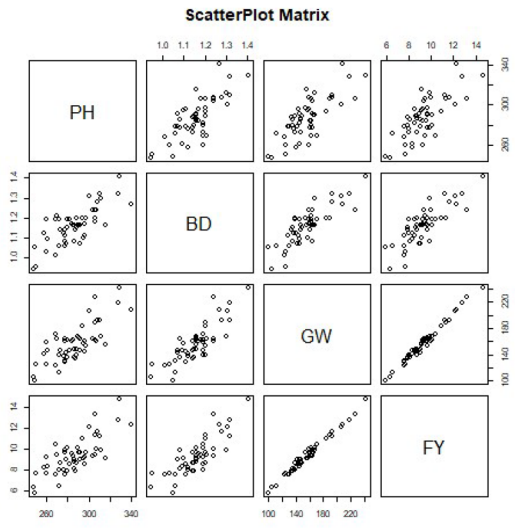

Fig. 3. Scatter plot depicting the variability in the genotypes and correlation between the traits.

The scatter plot matrix (Fig. 3) revealed a positive correlation for all the traits. Green weight showed a perfect positive correlation with fiber yield whereas other traits showed a weak correlation in between the accessions. The scree plot was generated for all the four principal components with respect to their eigen value (Fig. 4) and it showed that there was a sudden deviation in the slope after PC1 and became a normal continuous slope from PC2 towards PC3 and PC4.

CONCLUSION

The present investigation suggests that plant height, basal diameter, green weight and fiber yield would be a useful selection parameter to produce high fiber yielding jute varieties. According to the rescaled index value on the basis of all the traits together, three genotypes namely OIJ-218, OIN-915 and OIN-975 which secured the first three ranks can be used as one of the parental sources for further hybridization

process. Since green weight and fiber yield revealed high heritability coupled with high genetic advance hence these traits can be given more weightage during selection.

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