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## VARIABILITY AND MULTIVARIATE ANALYSIS IN WHITE JUTE (*CORCHORUS CAPSULARIS* L.) FOR YIELD ATTRIBUTING TRAITS AND BIOTIC STRESS COMPONENTS

S. K. Roy<sup>1</sup>, B. Thapa<sup>2\*</sup>, S. Vishnupriya<sup>1</sup>, B. Maying<sup>1</sup>, B. Sur<sup>1</sup>, M. Chakraborty<sup>1</sup>, L. Hijam<sup>1</sup>, S. Rout<sup>3</sup>,  
S. Das<sup>4</sup>, A. Roy<sup>5</sup> and G. Chakraborty<sup>6</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, U.B.K.V., Cooch Behar - 736 165, West Bengal, India.

<sup>2</sup>AICRP on Medicinal and Aromatic Plants, RRS, U.B.K.V., Kalimpong - 734 301, West Bengal, India.

<sup>3</sup>Department of Genetics and Plant Breeding, CUTM, Paralakhemundi - 761 200, Odisha, India.

<sup>4</sup>AICW & BIP, U.B.K.V., Pundibari, Cooch Behar, West Bengal (736165), India

<sup>5</sup>Department of Plant Pathology, U.B.K.V., Cooch Behar - 736 165, West Bengal, India.

<sup>6</sup>Department of Agricultural Entomology, B.C.K.V., Mohanpur, Nadia - 741 252, West Bengal, India.

\*Corresponding author E-mail : [bandan@ubkv.ac.in](mailto:bandan@ubkv.ac.in)

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### ABSTRACT

An experiment was conducted at Agricultural instructional and Research Farm, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, West Bengal, India to study and evaluate the performance of 77 white jute (*Corchorus capsularis* L.) genotypes for their variability. It was found that the white jute genotypes differed significantly for all the traits except root rot incidence. The D<sup>2</sup> analysis grouped 77 white jute accessions into three clusters. The genotypic co-efficient of variation (GCV) was moderate for green weight (14.60), yellow mite incidence (16.44) semi looper incidence (16.13) stem rot (14.63) and fibre yield (12.84). A high genetic advance and broad sense heritability was observed in the case of yellow mite incidence (28.99% & 0.73) and semilooper incidence (29.17% & 0.77) indicating the presence of additive gene action. The genotypic correlation analysis revealed that fibre yield was positively correlated with plant height (0.97\*\*), basal diameter (0.96\*\*), green weight (0.93\*\*), semilooper incidence (0.30\*\*) and stem rot (0.64\*\*). The path analysis revealed that plant height (0.97), basal diameter (0.96), green weight (0.93) and root rot incidence (0.97) had the maximum direct effect on fibre yield. Eight principal components were identified through Principal Component Analysis (PCA) and three principal components (PC1, PC2 and PC3) were found to have eigen values more than one. The traits fibre yield (0.49) and basal diameter (0.48) had the maximum positive value in PC 1. The total Rescaled Index (RI) ranking of genotypes revealed that CEX- 22 ranked first followed by JRC 517 (Check -1).

**Key words :** Correlation, Diversity, Jute, Path-analysis, Principal-components, Rescaled index.

### Introduction

Jute is a plant-based biodegradable lingo-cellulosic natural fibre producing crop bearing chromosome number  $2n=2x=14$  belonging the genus *Corchorus* and family Tiliaceae. Jute fibre is a secondary phloem fibre or bast fibre obtained from the bark of the stem of two cultivated species, namely *C. capsularis* L. and *C. oleriorius* by microbial breakdown (Yumnam *et al.*, 2015; Mukul, 2020). *C. capsularis* L. is more adaptable than other

cultivated species and can grow both in low and high land. *Corchorus* sp. is a member of the Malvaceae family with chromosome no.  $2n=2x=14$ , which includes 50–60 species that have become naturalised as annual herbs in tropical and subtropical parts of Africa, America, Australia, and Asia (Kundu *et al.*, 2013). It is also called Golden fibre due to its silky and golden texture making it important next to cotton in terms of global production, consumption and availability (Jana *et al.*, 2020; Miah *et al.*, 2020).

The selection of Jute varieties with finer and high-quality fibre which gained considerable attention over the years in China, Bangladesh, and India (Islam and Ali, 2017).

In 2020-21, India produced 0.434 million bales of raw jute fibre from 38.16 ha of land, with an average productivity of 2051 kg ha<sup>-1</sup> (Anonymous, 2022). India exported 20.5 mt of raw jute worth ₹ 120.93 crores in 2020-21. The yield levels of cultivated varieties have plateaued and with the increasing demand for this biodegradable fibre from western countries, there is an urgent need to increase yield levels and acreage with new promising high yielding varieties. The majority of the released varieties were generated from a small number of parents, resulting in a genetic base that is too limited for future crop development programmes (Benor *et al.*, 2012; Kundu *et al.*, 2013). It is a self-pollinated crop with narrow genetic base for which it becomes difficult for the plant breeders to develop potential high yielding varieties with the help existing germplasm as a result of which limited success has been attained to break the yield plateau (Sawarkar *et al.*, 2015).

High heterotic effects and desirable segregates are likely to be produced by the genetically diverse parents. Taking this into account, jute breeders have grown increasingly cognizant of the necessity of preserving genetic variety among types and strengthening the management of genetic resources through the preservation of traditional land races and germplasm (Das and Kumar, 2016). Jute genetic resources can be characterised morphologically to reveal the collection's richness and variability as well as to pinpoint key features (Satya *et al.*, 2014). The understanding of genetic parameters for fibre yield and yield attributing characters will allow the breeders to precisely execute their breeding and selection programmes (Anil Kumar *et al.*, 2016).

Semilooper and yellow mite are two of the most common and serious pests in jute which damages both cultivated species. It has been documented from every jute-growing region in the world and in some cases, is estimated to have damaged up to 90% of the plant's leaves (Hossain *et al.*, 2013). Yellow mite infestations have been increasingly frequent and severe in recent years, even reaching the level of outbreaks in a small number of jute-growing regions, especially during the crop's active growth period (Satpathy *et al.*, 2019). Keeping this in view, the present investigation was undertaken to measure the genetic variability, genetic diversity of 77 white jute (*C. capsularis*) cultivars for yield attributing and biotic stress attributing traits to identify suitable parents for improvement this species.

## Materials and Methods

The experimental material for the study comprised 77 white jute (*C. capsularis* L.) accessions, which were obtained from ICAR-Central Research Institute for Jute and allied Fibres, Barrackpore, West Bengal, India under the project AINP on Jute and Allied Fibres. The experiment was laid out in randomized complete block design (RBCD) with three replications at Agricultural instructional and Research Farm, Uttar Banga Krishi Vishwavidhyalaya, Pundibari, Coochbehar, West Bengal, India situated at of 26.5243° N latitude and 89.1075° E longitude April July over two years (2013 and 2014). The experiment was conducted during the months of. The details of weather parameters during the growth period of white jute are given in Table 1.

Observations were recorded on five randomly selected plants per replication for plant height (cm), basal diameter (cm), green weight (g plant<sup>-1</sup>), yellow mite incidence (number cm<sup>-2</sup> area), semilooper incidence (%), stem rot (PDI), root rot incidence (%) and fibre yield (g plant<sup>-1</sup>). The analysis of variance (ANOVA) was carried out for all the traits and then data was analyzed following multivariate analysis of Mahalanobis (1936) and genotypes were grouped into different clusters following Tocher's method (Rao, 1952) followed by Principal component analysis.

The genotypic and phenotypic components of variance were computed according to formulae suggested by Lush (1940) and Choudhary and Prasad (1968) for the observed statistics. The genotypic and phenotypic coefficients of variation were computed according to Burton and Devane (1953) and expressed as a percentage.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was categorized as low (0–10%), moderate (10–20%) and high (>20) as suggested by Sivasubramanian and Menon (1973). Broad sense heritability ( $h^2_b$ ) was estimated as the ratio of genotypic variance to phenotypic variance and expressed as a percentage. Heritability in the broad sense was categorized as low (0–30%), moderate (30–60%) and high (>60%) as described by Robinson *et al.* (1949). The extent of genetic advance to be expected by selecting 5% of the superior progeny was calculated using the following formula given by Robinson *et al.* (1949). Then genetic advance as a percent of the mean (GAM) was calculated. GAM was categorized as low (0–10%), moderate (10–20%) and high (>20) as suggested by Johnson *et al.* (1955). Microsoft Office Excel 2010 software was used for data entry and processing.

**Table 1** : Details of weather parameters during white jute (*C. capsularis* L.) germplasm growth period in 2013 and 2014.

Months	Temperature (°C)				Relative Humidity (%)				Total Rainfall (mm)	
	2013		2014		2013		2014		2013	2014
	Max	Min	Max	Min	Max	Min	Max	Min		
March	30.27	16.72	30.70	15.50	98.87	41.87	66.00	53.00	0.00	19.20
April	30.33	20.15	34.80	18.80	96.03	53.57	53.00	46.00	122.50	9.80
May	30.44	23.08	32.10	22.60	98.84	70.81	78.00	72.00	251.00	312.00
June	32.30	25.38	32.50	24.90	99.00	74.33	89.00	82.00	404.00	604.30
July	31.74	25.86	33.40	26.00	99.00	77.16	84.00	79.00	757.50	297.30
August	32.02	25.32	31.60	25.40	99.00	75.74	89.00	86.00	343.05	451.30
September	31.81	24.61	31.60	24.30	99.00	75.00	90.00	86.00	404.00	380.40

Analysis of variance (ANOVA), D<sup>2</sup> analysis, genetic parameters, genotypic correlation and genotypic path analysis was carried out using the software Genres (GENRES 1994, Version 3.11). Principal component analysis was computed using the IIRRI software STAR (Version 2.0.1, January 2014).

An overall ranking of 77 white jute accessions was performed for eight traits using Iyengar and Sudarshan's (1982) rescaling index approach.

$$Y_{id} = (X_{id} - \text{Min } X_{id}) / (\text{Max } X_{id} - \text{Min } X_{id}) \quad (1)$$

Where,  $X_{id}$  = mean of the trait,  $\text{Min } X_{id}$  and  $\text{Max } X_{id}$  are the minimum and maximum of ( $X_{i1}, X_{i2} \dots X_{in}$ ), respectively. The aforesaid formula for yield was used for positive traits *i.e.*, a trait which on enhancement is not expected to reduce fibre yields like plant height, basal diameter, green weight and fibre yield. In these traits, the genotypes with the highest value would have one (1) and the one with the lowest rescaled index value zero (0). In the case of traits that 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 scored the lowest rescaled index value. In the end, all the rescaled index values were added up and then the genotypes were ranked accordingly. The rescaled index values were unit less and were summed up to a total value and thereafter the ranking of the genotypes was done based on this total index. A similar ranking of genotypes has earlier been done by Rout *et al.* (2019).

## Results and Discussion

The ANOVA revealed that there was a significant difference among the genotypes for all the traits except root rot incidence, studied based on pooled mean data indicating the presence of wide variability in the white jute germplasm under the present study (Table 2). The mean performance of the 75 white jute accessions along with two checks over two years 2013-14 and 2014-15

are given in Table 3. The highest mean for the trait plant height was achieved by the check JRC 698+ (316.60 cm), CEX-22 (2.29 cm) for basal diameter, CEX-22 (447.33 gplant<sup>-1</sup>) for green weight, CIN-210 (35.15 number cm<sup>2</sup> area) for yellow mite incidence, CEX-28 (13.91%) for semilooper incidence, JRC 517+ (12.48 PDI) for stem rot, CIN 80 (8.88%) for root rot incidence and CIN 64 (17.37 gplant<sup>-1</sup>) for fibre yield. The overall mean was estimated for the traits plant height (273.48 cm), basal diameter (1.76 cm), green weight (252.46 gplant<sup>-1</sup>), yellow mite incidence (12.08 number cm<sup>2</sup> area), semilooper incidence (9.77%), stem rot (8.92 PDI), root rot (3.28%) and fibre yield (12.62 gplant<sup>-1</sup>). According to Mukul *et al.* (2021), genotypes with the highest plant height and basal diameter yield more fibre than other varieties. Hence, the jute accessions JRC 698+ (Check) and CEX-22, which possesses the maximum mean can be used as the parent for further crossing programs especially, when the objective is increasing the fibre content.

Traditionally, genetic divergence studies are based on differences in qualitative traits and morphological traits. Therefore, in the present investigation, genetic diversity present in 77 genotypes has been analyzed using D<sup>2</sup> analysis for genetic improvement for eight quantitative traits. Based on D<sup>2</sup> analysis, 77 accessions were grouped into three clusters (Table 4). A maximum number of genotypes were grouped into cluster II, which consisted of 40 accessions followed by cluster I, which included 29 accessions and finally cluster III included eight accessions. The intra cluster distance varied from 17.783 to 23.063 (Table 5). The maximum intra cluster distance was exhibited by cluster III (23.063) followed by cluster II (18.531) and by cluster I (17.783). This indicated that the genotypes in cluster III were highly divergent and could be selected as parents for a crossing program. The maximum inter cluster distance was observed between cluster I and cluster III (29.305) followed by cluster II

**Table 2:** ANOVA for fibre yield components, insect pest and disease incidence in white jute (*C. capsularis* L.) germplasm combined over two years (2013 and 2014).

Sources of variation	df	Mean Sum of Squares							
		Plant height (cm)	Basal diameter (cm)	Green weight (g plant <sup>-1</sup> )	Yellow mite incidence (number cm <sup>2</sup> area)	Semilooper incidence (%)	Stem rot (PDI)	Root Rot incidence (%)	Fibre yield (g plant <sup>-1</sup> )
Location	1	128290.00**	1.80*	412143.86*	95.22	7282.73*	3442.91**	316.37	11.98
Error	4	1820.04	0.25	20099.75	15.43	19.56	62.00	84.07	21.38
Genotypes	76	1960.47**	0.14**	14554.03**	33.24**	16.40**	10.83**	9.63	29.53**
Location×Genotypes	76	2265.02**	0.15**	17408.65**	21.35**	10.78**	8.01	10.95	39.28**
Error	304	744.92	0.05**	6375.81	3.60	1.41	6.04	9.03	13.51

\* Significant at 5% probability level, \*\* Significant at 1% probability level.

and cluster III (26.379) and minimum inter cluster distance was recorded between cluster I and cluster II (25.997) indicating greater genetic divergence in these clusters. The average intra and inter-cluster distance reflected that the accessions within the cluster had a minimum divergence from each other concerning the aggregate effects of the eight traits, which are under the present investigation. Since the distance is minimum, there is a low chance to obtain the promising recombinants in the segregating generations by crossing the members of the same cluster. Therefore, it is suggested that crosses should be carried out between the accessions belonging to clusters separated by large inter-cluster distances. According to Thomas and Lal (2012), to realize more variability and high heterotic effect in future generations, it is recommended that parents should be selected from two different clusters that are having wider inter-cluster distances. The inter cluster distances under study were higher than the intra cluster distance denoting the wider diversity among the accessions of the distant groups. Therefore, to obtain better recombinants with higher genetic variability, inter-crossing should be done between the genotypes from different clusters showing high mean performance. Hence, in this study, group constellation showed that cluster III consisting of (CEX-28, CEX-33, CEX-38, CEX-46, CEX-51, CEX-69, JRC-517 and JRC-698) was highly divergent from all the other genotypes and it can be used directly for the improvement of fibre yield and its component traits and may be used as parents in transgressive breeding. The more inter-cluster distance indicates greater genetic divergence between the accessions of those clusters, whereas lower inter cluster distance indicates that the members of those clusters are not much genetically diverse from each other, therefore, the members from cluster I and cluster III can be chosen as parents for a suitable crossing program. The different groups of divergent clusters help us to select the parents for the white jute improvement program with different objectives.

The distribution of white jute (*C. capsularis* L.) germplasm accessions exhibiting higher fibre yield along with tolerance to biotic stress components in three different groups of divergent clusters are described in Table 6. Group 1 comprised cluster I and cluster II, Group 2 comprised cluster I and cluster III and Group 3 consisted of the accessions from cluster II and cluster IV.

The cluster mean values (Table 7) revealed a wide range of variation for all the traits. The cluster means for various traits showed that different clusters responded differently for different traits. Cluster III expressed the highest mean value for plant height (276.60 cm), basal

**Table 3 :** Mean performance of the 75 white jute (*C. capsularis* L.) accessions along with two checks, over two years 2013 and 2014.

S. no.	Germplasm Accession	Plant height (cm)	Basal diameter (cm)	Green weight (g plant <sup>-1</sup> )	Yellow mite incidence (number cm <sup>-2</sup> area)	Semilooper incidence (%)	Stem rot (PDI)	Root rot incidence (%)	Fibre yield (g plant <sup>-1</sup> )
1	CIN-02	254.07	1.76	248.07	9.92	10.11	6.30	2.27	12.50
2	CIN-06	280.20	1.69	241.82	9.88	7.41	5.50	1.95	10.19
3	CIN-09	280.50	1.80	282.49	7.90	12.09	6.34	2.78	12.21
4	CIN-10	270.63	1.78	261.85	11.92	10.13	4.66	0.83	12.78
5	CIN-11	262.00	1.72	194.15	12.75	10.32	6.85	5.39	10.42
6	CIN-13	284.40	1.84	276.97	12.79	8.66	6.28	2.79	13.86
7	CIN-15	289.07	1.87	321.53	10.00	9.90	6.64	4.51	14.17
8	CIN-17	296.97	1.89	288.26	10.70	9.92	7.77	4.04	15.71
9	CIN-20	267.63	1.70	227.14	9.83	9.04	6.01	1.92	11.17
10	CIN-26	244.13	1.75	221.83	9.02	6.49	5.50	3.04	8.83
11	CIN-40	247.86	1.67	188.28	14.64	8.01	5.53	7.28	10.07
12	CIN-43	251.73	1.49	182.50	14.86	5.17	6.07	3.74	9.05
13	CIN-45	261.36	1.48	189.10	13.07	8.28	6.51	4.30	8.24
14	CIN-47	266.40	1.70	219.97	13.67	8.83	6.77	5.36	11.37
15	CIN-48	247.83	1.56	211.66	13.12	5.46	7.15	4.89	9.42
16	CIN-50	262.17	1.89	287.10	9.82	8.79	7.05	5.19	10.09
17	CIN-53	276.78	1.83	264.81	10.94	10.56	5.20	1.94	11.75
18	CIN-58	267.00	1.88	254.56	10.56	9.81	4.91	3.82	13.26
19	CIN-59	298.70	2.04	354.19	7.66	9.99	5.93	2.97	16.45
20	CIN-64	286.27	1.89	299.00	13.61	7.70	4.23	1.88	17.34
21	CIN-65	266.77	1.56	202.58	14.75	6.77	4.90	2.76	9.97
22	CIN-67	268.33	1.66	223.73	14.21	8.77	7.79	2.97	11.57
23	CIN-68	261.50	1.76	254.04	12.25	7.97	5.77	2.50	11.58
24	CIN-80	290.13	1.81	265.92	15.60	8.53	6.07	8.88	14.88
25	CIN-81	276.90	1.80	262.15	14.60	8.63	5.22	4.52	12.14
26	CIN-84	278.17	1.75	286.71	12.51	10.60	6.47	3.44	12.61
27	CIN-85	242.53	1.59	256.99	14.12	9.79	6.16	1.11	12.72
28	CIN-86	249.33	1.44	179.26	13.57	12.87	5.86	1.31	10.42
29	CIN-91	267.47	1.78	229.12	14.10	9.88	6.11	3.37	12.76
30	CIN-93	286.90	1.80	267.25	14.48	9.67	6.57	5.26	13.77
31	CIN-94	251.17	1.57	266.22	15.28	10.31	7.48	3.03	9.14
32	CIN-99	232.70	1.79	238.08	16.04	12.23	10.25	2.89	11.94
33	CIN-101	254.10	1.62	246.04	14.12	10.44	4.44	2.36	10.79
34	CIN-103	245.63	1.63	194.01	12.97	7.05	6.61	5.32	9.89
35	CIN-105	243.57	1.67	215.03	13.41	10.72	5.76	1.17	10.59
36	CIN-107	276.57	1.71	204.74	14.42	10.74	5.69	2.24	10.19
37	CIN-108	285.80	1.83	213.24	15.13	10.47	7.24	2.78	12.75
38	CIN-116	249.43	1.69	188.66	13.19	8.40	5.42	2.32	11.38
39	CIN-117	273.50	1.91	258.42	14.12	9.57	6.34	2.22	14.30
40	CIN-120	298.10	1.85	224.94	16.66	8.69	6.97	3.59	13.27
41	CIN-123	295.27	1.75	262.50	15.70	6.78	7.22	2.95	14.52

Table 3 continued...

**Table 3 continued...**

42	CIN-125	278.05	1.76	240.39	14.49	9.04	8.09	4.03	13.58
43	CIN-126	251.50	1.77	211.31	17.52	10.77	5.71	3.51	12.35
44	CIN-130	259.60	1.63	187.49	17.12	11.32	6.49	3.06	8.87
45	CIN-138	300.57	1.70	226.43	17.35	9.76	5.45	2.98	12.88
46	CIN-139	295.10	1.82	222.01	17.05	8.37	5.59	0.83	12.26
47	CIN-142	255.27	1.59	179.45	15.78	9.40	5.23	3.17	11.19
48	CIN-147	272.87	1.93	247.76	15.84	9.98	6.43	2.78	13.36
49	CIN-166	291.80	1.66	222.21	13.96	11.21	6.43	0.83	12.74
50	CIN-179	271.30	1.65	240.82	16.41	10.26	4.97	2.54	12.56
51	CIN-210	265.33	1.54	189.18	35.15	10.77	4.77	1.90	10.25
52	CIN-259	245.47	1.43	272.19	12.79	10.92	6.13	1.39	9.98
53	CIN-299	289.97	1.87	241.60	14.30	10.30	5.60	3.58	12.91
54	CIN-364	298.27	1.92	324.24	12.92	10.67	6.09	4.62	16.75
55	CIN-367	296.57	1.80	368.58	12.63	7.92	5.42	3.72	14.09
56	CIN-447	293.77	1.62	229.87	14.09	7.81	8.26	3.30	11.35
57	CIN-462	266.03	1.69	226.67	14.65	9.75	5.93	3.37	13.50
58	CIN-498	273.80	1.84	326.18	17.33	12.09	6.17	4.64	13.37
59	CIN-505	281.23	1.74	268.18	15.24	12.21	6.37	3.55	13.65
60	CIN-523	291.87	1.71	238.38	16.07	9.03	7.57	1.45	12.93
61	CIN-532	288.00	1.76	231.61	13.65	10.00	5.10	4.01	13.37
62	CIN-551	293.13	1.65	239.15	11.87	10.83	7.11	3.65	12.79
63	CEX-03	297.03	1.84	237.53	15.26	9.67	6.81	5.02	17.15
64	CEX-05	276.13	1.72	300.39	14.07	9.75	6.87	2.22	15.04
65	CEX-10	271.67	1.98	280.01	16.68	12.54	5.81	3.97	13.70
66	CEX-14	277.77	1.54	213.22	14.22	11.11	7.07	4.02	11.14
67	CEX-15	297.67	1.96	346.25	15.19	12.35	8.23	4.15	15.19
68	CEX-22	290.60	2.29	447.33	17.66	11.35	9.58	4.95	16.83
69	CEX-25	285.47	1.96	271.45	10.44	11.05	7.76	3.26	14.63
70	CEX-28	265.63	1.81	287.25	8.41	13.91	5.74	1.98	12.89
71	CEX-33	280.22	2.04	328.08	13.09	9.38	7.48	3.44	14.64
72	CEX-38	252.83	1.76	285.72	11.27	11.53	6.34	3.50	13.03
73	CEX-46	269.00	1.84	314.28	10.29	12.22	8.81	3.97	12.74
74	CEX-51	263.20	1.62	191.84	14.92	10.11	8.17	3.28	9.85
75	CEX-69	266.17	1.84	250.85	12.65	11.75	7.05	3.48	16.34
76	JRC 517+ (Check)	299.13	2.11	313.65	12.39	10.18	12.48	4.44	16.74
77	JRC 698+ (Check)	316.60	1.84	282.78	12.08	9.84	8.92	5.37	17.14
	Mean	273.48	1.76	252.46	13.51	9.77	6.51	3.28	12.62
	CV (%)	9.98	13.01	31.63	14.05	12.14	37.73	91.68	29.13
	Sem ( $\pm$ )	11.140	0.093	32.600	0.775	0.484	1.003	1.227	1.501
	CD (p=0.05)	26.00	0.22	76.06	1.81	1.13	2.34	-	3.50

**Table 4 :** Distribution of 77 white jute (*C. capsularis* L.) accessions in different clusters.

Cluster No.	Total number of germplasm accessions	Source	Name of germplasm accessions
I	29	ICAR-CRIJAF, Barrackpore, Kolkata, West Bengal	CIN-02, CIN-06, CIN-09, CIN-10, CIN-11, CIN-13, CIN-15, CIN-17, CIN-20, CIN-26, CIN-40, CIN-43, CIN-45, CIN-47, CIN-48, CIN-50, CIN-53, CIN-58, CIN-59, CIN-64, CIN-65, CIN-67, CIN-68, CIN-80, CIN-81, CIN-84, CIN-85, CIN-91, CIN-462
II	40	-do-	CIN-86, CIN-93, CIN-94, CIN-99, CIN-101, CIN-103, CIN-105, CIN-107, CIN-108, CIN-116, CIN-117, CIN-120, CIN-123, CIN-125, CIN-126, CIN-130, CIN-138, CIN-139, CIN-142, CIN-147, CIN-166, CIN-179, CIN-210, CIN-259, CIN-299, CIN-364, CIN-367, CIN-447, CIN-498, CIN-505, CIN-523, CIN-532, CIN-551, CEX-03, CEX-05, CEX-10, CEX-14, CEX-15, CEX-22, CEX-25
III	8	-do-	CEX-28, CEX-33, CEX-38, CEX-46, CEX-51, CEX-69, JRC-517, JRC-698

**Table 5 :** Average intra (diagonal) and inter-cluster (off-diagonal) D<sup>2</sup> values of 77 white jute (*C. capsularis* L.) germplasm accessions.

Cluster	I	II	III
I	17.783	25.997	29.305
II		18.531	26.379
III			23.063

It was revealed from Table 8 that the genotypic coefficient of variation (GCV) was moderate for the traits green weight (14.60), yellow mite incidence (16.44) semilooper incidence (16.13) stem rot (14.63) and fibre yield (12.84) and low for the traits plant height (5.13), basal diameter (7.01) and root rot incidence (4.76). The phenotypic coefficient of variation was high for the traits green weight (26.75), stem rot (29.11), root rot incidence

**Table 6 :** Distribution of white jute (*C. capsularis* L.) germplasm accessions exhibiting higher fibre yield along with tolerance to biotic stress components, in three different groups of divergent clusters.

Group	Clusters	Genotypes present in the cluster
1	I	CIN-02, CIN-06, CIN-09, CIN-10, CIN-11, CIN-13, CIN-15, CIN-17, CIN-20, CIN-26, CIN-40, CIN-43, CIN-45, CIN-47, CIN-48, CIN-50, CIN-53, CIN-58, CIN-59, CIN-64, CIN-65, CIN-67, CIN-68, CIN-80, CIN-81, CIN-84, CIN-85, CIN-91, CIN-462
	II	CIN-86, CIN-93, CIN-94, CIN-99, CIN-101, CIN-103, CIN-105, CIN-107, CIN-108, CIN-116, CIN-117, CIN-120, CIN-123, CIN-125, CIN-126, CIN-130, CIN-138, CIN-139, CIN-142, CIN-147, CIN-166, CIN-179, CIN-210, CIN-259, CIN-299, CIN-364, CIN-367, CIN-447, CIN-498, CIN-505, CIN-523, CIN-532, CIN-551, CEX-03, CEX-05, CEX-10, CEX-14, CEX-15, CEX-22, CEX-25
2	I	CIN-02, CIN-06, CIN-09, CIN-10, CIN-11, CIN-13, CIN-15, CIN-17, CIN-20, CIN-26, CIN-40, CIN-43, CIN-45, CIN-47, CIN-48, CIN-50, CIN-53, CIN-58, CIN-59, CIN-64, CIN-65, CIN-67, CIN-68, CIN-80, CIN-81, CIN-84, CIN-85, CIN-91, CIN-462
	III	CEX-28, CEX-33, CEX-38, CEX-46, CEX-51, CEX-69, JRC-517, JRC-698
3	II	CIN-86, CIN-93, CIN-94, CIN-99, CIN-101, CIN-103, CIN-105, CIN-107, CIN-108, CIN-116, CIN-117, CIN-120, CIN-123, CIN-125, CIN-126, CIN-130, CIN-138, CIN-139, CIN-142, CIN-147, CIN-166, CIN-179, CIN-210, CIN-259, CIN-299, CIN-364, CIN-367, CIN-447, CIN-498, CIN-505, CIN-523, CIN-532, CIN-551, CEX-03, CEX-05, CEX-10, CEX-14, CEX-15, CEX-22, CEX-25
	IV	CEX-28, CEX-33, CEX-38, CEX-46, CEX-51, CEX-69, JRC-517, JRC-698

The groups 1, 2 and 3 have been formed according to the genetic divergence of the clusters

diameter (1.86 cm), green weight (281.81 g plant<sup>-1</sup>), semi looper incidence (11.12%), stem rot (8.13 PDI), root rot incidence (3.68%) and for fibre yield (14.17 g plant<sup>-1</sup>). Cluster II showed the highest mean value only for yellow mite incidence (14.81 cm<sup>2</sup> area).

(67.22), and fibre yield (24.44) whereas, the traits basal diameter (11.15), yellow mite incidence (19.21) and semilooper incidence (18.38) exhibited a moderate value and low PCV was observed for plant height (8.85). The greater difference between GCV and PCV indicated the

**Table 7 :** Cluster means for eight traits of white jute (*C. capsularis* L.) germplasm accessions.

Cluster	Plant height (cm)	Basal diameter (cm)	Green weight (g plant <sup>-1</sup> )	Yellow mite incidence (number cm <sup>-2</sup> area)	Semilooper incidence (%)	Stem rot (PDI)	Root rot incidence (%)	Fibre yield (g plant <sup>-1</sup> )
I	269.43	1.75	249.08	12.19	8.87	6.06	3.41	12.09
II	275.80	1.75	249.04	14.81	10.16	6.53	3.11	12.70
III	276.60	1.86	281.81	11.89	11.12	8.13	3.68	14.17
Population mean	273.49	1.76	252.46	13.52	9.78	6.52	3.28	12.62
Percent contribution	1.47	2.05	2.12	10.66	16.61	6.32	16.85	43.92

**Table 8 :** Genetic parameters for the different traits of 77 germplasm accessions of white jute.

Traits	Mean	Range	GCV (%)	PCV (%)	Heritability (Broad Sense)	GA as percentage of Mean
Plant height (cm)	273.48	266.40–381.40	5.13	8.85	0.34	6.13
Basal diameter (cm)	1.76	1.56–2.83	7.01	11.15	0.40	9.09
Green weight (g plant <sup>-1</sup> )	252.46	205.20–997.60	14.60	26.75	0.30	16.40
Yellow Mite incidence (number cm <sup>-2</sup> area)	13.52	4.59–23.19	16.44	19.21	0.73	28.99
Semilooper incidence (%)	9.78	1.48–21.19	16.13	18.38	0.77	29.17
Stem rot (PDI)	6.52	5.94–18.23	14.63	29.11	0.25	15.15
Root Rot incidence (%)	3.28	0–13.33	4.76	67.22	0.01	0.69
Fibre yield (g plant <sup>-1</sup> )	12.62	5.40–25.56	12.84	24.44	0.28	13.89

**Table 9 :** Genotypic correlation between fibre yield components, insect pest and disease incidence in white jute.

Traits	Basal diameter (cm)	Green weight (g plant <sup>-1</sup> )	Yellow mite incidence (number cm <sup>-2</sup> area)	Semilooper incidence (%)	Stem rot (PDI)	Fibre yield (g plant <sup>-1</sup> )
Plant height (cm)	0.60**	0.49**	0.03	-0.04	0.49**	0.97**
Basal diameter (cm)		0.83**	-0.12	0.20*	0.65**	0.96**
Green weight (g plant <sup>-1</sup> )			-0.29**	0.32**	0.49**	0.93**
Yellow Mite incidence (number cm <sup>-2</sup> area)				-0.01	0.10	-0.04
Semilooper incidence (%)					0.25*	0.30**
Stem rot (PDI)						0.64**

\* Significant at 5% probability level, \*\* Significant at 1% probability level.

greater role of the environment in the phenotypic expression of these traits in the present study. This showed that the traits are dependent on environmental factors and genetic factors alone are not sufficient to explain their performance. There is a difference between the PCV and GCV where PCV is more than the GCV value. This result corresponds to Yadav *et al.* (2011).

The heritability ( $h^2_b$ ) in a broad sense is an approximate measure of the expression of a trait. Genotypic coefficient of variation (GCV) along with heritability generally gives the best estimate of the response that is expected from the selection. Higher broad sense heritability reveals that a large portion of the variation is heritable to the offspring. This suggests that



**Table 10 :** Direct (diagonal) and indirect (off-diagonal) effects of different yield components and biotic factors on fibre yield in white jute (*C. capsularis* L.).

Traits	Plant height (cm)	Basal diameter (cm)	Green weight (g plant <sup>-1</sup> )	Yellow mite incidence (number cm <sup>-2</sup> area)	Semilooper incidence (%)	Stem rot (PDI)	Correlation with fibre yield (g plant <sup>-1</sup> )
Plant height (cm)	0.71	0.12	0.24	0.00	-0.01	-0.10	0.97**
Basal diameter (cm)	0.46	0.20	0.41	-0.02	0.04	-0.12	0.96**
Green weight (g plant <sup>-1</sup> )	0.37	0.17	0.47	-0.04	0.06	-0.10	0.93**
Yellow mite incidence (number cm <sup>-2</sup> area)	0.02	-0.03	-0.14	0.13	0.00	-0.02	-0.04
Semilooper incidence (%)	-0.03	0.04	0.16	0.00	0.18	-0.05	0.30**
Stem rot (PDI)	0.37	0.13	0.25	0.01	0.05	-0.17	0.64**
Root Rot incidence (%)	0.71	0.12	0.24	0.00	-0.01	-0.10	0.97**

\* Significant at 5% probability level, \*\* Significant at 1% probability level, Residual Effect = 0.64.

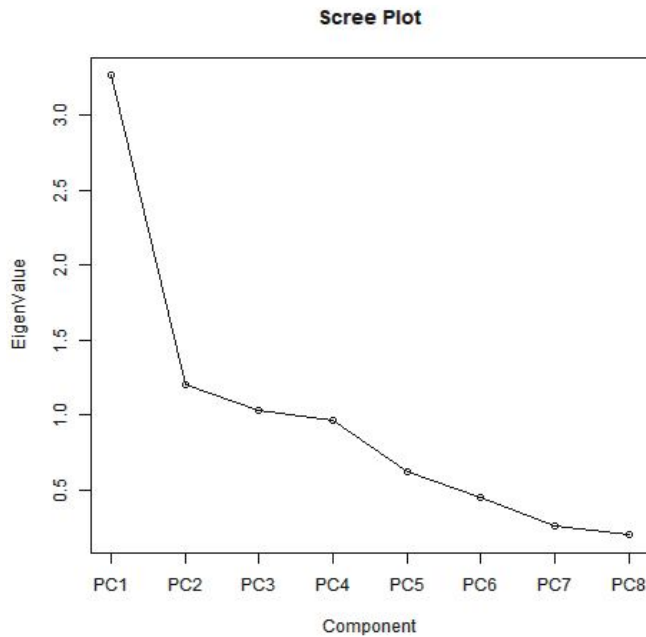
**Table 11 :** Principal Component analysis.

Statistics	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
Standard deviation	1.8070	1.0955	1.0172	0.9808	0.7874	0.6708	0.5152	0.4504
Proportion of variance	0.4081	0.1500	0.1293	0.1202	0.0775	0.0563	0.0332	0.0254
Cumulative proportion	0.4081	0.5582	0.6875	0.8077	0.8852	0.9415	0.9747	1.000
Eigen values	3.2651	1.2001	1.0347	0.9612	0.6200	0.4500	0.2654	0.2028

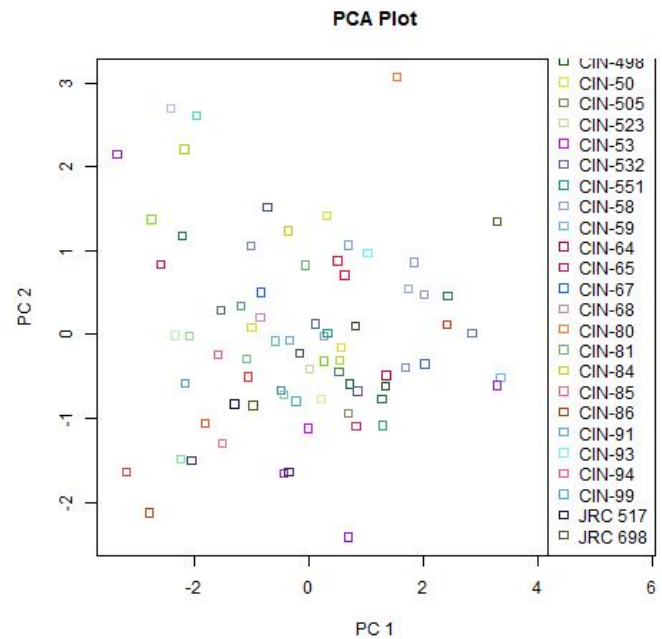
yield attributing traits are moderately heritable to the off-springs. The highest broad sense heritability was observed in yellow mite incidence (0.73) and semilooper incidence (0.77). A moderate heritability was found in plant height (0.34), basal diameter (0.40) and green weight (0.30). The traits stem rot (0.25) and fibre yield (0.28) possessed low heritability. Very low heritability (0.01) was observed for the trait root rot incidence. Knowledge of heritability alone is not at all sufficient for an efficient selection. Therefore, heritability along with genetic advance is considered more useful. A high genetic advance was observed in the case of yellow mite incidence (28.99%) and semilooper (29.17%). A moderate level of genetic advance was found in green weight (16.40%), stem rot (15.15%) and fibre yield (13.89%) whereas, the low genetic advance was found in plant height (6.13%), basal diameter (9.09%) and the very low genetic advance was recorded for root rot incidence (0.69%). High heritability coupled with high genetic advance as a percentage of the mean of yellow mite incidence and semilooper incidence indicates the presence of additive genes and shows the maximum possible for the improvement of these traits to develop tolerant genotypes through progeny selection, mass selection, family selection by any other suitable modified selection procedure, which targets to

exploit the additive gene effects.

The genotypic correlation coefficient reveals the type of relationship between any two traits. In the correlation analysis, one trait namely root rot incidence was not included as the germplasm accessions did not differ significantly for this trait. The genotypic correlation analysis (Table 9) revealed that fibre yield was positively and highly significantly correlated with plant height (0.97\*\*), basal diameter (0.96\*\*), green weight (0.93\*\*), semilooper incidence (0.30\*\*) and stem rot (0.64\*\*) whereas, yellow mite incidence was negatively correlated with green weight (-0.29). Significant genotypic correlation between the traits suggested a strong relationship between these traits at the genetic level. Path analysis always provides a depth of relationship through direct and indirect effects of traits and it measures the relative importance of every trait about the targeted trait, fibre yield. In the case of path analysis also root rot incidence was not included as the germplasm accessions did not differ significantly for this trait. Partitioning of genotypic correlation coefficients of various component traits with fibre yield per plant into direct and indirect contributions is given in Table 10. Plant height (0.97), basal diameter (0.96), green weight (0.93) and root rot incidence (0.97) had the maximum direct effect on fibre



**Fig. 1 :** Scree plot representation for all the eight principal components along with their eigen values.



**Fig. 2 :** PCA plot for the principal components PC 1 and PC 2.

**Table 12 :** The eight principal components along with their factor loadings.

Variables	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
PH	0.3975	0.0855	-0.2015	0.4372	-0.3268	0.5635	0.2571	0.3355
BD	0.4897	-0.0619	0.0549	0.0454	0.1426	-0.3535	-0.5511	0.5529
GW	0.4659	-0.1223	0.1659	0.0213	0.16656	-0.4562	0.7073	-0.0640
YM	-0.1221	-0.0804	-0.9223	0.1100	0.0420	-0.3321	0.0574	0.0224
SL	0.1718	-0.6587	-0.1529	-0.4639	0.3379	0.4197	0.0222	0.0842
SR	0.2678	0.2068	-0.1363	-0.6834	-0.6260	-0.0775	0.0048	-0.0445
RR	0.1694	0.6986	-0.1657	-0.2452	0.5811	0.2302	0.0654	-0.0296
FY	0.4901	-0.0796	-0.0935	0.2277	-0.0017	0.0628	-0.3489	-0.7531

yield followed by stem rot (0.64) and semilooper incidence (0.30). The direct and indirect effects showed that plant height (0.97 direct and 0.71 indirect) and root rot incidence (0.97 direct and 0.71 indirect) were positive and significantly correlated with fibre yield, mainly due to their direct effects. The same findings were expressed by Senapati *et al.* (2006). Based on the residual effect value (0.64), it is evident that about 40% of the total variations for fibre yield in jute were explained. Therefore, the path coefficient analysis revealed the role of plant height and root rot incidence for their contribution either directly or indirectly towards fibre yield, and hence it is suggested that these traits should be given the maximum attention during selection for developing high fibre-yielding jute genotypes.

Principal component analysis helps the breeders to differentiate significant relationships between traits. It is a multivariate analysis method to explain the correlation between a large set of variables in terms of a small

number of underlying independent factors (Badenes *et al.*, 2000). Eight principal components were identified through Principal Component Analysis (PCA) and three principal components (PC1, PC2 and PC3) were found to have eigen values more than one (Table 11), which showed an increased variability among the white jute accessions for the selection of the diverse accessions. When compared to other PCs, the scree plot (Fig. 1) exhibits that PC1 possesses the maximum variation. Hence, identifying the members from PC1 is favourable for genetic improvement. The eight principal components along with their factor loadings are given in Table 12. The loading values with both negative and positive values showed that the eight traits had both positive as well as negative correlation patterns between the components and variables. The results depicted that fibre yield had the maximum positive value (0.49) followed by basal diameter (0.48) in PC1 whereas, root rot incidence showed the maximum positive value (0.69) in PC 2. The

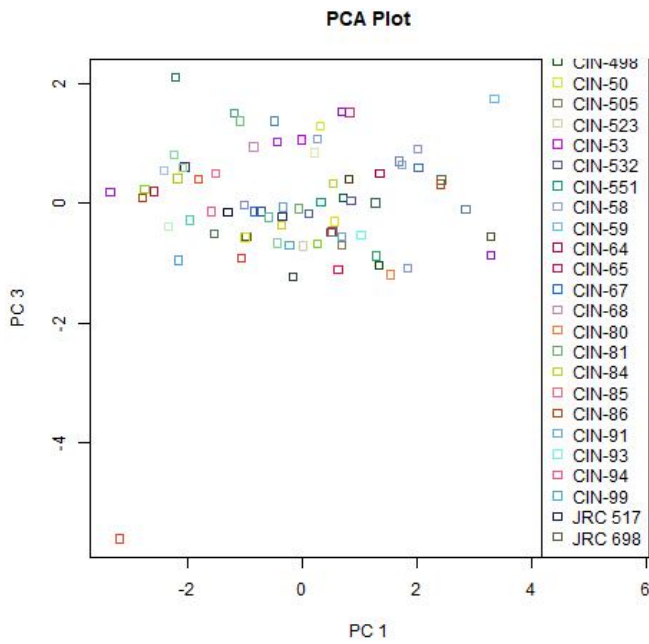
**Table 13 :** Ranking of white jute (*C. capsularis* L.) germplasm accessions on the basis of total rescaled index value.

Germplasm Accessions	Rescaled index value								Total RI (A+B+C+D+E+F+G+H)	Rank
	Plant height (cm) (A)	Basal diameter (cm) (B)	Green weight (g plant <sup>-1</sup> ) (C)	Yellow mite incidence (number cm <sup>2</sup> area) (D)	Semi-looper incidence (%) (E)	Stem rot (PDI) (F)	Root rot incidence (%) (G)	Fibre yield (g plant <sup>-1</sup> ) (H)		
CIN-02	0.25	0.38	0.26	0.28	0.57	0.25	0.18	0.47	2.63	47
CIN-06	0.57	0.30	0.23	0.28	0.26	0.15	0.14	0.21	2.14	58
CIN-09	0.57	0.43	0.39	0.22	0.79	0.26	0.24	0.44	3.33	27
CIN-10	0.45	0.41	0.31	0.33	0.57	0.05	<b>0.00</b>	0.50	2.62	48
CIN-11	0.35	0.34	0.06	0.36	0.59	0.32	0.57	0.24	2.81	44
CIN-13	0.62	0.48	0.36	0.36	0.40	0.25	0.24	0.62	3.32	28
CIN-15	0.67	0.51	0.53	0.28	0.54	0.29	0.46	0.65	3.93	13
CIN-17	0.77	0.53	0.41	0.30	0.54	0.43	0.40	0.82	4.20	9
CIN-20	0.42	0.31	0.18	0.27	0.44	0.22	0.14	0.32	2.30	55
CIN-26	0.14	0.37	0.16	0.25	0.15	0.15	0.27	0.06	1.56	68
CIN-40	0.18	0.28	0.03	0.41	0.32	0.16	0.80	0.20	2.39	54
CIN-43	0.23	0.07	0.01	0.42	<b>0.00</b>	0.22	0.36	0.09	1.40	69
CIN-45	0.34	0.06	0.04	0.37	0.36	0.28	0.43	<b>0.00</b>	1.87	65
CIN-47	0.40	0.31	0.15	0.38	0.42	0.31	0.56	0.34	2.88	41
CIN-48	0.18	0.15	0.12	0.37	0.03	0.35	0.50	0.13	1.84	66
CIN-50	0.35	0.53	0.40	0.27	0.41	0.34	0.54	0.20	3.06	35
CIN-53	0.53	0.47	0.32	0.31	0.62	0.12	0.14	0.39	2.87	12
CIN-58	0.41	0.52	0.28	0.29	0.53	0.08	0.37	0.55	3.04	36
CIN-59	0.79	0.71	0.65	0.21	0.55	0.21	0.27	0.90	4.29	6
CIN-64	0.64	0.53	0.45	0.38	0.29	<b>0.00</b>	0.13	<b>1.00</b>	3.42	23
CIN-65	0.41	0.15	0.09	0.41	0.18	0.08	0.24	0.19	1.75	67
CIN-67	0.42	0.27	0.17	0.40	0.41	0.43	0.27	0.37	2.73	46
CIN-68	0.34	0.38	0.28	0.34	0.32	0.19	0.21	0.37	2.43	53
CIN-80	0.68	0.44	0.32	0.44	0.38	0.22	<b>1.00</b>	0.73	4.23	7
CIN-81	0.53	0.43	0.31	0.41	0.40	0.12	0.46	0.43	3.08	34
CIN-84	0.54	0.37	0.40	0.35	0.62	0.27	0.32	0.48	3.36	26
CIN-85	0.12	0.19	0.29	0.40	0.53	0.23	0.03	0.49	2.28	56
CIN-86	0.20	0.01	<b>0.00</b>	0.38	0.88	0.20	0.06	0.24	1.97	63
CIN-91	0.41	0.41	0.19	0.40	0.54	0.23	0.32	0.50	2.98	37
CIN-93	0.65	0.43	0.33	0.41	0.51	0.28	0.55	0.61	3.77	15
CIN-94	0.22	0.16	0.32	0.43	0.59	0.39	0.27	0.10	2.49	52
CIN-99	<b>0.00</b>	0.42	0.22	0.45	0.81	0.73	0.26	0.41	3.29	30
CIN-101	0.26	0.22	0.25	0.40	0.60	0.03	0.19	0.28	2.22	57
CIN-103	0.15	0.23	0.06	0.36	0.22	0.29	0.56	0.18	2.05	60
CIN-105	0.13	0.28	0.13	0.38	0.64	0.19	0.04	0.26	2.04	61
CIN-107	0.52	0.33	0.10	0.41	0.64	0.18	0.18	0.21	2.55	51
CIN-108	0.63	0.47	0.13	0.43	0.61	0.36	0.24	0.50	3.36	26
CIN-116	0.20	0.30	0.04	0.37	0.37	0.14	0.19	0.35	1.95	64
CIN-117	0.49	0.56	0.30	0.40	0.50	0.26	0.17	0.67	3.33	27
CIN-120	0.78	0.49	0.17	0.47	0.40	0.33	0.34	0.55	3.54	19

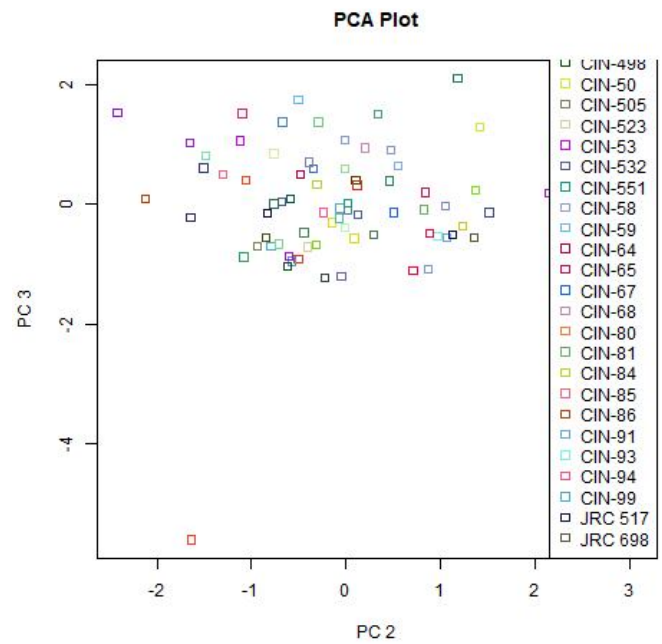
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**Table 13 continued...**

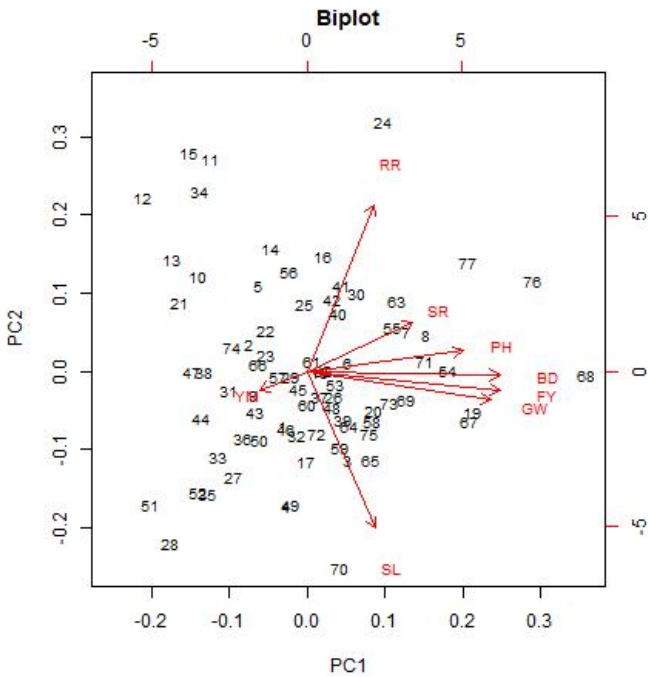
CIN-123	0.75	0.37	0.31	0.44	0.18	0.36	0.26	0.69	3.37	25
CIN-125	0.54	0.38	0.23	0.41	0.44	0.47	0.40	0.59	3.45	21
CIN-126	0.22	0.40	0.12	0.49	0.64	0.18	0.33	0.45	2.84	43
CIN-130	0.32	0.23	0.03	0.48	0.70	0.27	0.28	0.07	2.39	54
CIN-138	0.81	0.31	0.18	0.49	0.53	0.15	0.27	0.51	3.24	31
CIN-139	0.74	0.45	0.16	0.48	0.37	0.16	0.00	0.44	2.81	44
CIN-142	0.27	0.19	0.00	0.44	0.48	0.12	0.29	0.32	2.12	59
CIN-147	0.48	0.58	0.26	0.45	0.55	0.27	0.24	0.56	3.38	24
CIN-166	0.70	0.27	0.16	0.39	0.69	0.27	0.00	0.49	2.98	37
CIN-179	0.46	0.26	0.23	0.46	0.58	0.09	0.21	0.47	2.77	45
CIN-210	0.39	0.13	0.04	1.00	0.64	0.07	0.13	0.22	2.61	49
CIN-259	0.15	0.00	0.35	0.36	0.66	0.23	0.07	0.19	2.01	62
CIN-299	0.68	0.51	0.23	0.40	0.59	0.17	0.34	0.51	3.44	22
CIN-364	0.78	0.57	0.54	0.36	0.63	0.23	0.47	0.94	4.52	5
CIN-367	0.76	0.43	0.71	0.35	0.31	0.14	0.36	0.64	3.71	16
CIN-447	0.73	0.22	0.19	0.40	0.30	0.49	0.31	0.34	2.97	38
CIN-462	0.40	0.30	0.18	0.41	0.52	0.21	0.32	0.58	2.91	40
CIN-498	0.49	0.48	0.55	0.49	0.79	0.24	0.47	0.56	4.07	11
CIN-505	0.58	0.36	0.33	0.43	0.81	0.26	0.34	0.59	3.70	17
CIN-523	0.71	0.33	0.22	0.45	0.44	0.40	0.08	0.52	3.14	33
CIN-532	0.66	0.38	0.20	0.38	0.55	0.11	0.40	0.56	3.24	31
CIN-551	0.72	0.26	0.22	0.33	0.65	0.35	0.35	0.50	3.38	24
CEX-03	0.77	0.48	0.22	0.43	0.51	0.31	0.52	0.98	4.22	8
CEX-05	0.52	0.34	0.45	0.40	0.52	0.32	0.17	0.75	3.47	20
CEX-10	0.46	0.64	0.38	0.47	0.84	0.19	0.39	0.60	3.97	12
CEX-14	0.54	0.13	0.13	0.40	0.68	0.34	0.40	0.32	2.93	39
CEX-15	0.77	0.62	0.62	0.43	0.82	0.48	0.41	0.76	4.92	3
CEX-22	0.69	1.00	1.00	0.50	0.71	0.65	0.51	0.94	6.00	1
CEX-25	0.63	0.62	0.34	0.29	0.67	0.43	0.30	0.92	4.20	9
CEX-28	0.39	0.44	0.40	0.23	1.00	0.18	0.14	0.51	3.31	29
CEX-33	0.57	0.71	0.56	0.37	0.48	0.39	0.32	0.70	4.10	10
CEX-38	0.24	0.38	0.40	0.31	0.73	0.26	0.33	0.53	3.18	32
CEX-46	0.43	0.48	0.50	0.00	0.81	0.56	0.39	0.49	3.66	18
CEX-51	0.36	0.22	0.05	0.42	0.57	0.48	0.30	0.18	2.58	50
CEX-69	0.40	0.48	0.27	0.35	0.75	0.34	0.33	0.89	3.81	14
JRC 517 (Check)	0.79	0.79	0.50	0.35	0.57	1.00	0.45	0.93	5.39	2
JRC 698 (Check)	1.00	0.48	0.39	0.34	0.53	0.57	0.56	0.98	4.85	4



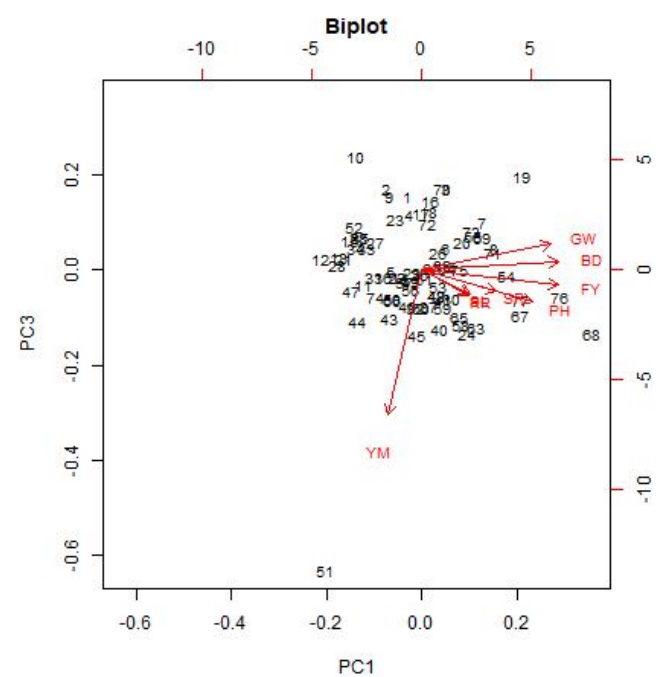
**Fig. 3 :** PCA plot for the principal components PC 1 and PC 3.



**Fig. 4 :** PCA plot for the principal components PC 2 and PC 3.



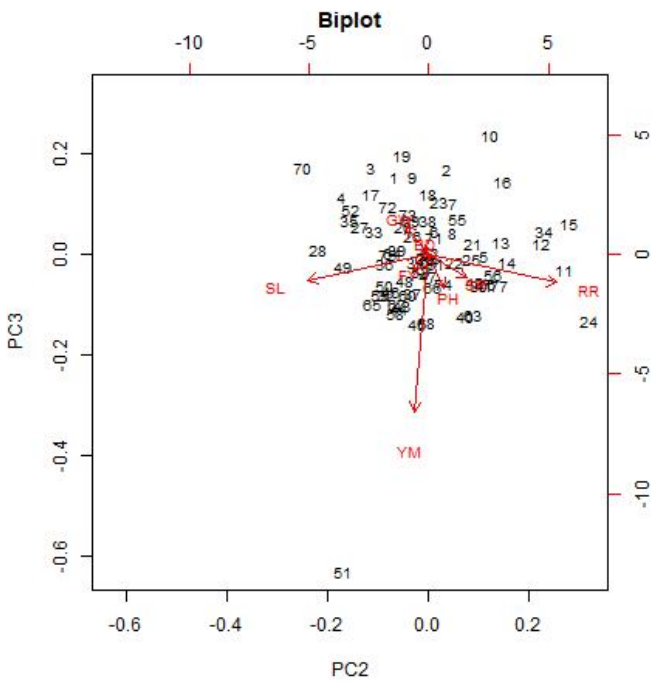
**Fig. 5 :** Biplot representation for the principal components PC 1 and PC 2.



**Fig. 6 :** Biplot representation for the principal components PC 1 and PC 3.

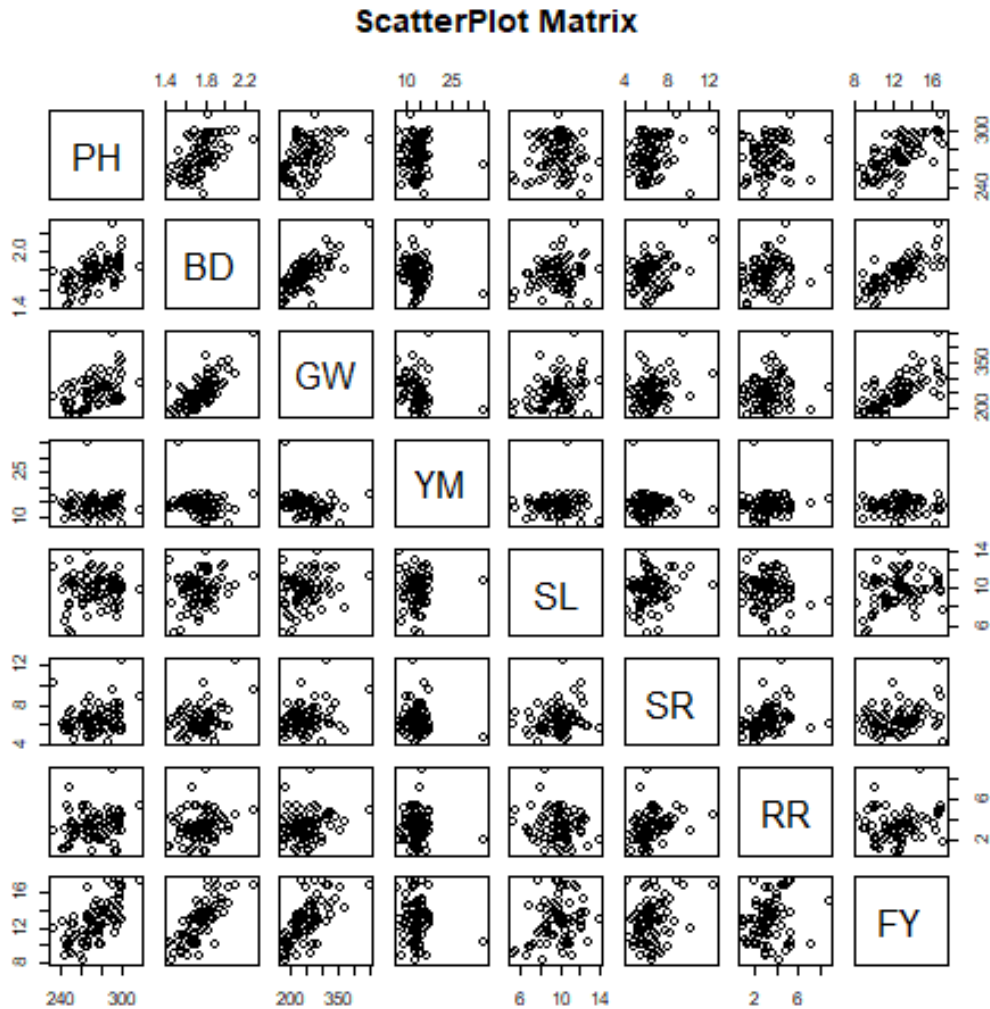
PCA plots generated for PC 1 with PC2, PC1 with PC 3, and between PC 2 and PC 3 (Figs. 2, 3 and 4) exhibited that 24 accessions were diversely related in both positive and negative distances for PC 1 and PC 2 whereas, the same accessions were comparatively closely related for PC 1 and PC 3. PCA plots of PC 2 and PC 3 revealed a slight change in the relationship of those accessions. Three of the eight PCs had more than 1.0 eigen values and PC1 contributed the maximum to the total variation. The maximum loaded value revealed that the traits that are

loaded favorably contribute to the maximum level of diversity that distinguishes the clusters most. The first two principal components (PC1 and PC 2) were layered against each other in a biplot to observe a relationship between the white jute accessions based on fibre yield and its attributing traits in the present study (Fig. 5). It shows the white jute accessions JRC 517 (check) and JRC 698 (check) were placed in the uppermost right corner (1<sup>st</sup> quadrant) and the accessions CEX-03 (No.63), CIN-367 (No.55), CIN-17 (No.8), CEX-33 (No.71) and



**Fig. 7 :** Biplot representation for the principal components PC 2 and PC 3

CIN 364 (No.54) were also placed in the same quadrant and they were highly influenced by plant height, stem rot, and root rot traits. Another observable feature was that the accessions-22 (Sr. No.68) was near basal diameter, green weight, and fibre yield and it was highly influenced by these traits. Also, the accession CIN-80 (Sr. No. 24) was near root rot incidence, which meant that this accession was highly susceptible to root rot incidence with the highest value of 8.88. The biplot of PC 1 and PC 3 (Fig. 6) placed CIN-59 (No.19) in the uppermost positive side and the accessions CIN-15 (No.7), CEX-25 (No.69), CIN-64 (No.20), CEX-46 (No. 73), CIN-50 (No. 16) and JRC 698 (No. 77) in the same quadrant and they are highly influenced by green weight and basal diameter. Another observable feature in this biplot of PC1 and PC3 was again the position of accession CEX-22 (Sr. No. 68), which was near the trait plant height which was positively correlated with fibre yield (Table 9). The biplot of PC 2 and PC 3 (Fig. 7) placed CIN-26 (No.10) and CIN-50 (No.16) in the uppermost positive side and other accessions namely CIN-45 (NO.13), CIN-103



**Fig. 8 :** Scatter Plot matrix for all the eight traits indicating the variability and the correlation among the traits.

(No.34), CIN-48 (No. 15), CIN-43 (No. 12), CIN-6 (No.2), CIN-108 (No.37), CIN-367 (No.55), CIN-17 (No.8) and CIN 65 (No.21) in the same quadrant and they were highly influenced by basal diameter. The scattered plot (Fig. 8) depicted the distribution of genotypes concerning the particular traits and the correlation between them and confirms with Table 9. A scree plot was developed by a graph between eigenvalues and PC numbers, which was used to explain the percentage of variation that is connected with each PC. In the present study, PC1 revealed 40% of variability with an eigen value of 3.26 which rapidly fell after that (Fig. 1). An inclined line was noticed after PC2 with some fluctuation in each PC. More deviation was observed in PC4. By analyzing all the biplots, it was clear that the trait basal diameter was the prominent trait that was highly influencing the genotypes. Hence, the trait basal diameter had to be considered an unavoidable trait in any jute improvement program.

The rescaled index value was calculated using the formula given by Iyengar and Sudarshan's (1982) rescaling approach, where the ranking of 77 white jute accessions was carried out for 8 traits (Table 13). The cumulative ranking for both years (2013 and 2014) showed that the first rank recorded for plant height was by the genotype JRC 698 (check), CEX-22 for basal height and green weight, CIN-210 for yellow mite incidence, CEX-28 for semilooper incidence, JRC 517 (check) for stem rot, CIN 80 for root rot incidence and CIN 64 for fibre yield. The total rescaled index (RI) ranking revealed that CEX- 22 ranked first (Total RI value = 6.00) followed by JRC 517 (check) at rank two (Total RI value = 5.39), CEX-15 (Total RI Value = 4.92) at rank 3, JRC 698 (check) [Total RI Value = 4.85] at rank 4 and CIN 364 (Total RI value = 4.52) at rank 5. The findings of PCA biplots are in close conformity with the ranking of the genotypes as per the rescaled index values since the top-ranking accessions showed close affinity to the traits like plant height, basal diameter, and green weight, which were positively correlated with fibre yield along with high direct effect.

### Conclusion

Based on the genetic diversity analysis and principal component analysis the accession CEX 22 ranked top as per the rescaled index showing close affinity to the traits like plant height, basal diameter, and green weight, which were positively correlated with fibre yield along with high direct effect. CEX 15 and CIN 364 also showed high mean values for fibre yield and yield attributing traits can be utilized as one of the parents for the hybridization

program for the development of high fibre-yielding genotypes.

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### Conflict of interests

The authors have declared no conflict of interest exists.

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