

ASSESSMENT OF PHENOTYPIC VARIATION AMONG KENAF (*Hibiscus cannabinus* L.) GENOTYPES BY MORPHO-AGRONOMIC TRAITS**A. Miah^{1*}, A. K. M. S. Hossain¹, M. N. H. Rony², I. J. Mumu³ and M. Z. Tareq⁴**¹Genetic Resources and Seed Division, Bangladesh Jute Research Institute, Dhaka, Bangladesh²BARJ-project, Bangladesh Jute Research Institute, Dhaka, Bangladesh³Department of Genetics and Plant Breeding, BSMRAU, Gazipur, Bangladesh⁴Jute Agriculture Experimental Station, BJRI, Jagir, Manikganj, Bangladesh

*Corresponding author's email: arjumia146@gmail.com

ABSTRACT

Thirty-seven kenaf (*Hibiscus cannabinus* L.) genotypes (34 accessions and 3 variety) originated in different parts of the world were studied in BJRI to assess genetic variation using morpho-agronomic traits. A total of 20 morpho-agronomic traits was selected for study and found that the genotypes varied significantly ($p < 0.01$) in these traits. The major production traits such as stick weight and fiber weights were found highly correlated with other traits. Considerable ranges of variability were observed in stem colour, petiole colour, stipule colour, plant technical height, base diameter, dry fiber weight and dry stick weight. Based on major yield contributing characters accession 3569, 5027, 2048, and 5029 were better than other genotypes.

Key words: Kenaf genotypes, morpho-agronomic trait, genetic diversity, kenaf breeding program.

Introduction

Kenaf (*Hibiscus cannabinus* L.) is a traditional fiber producing plant belonging to the family Malvaceae. In the present global environmental needs and inadequate green fiber resources, kenaf is a potential crop with higher tensile strength fiber (Faruq *et al.*, 2013) and because of lower production cost and labor requirements it is now replacing jute plants traditionally used for fiber production (Golam *et al.*, 2011). To date, kenaf has been utilized for manufacturing various industrial products such as pulping and paper making. Good quality kenaf fiber can be utilized for producing industrial filter and the core can be utilized as a bio-remediation agent, animal bedding, and low-density particle board (Baldwin and Graham, 2006). In order to expand its industrial use and maintain the economic viability, it is important to study the genetic diversity of different kenaf genotypes for developing an effective breeding program that will yield high fiber or stick (Bitzer *et al.*, 2000). The widespread method to define the variability of kenaf is the study of morpho-agronomic traits. Raw morphological properties play important roles to classify kenaf varieties. However, defining the kenaf genotype by common traits such as plant height, leaf shape and maturity etc. are sometimes difficult. For instance, morphological traits cannot be utilized in early selection of potential kenaf genotypes. In addition, genetic variability detection using morphological traits is not worthy when the target gene expression changes with environmental condition and plant development stages (Kalpana *et al.*, 2012). It is also important to define the circulating seeds in the market to secure farmer's interest from potential fraudulent admixtures (Cheng *et al.*, 2002). Traditional genetic variation analysis was on morphological and agronomical traits and due to the difficulty to identify cultivars based entirely on these traits effective recently molecular technologies are introduced (Islam *et al.*, 2014). For characterization of genetic variation in plants certain molecular DNA based markers, such as RAPD, RFLP, AFLP and SSR (Faruq *et al.* 2013) can be applied (Islam *et al.*, 2014). At present a large number of germplasm are now being maintained in the Gene Bank of Bangladesh Jute Research Institute (BJRI). There are 675 germplasms of kenaf of both indigenous and exotic sources in the Gene Bank of BJRI. The use of plant genetic resources in breeding research is largely dependent on the available information of their genetic variability. In this study thirty one accessions of kenaf germplasm received from different sources. This study was, therefore, conducted to determine the genetic diversity in different kenaf genotypes of diverse origin in tropical and sub-tropical environment of the World using morphological traits.

Materials and Methods

The experiment conducted at the experimental fields of Jute Agriculture Experimental Station (JAES), Manikganj 2016. Thirty seven accessions of kenaf were taken for this study. The experiment was laid out in Rod Row design. Seeds were sown in single row of three meter long with spacing of 30, 60 and 10 cm between rows, replications and plants, respectively. Standard production technology was adopted to raise a good crop under optimum management. The seeds were sown 07 April, 2016. Intercultural operations were done at proper time for ensuring proper growth of the crop. The data on different morphological parameters were recorded from 10 randomly selected plants of each accession. Observations were recorded on different morphological characters on the basis of IJO developed *Hibiscus* descriptor. The collected data on different parameters were statistically analyzed.

Results and Discussion

The mean performance of the major yield contributing characters and co-efficient of variation are presented in Table 1. Pigmentation data on stem colour, leaf colour, vein colour, petiole colour, stipule colour, bud colour, and fruit colour are presented in Table 2. The plant technical height at harvest (120 days) ranged from 1.89-3.63m. The highest score was observed in accession 3569 (3.63 m/plant) followed by accessions 5027 (3.52 m/plant), 2048 (3.51 m/plant) and accession 5029 (3.32 m/plant). Dry fiber weight ranged from 14.82-25.44 g/plant. The highest score was observed in accession 3569 (25.44 g/plant) followed by accession 5027 (24.98 g/plant), accession 2048 (24.75 g/plant) and accession 5029 (24.63 g/plant). Dry stick weight ranged from 29.45-65.63 g/plant. The highest score was recorded in accession 3569 (65.63 g/plant) followed by accession 5027 (64.38 g/plant), 2048 (63.95 g/plant) and accession 5029 (63.55 g/plant). Similar result was found in Annual Research Report (2016) BJRI in different accession. Among the characterized accession, four accession viz. 3569, 5027, 2048 and 5029 performed better than the control varieties HC-2, HC-3 and HC-95. Hence, these accessions may be selected for further study. The analysis of variance (ANOVA) for fiber yield and yield contributing components like plant height, base diameter, core diameter, dry stick weight etc. in kenaf germplasm, is described in Table 3. The ANOVA revealed significant difference as the source of variation, for the traits plant height (m), base diameter (cm), fiber weight (g/plant) and stick weight (g/plant). All parameters are significantly different at 1% level of significance. The finding of this study is supported by Roy *et al.* (2018).

The phenotypic coefficient of variation (PCV) was found to be greater than the genotypic coefficient of variation (GCV) in case of all the characters (Table 4). The percentage (%) of PCV of plant height 16.67, base diameter 12.41, dry fiber weight 15.47 and dry stick weight 22.85 and the percentage (%) of GCV of plant height 15.60, base diameter 11.73, dry fiber weight 15.09 and dry stick weight 22.64 were found in this study. The GCV and PCV were found to differ significantly for all the fiber yield components. This is in agreement with the findings of Sawarkar *et al.* (2014). The percentage (%) of heritability of plant height 87.50, base diameter 89.31, dry fiber weight 95.12 and dry stick weight 98.15 and the percentage (%) of genetic advance (GA) of plant height 30.06, base diameter 22.83, dry fiber weight 30.32 and dry stick weight 46.21 were found in this study. The heritability and genetic advance (% of mean) were also found to be high for all the traits and this is similar to the findings of Roy *et al.* (2015) who reported that higher heritability and genetic advance for fiber yield components of kenaf.

All genotypes were distributed in distinct divergent clusters. The distribution of the kenaf germplasm accessions exhibiting higher fiber yield along with the different morpho-agronomic factors in the five groups of divergent clusters are presented in Table 5. In the first group of divergent clusters consisting of cluster-I, nine genotypes having higher average rank namely serial no. of Ac 01, Ac 02, Ac 06, Ac 10, Ac 15, Ac 17, Ac 23, Ac 29 and Ac 35 belonged to cluster-I. In the second group of divergent clusters consisting of cluster-II, fifteen genotypes namely serial no. of Ac 03, Ac 08, Ac 09, Ac 11, Ac 13, Ac 16, Ac 19, Ac 22, Ac 26, Ac 28, Ac 31, Ac 32, Ac 34, Ac 36 and Ac 37 belonged to cluster-II. In the third group of divergent clusters consisting of cluster-III, six genotypes namely serial no. of Ac 04, Ac 07, Ac 12, Ac 14, Ac 18 and Ac 25 belonged to cluster-III. In the fourth group of divergent clusters consisting of

cluster-IV, four genotypes namely serial no. of Ac 05, Ac 20, Ac 21 and Ac 30 belonged to cluster-IV. In the fifth group of divergent clusters consisting of cluster-V, three genotypes namely serial no. of Ac 24, Ac 27 and Ac 33 belonged to cluster-V. These findings are in agreement with Das *et al.* (2016).

Table 1. Range, Mean and co-efficient of variation (CV %) of twelve characters of twenty nine *Hibiscus cannabinus* germplasm

Acc. No.	TH (m)	LA (dg)	LL (cm)	LW (cm)	PL (cm)	Node no.	BD (mm)	MD (mm)	TD (mm)	CD (mm)	DFW (g)	DSW (g)
1821	3.24	45	12.39	14.45	21.24	104	27.10	14.77	7.98	23.75	24.52	63.12
HC-2	3.13	48	11.95	13.98	20.92	98	26.89	14.41	6.95	23.51	23.88	62.47
1823	2.31	54	8.98	9.55	14.79	82	20.65	11.25	5.54	18.52	17.44	42.85
1824	2.75	50	10.58	11.51	16.17	85	23.69	12.54	6.85	19.73	21.24	49.98
1825	2.17	55	8.65	8.27	10.32	74	20.27	10.25	5.22	15.61	15.27	32.45
HC-95	3.21	49	12.15	14.09	21.02	101	26.85	14.51	7.91	22.98	23.85	58.86
1826	2.77	50	10.86	11.54	15.73	93	22.89	12.57	6.75	20.75	18.48	42.57
HC-3	2.48	52	9.87	9.78	14.78	78	20.45	11.41	5.87	19.27	17.45	35.54
1983	2.54	50	9.89	10.71	15.09	85	21.66	12.12	6.41	20.23	19.64	39.69
1984	3.02	50	11.46	13.69	20.85	95	25.96	14.08	6.99	22.89	22.45	60.51
1985	2.27	55	9.74	8.95	13.26	78	20.87	10.68	5.32	17.41	16.85	39.65
1993	2.88	50	10.98	12.62	17.26	88	23.49	13.21	6.79	21.24	20.53	42.75
1995	2.53	51	9.87	11.56	15.77	86	21.25	12.28	6.45	18.95	18.84	37.74
1996	2.59	53	10.25	11.11	16.68	87	22.19	12.14	6.35	20.65	20.65	45.64
2002	3.22	47	12.12	13.89	20.86	97	27.07	14.57	7.89	23.11	24.12	61.41
2003	2.47	51	9.85	10.48	15.85	83	21.45	11.05	6.62	18.74	17.58	36.56
2005	3.12	49	12.28	13.87	20.98	96	27.05	14.58	6.79	22.55	23.87	56.58
2006	2.85	50	11.75	11.52	16.27	91	24.86	13.26	7.12	21.14	21.65	55.89
2008	2.45	58	11.23	10.85	14.58	88	21.48	10.31	6.14	18.85	18.79	45.85
2009	2.11	56	8.55	9.11	10.82	78	20.85	10.42	5.18	15.52	15.66	42.75
2016	1.98	58	7.96	8.12	10.26	75	19.85	9.98	5.12	15.23	15.48	35.47
2043	2.53	50	9.86	9.89	15.45	80	21.17	11.72	6.33	19.85	19.74	38.55
2045	3.22	50	12.41	14.15	21.35	99	26.65	14.25	8.06	22.84	23.96	62.44
2048	3.51	43	12.75	14.69	21.79	106	27.66	15.02	7.98	23.09	24.75	63.95
2107	2.74	51	10.45	11.61	14.89	94	24.28	12.54	7.12	20.64	21.41	59.27
3568	2.56	55	10.25	10.48	14.25	92	22.24	11.46	6.55	19.55	20.61	52.46
3569	3.63	40	13.25	15.23	22.57	110	28.24	15.75	8.59	23.54	25.44	65.63
4118	2.46	52	10.85	9.87	12.57	79	21.44	11.11	6.05	18.57	17.24	35.28
4214	3.00	50	11.28	14.04	20.15	98	25.55	13.98	7.41	22.64	23.27	62.63
4971	1.89	60	7.45	7.58	9.89	70	18.51	9.89	4.68	14.23	14.82	29.45
4973	2.41	56	9.87	9.55	12.95	78	20.72	10.23	6.28	18.65	18.67	38.65
4979	2.55	55	9.24	9.36	12.56	75	22.65	10.69	5.87	18.74	18.52	41.45
5027	3.52	43	12.85	14.85	21.98	107	27.89	15.19	8.26	23.12	24.98	64.38
5028	2.58	56	10.12	9.89	14.25	79	21.69	10.68	6.35	20.22	20.22	46.34
5029	3.32	45	12.56	14.50	21.77	105	27.12	14.54	7.83	22.56	24.63	63.55
5033	2.54	50	10.21	10.41	12.69	81	21.47	11.21	6.14	19.32	20.21	45.54
5034	2.65	52	10.26	10.36	13.85	80	22.58	11.65	6.25	19.50	19.32	45.85
Range	1.89-3.63	40-60	7.45-13.25	7.58-15.23	9.89-22.57	70-110	18.51-28.24	9.89-15.75	4.68-8.59	14.23-23.54	14.82-25.44	29.45-65.63
Mean	2.73	51.05	10.67	11.51	16.39	8.50	3.42	2.46	6.62	20.20	9.50	48.48
CV%	8.47	9.27	15.98	18.57	16.88	10.95	11.79	10.73	14.35	12.61	19.87	22.15

* Check Variety

Technical height (TH), leaf angle (LA), leaf length (LL), leaf width (LW), petiole length (PL), base diameter (BD), middle diameter (MD), top diameter (TD), core diameter (CD), dry fiber weight (DFW), dry stick weight (DSW)

Table 2. Pigmentation of *Hibiscus cannabinus* genotypes

Acc. No.	Stem color	Leaf color	Vein color	Petiole color	Stipule	Stipule color	Bud color	Fruit color
1821	G	G	G	G	+	G	P	B
HC-2	G	G	G	G	+	G	P	B
1823	G	G	G	G	+	G	P	B
1824	G	G	G	G	+	G	Y	B
1825	G/R	G	G	G/R	+	G	Y	B
HC-95	G	G	G	G	+	G	Y	B
1826	G/R	G	G	G/R	+	G	Y	B
HC-3	G/R	G	G	G/R	+	G	Y	B
1983	G	G	G	G	+	G	P	B
1984	G	G	G	G	+	G	Y	B
1985	G	G	G	G	+	G	Y	B
1993	G/R	G	G	G/R	+	G	Y	B
1995	G	G	G	G	+	G	P	B
1996	G	G	G	G	+	G	Y	B
2002	G/R	G	G	G/R	+	G	Y	B
2003	G/R	G	G	G/R	+	G	Y	B
2005	G/R	G	G	G/R	+	G	Y	B
2006	R	G/R	G	R	+	G	Y	B
2008	G/R	G	G	G/R	+	G	P	B
2009	R	G	G	G/R	+	G	P	B
2016	G/R	G	G	G/R	+	G	Y	B
2043	G/R	G	G	G/R	+	G	Y	B
2045	G/R	G	G	G/R	+	G	P	B
2048	G/R	G	G	G/R	+	G	Y	B
2107	G	G	G	G	+	G	Y	B
3568	G/R	G	G	G	+	G	Y	B
3569	G	G	G	G	+	G	Y	B
4118	G/R	G	G	G/R	+	G	Y	B
4214	R	RG	R	R	+	R	Y	B
4971	G/R	G	G	G/R	+	G	Y	B
4973	G	G	G	G	+	G	Y	B
4979	G	G	G	G	+	G	P	B
5027	G/R	G	G	G/R	+	G	Y	B
5028	G/R	G	G	G/R	+	G	Y	B
5029	R	G	G	G/R	+	G	Y	B
5033	G/R	G	G	G/R	+	G	Y	B
5034	G/R	G	G	G/R	+	G	Y	B

G= Green, R= Red, LR= Light Red, B=Brown, "+"= Present, * Check variety

Table 3. Analysis of variance (mean square)

SOV	df	TL (m)	LA (dg)	LL (cm)	LW (cm)	PL (cm)	Node No.	BD (mm)	MD (mm)	TD (mm)	CD (mm)	DFW (g)	DSW (g)
Rep.	2	0.051	14.75	0.025	0.102	0.023	17.75	0.247	0.010	0.150	0.741	0.335	0.255
Acc.	36	0.572 **	58.16 **	6.122 **	14.58 **	44.65 **	346.3 **	23.54 **	9.337 **	2.820 **	19.27 **	29.05 **	367.8 **
Error	72	0.026	9.423	0.103	0.211	0.210	11.17	0.903	0.204	0.076	0.771	0.488	2.298

SOV = Source of variation, Rep. = Replication, Acc. = Accession

** = Significant at 1% level of probability

Table 4. Variability, heritability (h²b), genetic advance (GA) and GA in percent of mean for twelve yield and its related characters of *H. cannabinus*

Charac- ters	Min.	Max.	Mean	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (h ² b)	GA	GA (%)
TH	1.89	3.63	2.74	0.18	0.21	15.60	16.67	87.50	0.82	30.06
LA	40.00	60.00	51.05	16.245	25.67	7.89	9.92	63.29	6.61	12.94
LL	7.45	13.25	10.68	2.006	2.109	13.27	13.60	95.12	2.85	26.66
LW	7.58	15.23	11.52	4.79	5.00	19.00	19.42	95.78	4.41	38.31
PL	9.89	22.57	16.39	14.81	15.02	23.48	23.65	98.60	7.87	48.03
Node	70.00	110.00	88.51	111.700	122.870	11.94	12.52	90.91	20.76	23.45
BD	18.51	28.24	23.42	7.544	8.447	11.73	12.41	89.31	5.35	22.83
MD	9.89	15.75	12.44	3.044	3.248	14.03	14.49	93.72	3.48	27.97
TD	4.68	8.59	6.65	0.915	0.991	14.39	14.97	92.33	1.89	28.47
CD	14.23	23.75	20.21	6.166	6.937	12.29	13.03	88.89	4.82	23.87
DFW	14.82	25.44	20.43	9.509	9.997	15.09	15.47	95.12	6.20	30.32
DSW	29.45	65.63	48.75	121.827	124.125	22.64	22.85	98.15	22.53	46.21

Technical height (TH), leaf angle (LA), leaf length (LL), leaf width (LW), petiole length (PL), base diameter (BD), middle diameter (MD), top diameter (TD), core diameter (CD), dry fiber weight (DFW), dry stick weight (DSW)

Table 5. Number, percent and name of genotypes in different cluster

Cluster number	Number of varieties	Percent (%)	Name of Accessions
I	9	24.32	Ac 01, Ac 02, Ac 06, Ac 10, Ac 15, Ac 17, Ac 23, Ac 29 and Ac 35
II	15	40.54	Ac 03, Ac 08, Ac 09, Ac 11, Ac 13, Ac 16, Ac 19, Ac 22, Ac 26, Ac 28, Ac 31, Ac 32, Ac 34, Ac 36 and Ac 37
III	6	16.22	Ac 04, Ac 07, Ac 12, Ac 14, Ac 18 and Ac 25
IV	4	10.81	Ac 05, Ac 20, Ac 21 and Ac 30
V	3	8.11	Ac 24, Ac 27 and Ac 33

Table 6. Cluster mean for twelve yield and yield characters of *H. sabdariffa*

Characters	I	II	III	IV	V
TH	3.16	2.49	2.76	2.04	3.55
LA	48.11	53.13	50.67	57.25	42.00
LL	12.07	10.01	10.81	8.15	12.95
LW	14.07	10.11	11.65	8.27	14.92
PL	21.02	14.18	16.17	10.32	22.11
Node	99.22	81.60	89.67	74.25	107.67
BD	26.69	21.45	23.57	19.87	27.93
MD	14.41	11.19	12.71	10.14	15.32
TD	7.53	6.14	6.83	5.05	8.28
CD	22.98	19.09	20.69	15.15	23.25
DFW	23.84	18.74	20.66	15.31	25.06
DSW	61.29	41.47	49.35	35.03	64.65

Technical height (TH), leaf angle (LA), leaf length (LL), leaf width (LW), petiole length (PL), base diameter (BD), middle diameter (MD), top diameter (TD), core diameter (CD), dry fiber weight (DFW), dry stick weight (DSW)

The diversity in the present materials was also supported by the appreciable amount of variation among cluster means for different characters (Table 6). Cluster V showed highest mean for plant height (3.55 m), Base diameter (27.93 mm), dry stick weight (64.65 g) and dry fiber weight (25.06 g). Similar result was found by Das *et al.* (2016).

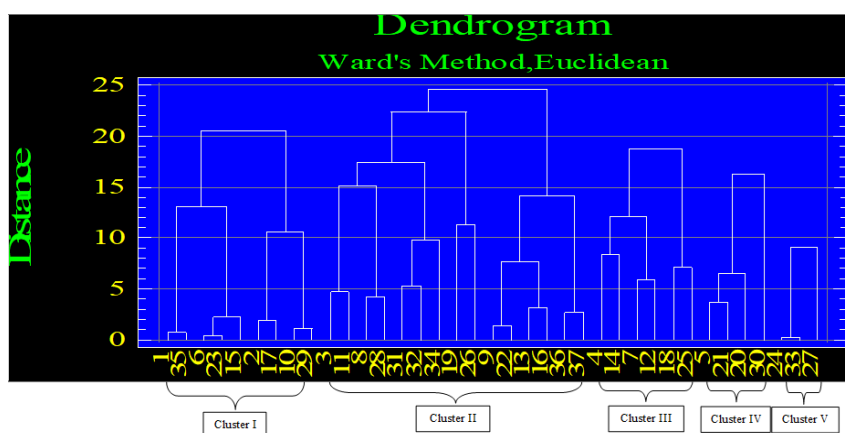


Fig. 1. Dendrogram of 37 kenaf genotypes

Conclusion

The highest score of fiber weight was observed in accession 3569 (25.44 g/plant). The highest score of stick weight was recorded in accession 3569 (65.63 g/plant). Among the characterized accession, four accession viz. 3569, 5027, 2048 and 5029 performed better than the control varieties HC-2, HC-3 and HC-95. High positive relationship of the major agronomic traits such as fiber and stick yield with other traits will help for the selection of better kenaf plant.

References

- Annual Research Report. 2016. Bangladesh Jute Research Institute. Manik Mia Avenue, Dhaka-1207.
- Baldwin, B. S. and Graham, J. 2006. Population density and row spacing effects on dry matter yield and bark content of kenaf (*Hibiscus cannabinus* L.). *Ind. Crop Prod.*, 23: 244–248
- Bitzer, M. J., Cook, C. G. and Baldwin, B. S. 2000. The development of kenaf varieties in United States. In: Proceedings of the International Kenaf Symposium, pp: 91–94. Hiroshima, Japan
- Cheng, Z., Lu, B. R., Baldwin, B. S., Sameshima, K. and Chen, J. K. 2002. Comparative studies of genetic diversity in kenaf (*Hibiscus cannabinus* L.) varieties based on analysis of agronomic and RAPD data. *Hereditas*, 136: 231–239
- Das, A. and Kumar, D. 2016. Genetic Divergence and Character Association for Yield and Quality Attributing Characters in Jute Cultivars (*Corchorus* spp.). *Elect. J. Plant Breed.*, 7(3): 529–537.
- Faruq, G., Alamgi, M. A., Rahman, M. M., Motior, M. R., Zakaria, H. P., Marchalina, B. and Mohamed, N. A. 2013. Morphological characterization of kenaf (*Hibiscus cannabinus* L.) in Malaysian tropical environment using multivariate analysis. *J. Anim. Plant. Sci.*, 23: 60–67
- Golam, F., Alamgir, M., Rahman, M., Subha, B. and Motior, M. 2011. Evaluation of genetic variability of kenaf (*Hibiscus cannabinus* L.) from different geographic origins using morpho-agronomic traits and multivariate analysis. *Aust. J. Crop. Sci.*, 5: 1882–1890
- Islam, A. K. M. A., Jahan, M. A., Yaakob, Z. and Osman, M. 2014. Genetic relationship between roselle (*Hibiscus sabdariffa* L.) and kenaf (*Hibiscus cannabinus* L.) accessions through optimization of PCR based RAPD method. *Emir. J. Food Agric.*, 26: 247–258
- Kalpana, D., Choi, S. H., Choi, T. K., Senthil, K. and Lee, Y. S. 2012. Assessment of genetic diversity among varieties of mulberry using RAPD and ISSR fingerprinting. *Sci. Hort.*, 134: 79–87.
- Roy, S. K., Chakraborty, Hijam, H. M., Mondal, H. A., Surje, D. T., Roy, A., Mondal, A., Pal, S., Kundu, A., Das, S., Sarkar, P., Kheroar, S., Chakraborty, G. and Mitra, S. 2018. Studies on genetic variability and screening for fiber yield components and biotic stress factors in tossa jute (*Corchorus olitorius* L.) germplasm under Terai region of West Bengal. *Elect. J. Plant Breed.*, 9 (2): 409–423