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Research Article
Genetic Diversity Analyses of Twelve Tossa Jute (*Corchorus olitorius* L.) Genotypes Based on Variability, Heritability and Genetic Advance for Yield and Yield Attributing morphological Traits

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Abstract

Background and Objective: Improvement of qualitative and quantitative traits of Tossa Jute through hybridization is problematic due to narrow genetic base and high sensitivity to light and temperature. Twelve Tossa Jute genotypes were studied to estimate their genetic diversity for fiber yield based on variances, heritability and genetic advance. **Materials and Methods:** This investigation was done in a randomized complete block design with three replications. Plants were harvested at 110 days of age. Data on plant height, base diameter, green weight, fiber yield and stick yield were recorded carefully. **Results:** The Acc. 1318 showed maximum plant height (3.22 m), stem base diameter (16.63 mm), dry fiber weight/plant (16.93 g), dry fiber yield per hectare area (3.55 t) followed by Acc. 1306, O-0512-6-2,O-043-7-9, BJRI Tossa pat-5, O-049-1-3, O-0411-10-4, JRO-524 (green), BJRI Tossa pat-8, JRO-524 (red), O-0419-3-1 and O-0412-9-4. Highly significant differences indicating variability were found for all characters among the genotypes which are helpful for varietal development. For all traits, phenotypic co-variances were relatively greater, but nearest to the genotypic co-variances indicating high contribution of genotypic effects for phenotypic expression. High heritability coupled with high genetic advance per percent of mean obtained for all characters except plant height, base diameter reflecting the presence of additive gene action for the expression of these traits and improvement of these characters through selection. **Conclusion:** Proper hybridization between wild and cultivated species will develop novel plant types with good characters. Acc. 1318, Acc. 1306, O-0512-6-2, O-049-1-3 performed good results on variability, heritability and genetic advance for fiber yield which will be used as breeding materials.

Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Tossa Jute (*Corchorus olitorius* L.) is the main cash crop of Bangladesh and a natural fiber popularly known as the golden fiber which is second to cotton plant in respect of textile fiber production in world[1-3]. It is an annual fibrous plant belongs to the genus *Corchorus*, family Tiliaceae[4,5] with diploid chromosome number 2n = 2x = 24, genetically self-pollinated[6] and distributed in warm regions throughout the world[7,8]. Approximately 5% out crossing may occur which is assisted by some pollinators like; honey bees, butterflies and moths[9]. There are commonly 2 species of Jute plant viz., Deshi Jute (*Corchorus capsularis* L.) and Tossa Jute (*C. olitorius* L.) cultivated in Bangladesh. Jute was previously named 'pat'. The fiber of Jute plant is totally biodegradable, comfortable and extremely attractive renewable resource. Tossa Jute is economically important for fiber production, the wild species are considered important genetic resources for biotic and abiotic stress tolerance and fine fiber trait. *Corchorus* germplasms occur in diverse ecological conditions and habitats like; riverbanks, dry river bed, low altitude valley within mountain folds, hill cliffs, forest floors with open canopy, marshy lands road side fallow, ditches and cultivable as well as homestead lands. *Corchorus* is a genus of about 40-100 species of flowering plants in the family Malvaceae, native to tropical and subtropical regions throughout the world. The plants are usually annual herbs, reaching a height of 2.0-4.5 m, unbranched or with side branches and is an erect woody herb. The leaves are alternate, simple, lanceolate, 5-15 cm long, with an acuminate tip and a finely serrated or lobed margin. The flowers are small (2-3 cm diameter) and yellow with 5 petals, the fruit is a many-seeded capsule[5]. The Jute fiber is also known as Pat, kosta, Nalita[2]. It is a lingo-cellulosic multi-cellular fiber composed of cellulose, lignin, hemi-cellulose, waxes, pectin, protein and mineral matters. Fiber is extracted from the bark of the plants[10,11].

According to Islam and Ali[2], Bangladesh Jute Research Institute (BJRI) was established in 1951 with the mandate to complete research on both agricultural and industrial aspects on Jute and allied fiber crops. The total land area of Bangladesh is 13 million ha of which 8.44 million ha belongs to agricultural land. In 2010-11, 0.803 million ha land cultivated for Jute. Jute cultivation area was 6% of total land area. Jute cultivation area was 10% of agricultural land area. Jute production was 26% as of all agricultural crops. However, national average yield is increased from 1.59-1.98 t ha^{-1} from the decades 1970-1980 to present (2018-2019). It is happened due to use of high yielding Jute varieties and production technologies, which together contributed toward higher yield.

Jute is still contributing about 4% GDP to the national economy and earns about 5% of foreign exchange as well.

The cultivated species *C. olitorius* L. is globally important for fiber yield, the wild species are potential donor for abiotic and biotic stress tolerance like; fine fiber trait, disease resistance, drought tolerance and proved to be important genetic resources. Interspecific hybridization between wild and cultivated species may lead to conserve the wild germplasms and to create genetic diversity for enrichment of Jute trade in future[12]. In this regard, adequate information on morphological, cytological, anatomical, biochemical and molecular aspects helps to ascertain interrelationship between the germplasms for their successful exploitation in inter-specific hybridization and crop improvement[13].

The fiber yield of Jute crops varies from time to time due to many factors including biotic (disease, insect and virus) and abiotic (drought, heat, low soil fertility, etc.). Therefore, tailoring new variety of Jute crop have high potential yield, resistance to disease and good adaptability in different regions through breeding works must be a high priority. The systematic breeding works involved the several steps like; collection of germplasm, assessing of genetic variability, creating of genetic variability, implementing of selection and developing of selected genotypes to be released as commercial variety[14,15]. For efficient and effective breeding work, investigation and better understanding of the variability existing in a population base of crop is required so, that it can be exploited by plant breeder for crop improvement. Moreover, the success of any crops improvement program depends not only on the amount of genetic variation present in a crop, but also on magnitude of variation which is heritable from the parent to the progeny[16]. Knowledge on genetic variability of the local jute genotypes in the cultivable land was limited.

Therefore, there is a need to generate information on genetic variability, genotypic coefficient of variation, heritability and genetic advance of the Tossa Jute to estimate the progress of their breeding program in future. Heritability estimate of a character is important for plant breeder because it provides information on the extent to which a particular character can be transmitted from the parent to the progeny[17]. Similarly, genetic advance is also considered important because genetic advance shows the degree of the gain obtained in a character from one cycle of selection. High genetic advance coupled with high heritability estimates offers the most suitable condition to decide the criteria of selection[17]. In view of these, the present study was conducted the objectives to assess genetic variability, heritability and genetic advance of 12 local Tossa Jute genotypes cultivated or used to develop new variety in Bangladesh.

MATERIALS AND METHODS

Experimental materials and sites: The experiment was conducted at Jute Agricultural Experiment Station of BJRI at Manikganj district during the crop season from March-December, 2019.

As the experimental field having loamy soil, organic carbon 0.76%, soil pH 6.85, annual average temperatures 12.7-36°C, annual rainfall 2,376 mm with the elevation level of 49.21 ft above mean sea level and geographic coordinates[18] of 23°51 451″N, 90°04 01″E. The authors raised plants of individual species of *Corchorus* during the period of March-September and documented their morphological parameters (Table 1). Twelve of Tossa Jute genotypes including 2 accessions (Acc. 1306, Acc. 1318), 6 advanced breeding lines (O-043-7-9, O-049-1-3, O-0412-9-4, O-0411-10-4, O-0419-3-1, O-0512-6-2), 1 segregate (JRO-524-red) and 3 varieties [BJRI Tossa pat-5, JRO-524 (green) and BJRI Tossa pat-8] were used in this study. The germplasm accessions are maintained at Breeding Division of Bangladesh Jute Research Institute (BJRI), Manik Mia Avenue, Dhaka, Bangladesh.

Experimental design: The experiment was carried out in a Randomized Complete Block Design (RCBD) with three replications[19]. In each plot, the area was 6 m^2 (3×2 m) where line to line distance was 25 cm and plant to plant was 12-15 cm maintained to accommodate 30-35 plants m^2 area. All recommendation agricultural practices of Jute cultivations were followed to ensure normal plant growth.

Data collection: Ten plants were selected randomly from each plot and observation on plant height, stem basal diameter, green weight with leaves per plant, green weight without leaves per plant, dry fiber yield per plant, dry fiber yield per hectare of land and dry stick yield per plant were collected according to International Plant Genetic Resource Institute Bangladesh to evaluate the genotypes[20].

Statistical analysis: The data collected for each character was subjected to analysis of variance (ANOVA) by using RCB design to test the variations among genotypes. The analysis of variance was calculated by using Statistical Analysis System (SAS) software version 9.2[21]. After testing the ANOVA assumption, treatment means were tested with Duncan Multiple Range Testing (DMRT) at 5% probability levels[21].

Estimates of variance components: The variability present in the population was estimated by measure mean, phenotypic and genotypic variance and coefficient of variation. To estimate the phenotypic and genotypic variance, genotypic and phenotypic coefficients of variation were estimated based on formula[17] as follow:

σ^2_G = [(MSG)-(MSE)]/r
σ^2_P = [σ^2_G+σ^2_E]
σ^2_E = EMS/r

Where:

σ^2_G = Genotypic variance
σ^2_P = Phenotypic variance
σ^2_E = Environmental variance (Error mean square from the analysis of variance)
MSG = Mean square of genotypes
MSE = Error mean square
r = Number of replications:

$$\text{Genotypic coefficient of variation (GCV)} = [\sqrt{(\sigma^2_G)} / \bar{x}] \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)}] = [\sqrt{(\sigma^2_P)}/\bar{x}] \times 100$$

Where:

σ^2_G = Genotypic variance
σ^2_P = Phenotypic variance
$\bar{x}$ = Grand mean of a character

Estimation of heritability in broad sense: Broad sense heritability (h^2_{bs}) of the all traits were calculated according to the formula as described by Allard[14] as follow:

$$h^2_{bs} = \frac{\sigma^2_G}{\sigma^2_P} \times 100$$

Where:

h^2_{bs} = Heritability in broad sense
σ^2_G = Genotypic variance
σ^2_P = Phenotypic variance

Estimation of genetic advance: Genetic Advance (GA) was determined as described by Johnson *et al.*[22]:

$$GA = \frac{K \times \sigma_P \times h^2_{bs}}{100}$$

Where:

K = Selection differential (K = 2.06 at 5% selection intensity)

σ_P = Phenotypic standard deviation (STDEV.S) of the character

h^2_{bs} = Broad sense heritability

The genetic advance as percentage of the mean (GAM) was calculated as described by Johnson *et al.*[22] as follow:

$$GAM\ (\%) = \frac{GA}{\bar{x}} \times 100$$

Where:

GAM = Genetic advance as percentage of the mean
GA = Genetic advance
$\bar{x}$ = Grand mean of a character

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) and DMRT: The analysis of variance showed that genotype mean squares for all traits studied were highly significant (Table 1). It reflected the existing of large variability among tested genotypes and this variability can be further utilized for Tossa Jute plant improvement program. The Duncan Multiple Range Test (DMRT) was applied to know the variation between genotypes for all the characters (Table 2).

Analyses results for fiber yield revealed that, Acc. 1318 genotype attained maximum dry fiber yield per hectare area followed by O-0512-6-2, JRO-524 (green), BJRI Tossa pat-5 (Fig. 1).

Performance of all the genotypes by using DMRT (Table 2) indicated that Acc. 1318 genotype attained maximum plant height (3.22 m) followed by O-049-1-3 (3.18 m), stem base diameter (16.63 mm) followed by O-049-1-3 (16.23 mm), green weight with leaves per plant (261.93 g) followed by Acc. 1306 (260.27 g), O-0512-6-2 (260.17 g), green weight without leaves per plant (247.67 g) followed by Acc. 1306 (246.13 g), O-0512-6-2 (245.27 g), dry fiber weight per plant (16.93 g) followed by Acc. 1306 (13.83 g), O-0512-6-2 (13.50 g), JRO-524 (green) (13.43 g), BJRI Tossa pat-5 (13.20 g), dry fiber yield per hectare area (3.55 t) followed by Acc. 1306 (3.45 t), O-0512-6-2 (3.38 t) and JRO-524 (green) (3.35 t), BJRI Tossa pat-5 (3.30 t) (Fig. 1) and dry stick yield (52.70 g)

Table 1: Analysis of variance (ANOVA) for different quantitative characters studied

									F-value (Tabulated)	
SV	df (n-1)	PH	BD	GWL	GWL₁	FY	FY₁	STY	5%	1%
GMS	11	0.072**	4.945**	2495.58**	2304.84**	15.735**	0.736**	201.55**	2.27	3.19
BMS	2	0.009	1.293	153.88	27.22	3.315	0.12	27.3	3.44	5.72
EMS	22	0.002	0.466	6.05	23.57	0.44	0.023	4.032		
F (Calculated)		39.69	10.60	412.63	97.79	35.74	31.86	49.99		
Total df = 35										

SV: Source variation, GMS: Genotype mean square, BMS: Block mean square, EMS: Error mean square, PH: Plant height (m), BD: Stem base diameter (mm), GWL: Green weight with leaves per plant, GWL₁: Green weight without leaves per plant (g/pant), FY (g/plant): Dry fiber yield per plant, FY₁: Dry fiber yield per hectare (t ha⁻¹), STY: Dry stick yield per plant (g/plant), df: Degree of freedom, **Significant at 0.01 level of probability

Table 2: Performance mean of 12 Tossa Jute genotypes for morphological traits studied

Var/Lines	PH (m)	BD (mm)	GWL (g)	GWL₁ (g/plant)	FY (g/plant)	FY₁ (t ha⁻¹)	STY (g)
Acc. 1306	3.15ᵃᵇᶜ	15.40ᵇ	260.27ᵃ	246.13ᵃ	13.83ᵇ	3.45ᵇ	51.40ᵃ
Acc. 1318	3.22ᵃ	16.63ᵃ	261.93ᵃ	247.67ᵃ	16.93ᵃ	3.55ᵃ	52.70ᵃ
O-043-7-9	2.88ᶠᵍ	15.60ᵃᵇ	214.80ᵈᵉ	199.00ᶜᵈ	10.13ᵉᶠ	2.50ᶠᵍ	34.80ᶜ
O-049-1-3	3.18ᵃᵇ	16.23ᵃᵇ	213.80ᵈᵉ	195.87ᵈ	11.07ᵈᵉ	2.92ᵈᵉ	39.40ᵇ
O-0512-6-2	3.15ᵇᶜ	16.22ᵃᵇ	260.17ᵃ	245.27ᵃ	13.50ᵇ	3.38ᵇ	40.40ᵇ
O-0412-9-4	2.73ʰ	14.00ᶜ	208.87ᶠ	206.80ᵇᶜ	9.20ᶠ	2.27ᵍ	35.00ᶜ
O-0411-10-4	2.95ᶠ	16.13ᵃᵇ	217.53ᵈ	213.87ᵇ	12.10ᶜᵈ	3.00ᵈ	40.00ᵇ
O-0419-3-1	3.10ᶜᵈᵉ	16.07ᵃᵇ	227.87ᶜ	211.47ᵇ	9.63ᶠ	2.71ᵉᶠ	37.00ᵇᶜ
BJRI Tossa pat-5	3.13ᵇᶜᵈ	15.13ᵇᶜ	212.20ᵉᶠ	198.80ᶜᵈ	13.20ᵇᶜ	3.30ᵇᶜ	22.80ᵉ
JRO-524 (green)	3.07ᵈᵉ	16.20ᵃᵇ	248.33ᵇ	214.33ᵇ	13.43ᵇ	3.35ᵇ	38.20ᵇᶜ
JRO-524 (red)	3.04ᵉ	15.40ᵇ	224.07ᶜ	213.07ᵇ	12.23ᶜ	3.05ᶜᵈ	38.20ᵇᶜ
BJRI Tossa pat-8	2.84ᵍ	12.00ᵈ	161.33ᵍ	146.67ᵉ	11.50ᵈᵉ	2.80ᵉᶠ	29.00ᵈ
Maximum	3.22	16.63	261.93	247.67	16.93	3.55	52.70
Mean	3.04	15.42	225.93	211.58	12.06	3.02	38.24
LSD₍₀.₀₅₎	0.07**	1.16**	4.16**	8.22**	1.12**	0.26**	3.40**
CV (%)	1.47	4.43	1.09	2.29	5.50	5.02	5.25

CV: Coefficient of variation) = (√EMS/Mean)×100, LSD (0.05): Least significant difference at 5% probability level, values with same letters are statistically insignificant for same variable, PH: Plant height (m), BD: Stem base diameter (mm), GWL: Green weight with leaves per plant, GWL₁: Green weight without leaves per plant (g/plant), FY (g/plant): Dry fiber yield per plant, FY₁: Dry fiber yield per hectare (t ha⁻¹), STY: Dry stick yield per plant (g/plant), df: Degree of freedom, **Significant at 0.01 level of probability
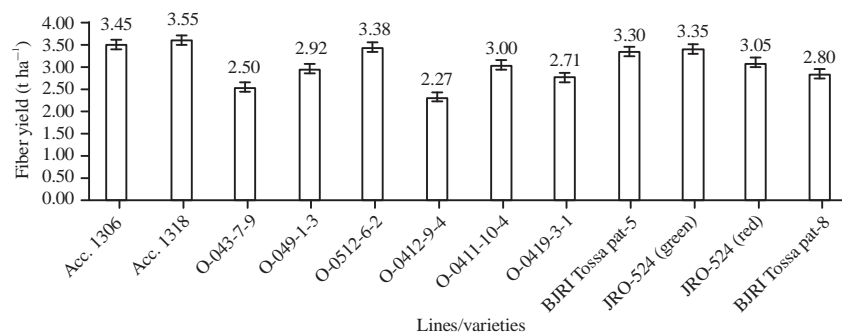
Fig. 1: Fiber yield performance of selected 12 Tossa Jute genotypes

Table 3: Correlations among the morphological traits studied in Tossa Jute genotypes

Characters	PH (m)	BD (mm)	GWL (g/plant)	GWL$_1$ (g/plant)	FY (g/plant)	FY$_1$ (t ha^{-1})	STY (g)
PH	1.000						
BD	0.684*	1.000					
GWL	0.670*	0.786*	1.000				
GWL$_1$	0.577*	0.743*	0.962*	1.000			
FY	0.728**	0.557**	0.750*	0.712*	1.000		
FY$_1$	0.842**	0.644**	0.800*	0.742*	0.976*	1.000	
STY	0.450*	0.522*	0.737*	0.757*	0.586*	0.577*	1.000

PH: Plant height (m), BD: Stem base diameter (mm), GWL: Green weight with leaves per plant, GWL$_1$: Green weight without leaves per plant (g/plant), FY (g/plant): Dry fiber yield per plant, FY$_1$: Dry fiber yield per hectare (t ha^{-1}), STY: Dry stick yield per plant (g/plant), df: Degree of freedom, **Significant at 0.01 level of probability

followed by Acc. 1306 (51.40 g), O-0512-6-2 (40.40 g), O-0411-10-4 (40.00 g), O-049-1-3 (39.40 g) and JRO-524 green and red (38.20 g), O-0419-3-1 (37.00 g).

Based on performance mean of selected 12 genotypes for some of their morphological traits, the genotypes Acc. 1318, Acc. 1306, O-0512-6-2, O-049-1-3 gave good results which will be considered for further improvement of Tossa Jute in Bangladesh.

Estimates of correlations among the characters studied: The positive significant correlations were observed for all the characters considering all genotypes. Highly significant and positive correlations were recorded between plant height, stem base diameter and fiber yield (Table 3).

Estimates of variance components: The estimates of phenotypic variances (σ^2_P), genotypic variances (σ^2_G), Phenotypic Coefficients of Variation (PCV) and Genotypic Coefficients of Variation (GCV) are given in Table 4. Genetic variance and phenotypic variance values ranged from 0.023-829.843 and 0.024-831.860 for plant height and green weight with leaves per plant, respectively. The GCV and PCV values were ranged from 5.026-21.218% and 5.090-21.434% for plant height and dry stick weight per plant, respectively (Table 4). According to Deshmukh *et al.*[23], PCV and GCV values greater than 20% are regarded as high and values between 10 and 20% to be medium, whereas, values less than 10% are considered to be low.

Estimates of co-variance components: Accordingly, high PCV and GCV were recorded for dry stick weight per plant, while traits with moderate PCV and GCV were recorded for green weight with leaves per plant, green weight without leaves per plant, dry fiber yield per plant and dry fiber yield per hectare, while traits with low PCV and GCV were found for plant height and stem base diameter. High and moderate values of PCV and GCV indicated the existence of substantial variability for such characters and selection may be effective based on these characters. Similar finding was reported by earlier researchers for plant height, stem base diameter, dry fiber yield per plant, dry fiber yield per hectare of land, dry stick yield per plant[13], for green weight with leaves per plant and green weight without leaves per plant[24].

In this study, the PCV was relatively greater than GCV for all traits however, GCV was near to PCV for all characters (Table 3), indicated high contribution of genotypic effect for phenotypic expression of such characters. Similar result was reported for plant height, stem base diameter, dry fiber weight and dry stick yield[24]. In other traits, there are wider gaps between estimate of PCV and GCV showed distinct contribution of environmental factors in addition to genotypic effect for expression of the traits. Similar finding was reported by Sharma *et al.*[25]. Genotypic coefficient of variance provides information on the genetic variability present in quantitative characters in base population, but it is not possible to determine the amount of the variation that was heritable only from the genotypic coefficient of variance. Genetic coefficient
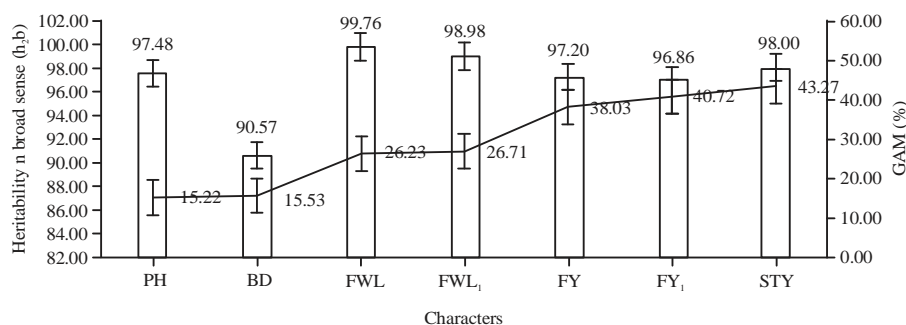
Fig. 2: h$_2$b and GAM (%) for different characters studied

Table 4: Range, mean, variances, covariances, heritability and genetic advances of morphological traits studied

Characters	Range	±SE	GV (σ²$_G$)	PV (σ²$_P$)	GCV (%)	PCV (%)	h²$_{bs}$ (%)	GA	GAM (%)
PH (m)	3.22-2.73	3.04±0.025	0.023	0.024	5.026	5.090	97.476	0.311	15.216
BD (mm)	16.63-12.00	15.42±0.39	1.493	1.648	7.924	8.326	90.569	2.395	15.534
GWL (g/plant)	261.93-161.33	225.93±1.42	829.843	831.860	12.750	12.766	99.758	59.270	26.234
GWL$_1$ (g/plant)	247.67-146.67	211.58±2.80	760.423	768.280	13.033	13.101	98.977	56.515	26.711
FY (g/plant)	16.93-9.20	12.06±0.38	5.098	5.245	18.723	18.990	97.202	4.586	38.025
FY$_1$ (t ha⁻¹)	3.92-2.27	3.02±0.09	0.238	0.245	16.156	16.416	96.861	0.988	40.723
STY (g/plant)	51.70-22.80	38.24±1.16	65.840	67.184	21.218	21.434	98.000	16.547	43.272
Maximum		225.93±1.42	829.843	831.860	21.218	21.434	99.758	59.270	43.272
Minimum		3.02±0.09	0.023	0.024	5.026	5.090	90.569	0.311	10.216

SE: Standard error, GV (σ²$_P$): Genotypic variation, PV (σ²$_P$): Phenotypic variation, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h²$_{bs}$: Heritability in broad sense, GA: Genetic advance, GAM (%): Genetic advance as percentage of the mean

of variance together with heritability estimates would give the best picture of the amount of advance to be expected from selection[26]. Thus, the heritable portion of the variation could be more useful with help of heritability estimates.

Heritability: Heritability values are helpful in predicting the expected progress to be achieved through breeding and selection processes. Estimates of heritability in broad sense ranged from 90.569% for base diameter to 99.758% for green weight with leaves per plant (Fig. 2). According to Singh[27], that heritability values greater than 80% were very high, values from 60-79% were moderately high, values from 40-59% were medium and values less than 40% were low. Accordingly, the estimate of heritability of all characters studied was very high (Table 4).

The characters having very high heritability indicated relative small contribution of the environment factors to the phenotype and selection for such characters could be fairly easy due to high additive effect[28]. High estimates of broad sense heritability have also been reported by previous researchers for plant height, stem base diameter[29], for fresh weight with and without leaves[24], dry fiber yield and stick yield per plant[30].

Genetic advance: Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotype. Hence, knowledge on

heritability coupled with genetic advance is more useful. Genetic Advance (GA) under selection referred to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at given selection intensity[25].

Furthermore, Hamdi *et al.*[31] stated that Genetic Advance (GA) is importance to predicting the expected genetic gain from one cycle of selection. Estimates of GA values for all characters studied are displayed in Table 4.

Estimates of genetic advance for dry fiber yield per plant was 4.586 g, indicated that whenever the best, 5% high yielding genotypes as parents, mean dry fiber yield per plant of the offspring could be improved a large of 4.586 g, that is, mean genotypic value of the new population for dry fiber yield per plant will be improved from 12.06-16.646 g. In the same way, plant height will be improved from 3.04-3.351 m, 15.42-17.815 mm for stem base diameter, 3.02-4.008 t for fiber yield per hectare of 1 and 38.24-54.787 g for dry stick yield per plant (Table 4).

Genetic advance in percent of mean: Genetic Advance as mean percentage (GAM) in this study ranged from 10.216- 43.272% for plant height and dry stick yield per plant, respectively (Table 4). According to Johnson *et al.*[22] that the value of genetic advance as mean percentage is categorized as low (<10%), moderate (10-20%) and high (>20%). The GAM

of plant height and stem base diameter were classified as moderate, whereas other characters were high (Table 4). According to Johnson *et al.*[22], high heritability estimates along with the high genetic advance as per mean is usually more helpful in predicting gain under selection than heritability alone. In the present study, high heritability with moderate genetic advance as percent of the mean are exhibited by plant height and stem base diameter, while the other characters were exhibited high heritability with high genetic advance as mean percentage (Fig. 2) reflecting the presence of additive gene action for the expression of these traits which is fixable for next generations and selection in next population based on this character would be ideal. Similar results were also reported by Sreelathakumary and Rajamory[30] in local chili pepper. Nagaraju *et al.*[32] reported high heritability combined with high genetic advance for yield per plant.

The traits having high values of heritability coupled with moderate genetic advance as percent of the mean viz. plant height and stem base diameter suggested that selection for improvement of these characters may be rewarding. It also indicated that greater role of non-additive gen action in their inheritance. Yadeta *et al.*[24] was also reported that plant height character had high heritability and moderate genetic advance.

CONCLUSION

Based on the findings in this study, it is concluded that seven characters viz. plant height, stem basal diameter, green weight with leaves per plant, green weight without leaves per plant, dry fiber yield per plant, dry fiber yield per hectare of land and dry stick yield per plant could be used as good criteria for selection in the Jute plant improvement because these characters had high genotypic coefficient of variation, heritability estimate and genetic advance as percent of the mean. Among all the genotypes, the accessions Acc. 1318, 1306, advanced lines viz., O-0512-6-2, JRO-524 (green), BJRI Tossa pat-5 and JRO-524 (red) performed well in respect of plant height, stem base diameter and fiber yield. These materials would be considered for breeding purpose for the improvement of Tossa Jute crop through hybridization techniques.

SIGNIFICANCE STATEMENT

This study identified some Tossa Jute genotypes with genetic variabilities for different morphological characters which will help the plant breeders to choose the breeding materials for good hybridization and new variety development. The genotype with high heritability and genetic advance will contribute in developing new high yielding varieties of Tossa Jute in Bangladesh.

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