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Genetic variability, heritability and genetic advance for yield related characters of tossa jute (*Corchorus olitorius*) genotypes

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ABSTRACT

The genetic parameters of variability were studied for seven yield related characters in forty-seven genotypes of tossa jute. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Highly significant genotypic differences were reported for all the characters. The maximum co-efficient of range were reported for green weight (g)/plant and stick weight (g)/plant followed by fibre weight (g)/plant, green bark thickness (mm) and core diameter (mm). The phenotypic and genotypic variances were the highest in green weight (g)/plant. The high PCV and GCV values recorded in stick weight (g)/plant. The maximum estimates of broad-sense heritability were recorded in stick weight (g)/plant followed by fibre weight (g)/plant, green weight (g)/plant and plant height (m). The result from this study leads to the conclusion that green weight (g)/plant, fibre weight (g)/plant and stick weight (g)/plant should be considered during selections for yield in *C. olitorius*.

Key Words: Tossa jute, *Corchorus olitorius*, Variability and Genotype

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I. Introduction

Jute is the second most important natural fibre crop after cotton (*Gossypium* sp. L.) in the Indian subcontinent. In Bangladesh jute cultivation area covered 698000 ha and production 7897100 MT in 2016-17 season. Among the total jute production area tossa jute occupied 98% area and produced 95% jute production of total production. Tossa jute (*Corchorus olitorius*) is an Afro-Arabian variety characterized by soft, silkier and stronger fibre than white jute (*Corchorus capsularis*). This variety astonishingly shows good sustainability in the climate of the Ganges Delta. However, the crop demands of the immediate attention of plant breeders. The available elite cultivars of tossa jute are essentially derived either through pure line selection or hybridization followed by selection from a few common accessions. Varietal improvement in jute, a predominantly self-pollinated crop, has been impaired due to lack of adequate genetic diversity within the available genetic stock (Singh, 1980;

Joshua and Thakare, 1984). The rates of genetic exploitation of the variation for production of improved cultivars and yield have not received sufficient attention. Rapid genetic improvement of crop depends on the availability of sufficient genetic diversity, which could be selected and combined in various forms to produce reasonable improvement (Denton and Nwangburuka, 2011; Wani *et al.* 2011). Various methods have been employed in the determination of heritability estimates (Wray and Visscher, 2008; Jindal *et al.*, 2010; Denton and Nwangburuka, 2011; Nwangburuka *et al.*, 2012). Estimates of heritability values become more reliable and meaningful when combined with genetic advance (Denton and Nwangburuka, 2011). High heritability and genetic advance in a trait indicates the presence of additive genes in such trait and further suggest reliable crop improvement through selection of such a trait (Panse, 1957). The present study was aimed at evaluation of genotypes of *C. olitorius* and determination of the genetic variability, heritability and genetic advance of the characters for their use in a varietal improvement programme.

II. Materials and Methods

The experimental material comprised of 47 genotypes of Tossa Jute (*Corchorus olitorius*) collected from Gene Bank Department of Bangladesh Jute Research Institute (BJRI). The test genotypes are listed in table 01. The experiment was conducted at the Jute Agriculture Experimental Station, Jagirs, Manikganj of Bangladesh Jute Research Institute during the period from April 2016 to September 2016. The experiment was laid out in the Randomized Complete Block Design (RCBD) with three replications. Seeds were sown in single row of 3m long with spacing of 30 cm, 60 cm and 5-7 cm between rows, replications and plants, respectively. Standard production technology from *Hand Book on Agricultural Technologies of Jute, Kenaf and Mesta crops* (2008) was adopted to raise a good crop under optimum management. The seeds were sown on 10 April, 2016. Intercultural operations were done at proper time for ensuring proper growth of the crop. The data were recorded from 10 randomly selected plants of each accession from each replication for yield traits viz., plant height (m), base diameter (mm), core diameter (mm), green bark thickness (mm), green weight (g)/plant, fibre weight (g)/plant and stick weight (g)/plant.

Table 01. List of the genotypes used in this experiment

Sl. No.	Genotypes	Source/Origin	Sl. No.	Genotypes	Source/Origin
01.	Acc.-1080	Bangladesh	25.	Acc.- 2690	Bangladesh
02.	Acc.-1108	Bangladesh	26.	Acc.- 2963	Bangladesh
03.	Acc.-1127	Bangladesh	27.	Acc.- 2995	Bangladesh
04.	Acc.-1156	Bangladesh	28.	Acc.- 3375	Bangladesh
05.	Acc.- 1207	Bangladesh	29.	Acc.- 3702	Kenya
06.	Acc.- 1210	Bangladesh	30.	Acc.- 3705	Kenya
07.	Acc.- 1216	Bangladesh	31.	Acc.- 3808	-
08.	Acc.- 1278	Bangladesh	32.	Acc.- 3988	Syria
09.	Acc.- 1283	Bangladesh	33.	Acc.- 3990	Syria
10.	Acc.- 1337	Cairo	34.	Acc.- 4025	Bangladesh
11.	Acc.- 1339	USSR	35.	Acc.- 4172	Tanzania
12.	Acc.- 1348	Denmark	36.	Acc.- 4178	Tanzania
13.	Acc.- 1349	Mozambique	37.	Acc.- 4234	Tanzania
14.	Acc.- 1352	India	38.	Acc.- 4483	USA
15.	Acc.- 1355	India	39.	Acc.- 4546	Thailand
16.	Acc.- 1356	USSR	40.	Acc.- 4566	Nepal
17.	Acc.- 1360	Denmark	41.	Acc.- 4569	Nepal
18.	Acc.- 1390	Bangladesh	42.	Acc.- 4570	Nepal
19.	Acc.- 1478	-	43.	Acc.-4702	Nepal
20.	Acc.- 1532	-	44.	Acc.- 4739	China
21.	Acc.- 1776	Bangladesh	45.	Acc.- 5001	China
22.	Acc.- 1795	Bangladesh	46.	O-9897	BJRI
23.	Acc.- 1823	-	47.	O-795	BJRI
24.	Acc.- 2378	Bangladesh			

Statistical Analyses: Analysis of variance was done based on RCBD as suggested by [Panse and Sukhatme \(1985\)](#) for each of the characters separately. Coefficient of range was calculated using following formula:

$$\text{Coefficient of range} = (H - L) / (H + L) \dots\dots\dots(1)$$

Where,

H is the highest value in a set of observation and

L is the lowest value in a set of observation

The yield and yield component were used to determining the genotypic and phenotypic variances according to [Prasad et al. \(1981\)](#) as follows:

$$\text{Genotypic variance } (\delta^2g) = (MSG - MSE) / r \dots\dots\dots(2)$$

$$\text{Phenotypic variance } (\delta^2ph) = MSG / r \dots\dots\dots(3)$$

$$\text{Error variance } (\delta^2e) = MSE / r \dots\dots\dots(4)$$

Where,

MSG = Genotypic mean squares

MSE = Mean squares error

r = Number of replications

The variance component was used to computing the Genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), estimates of broad-sense heritability and genetic advance (GA) according to [Burton \(1952\)](#); [Johnson et al. \(1955\)](#) and [Kumar et al. \(1985\)](#) as follows:

$$\text{Genotypic Coefficient of Variability (GCV)} = 100 \times (\delta g / \bar{x}) \dots\dots\dots(5)$$

$$\text{Phenotypic Coefficient of Variability (PCV)} = 100 \times (\delta ph / \bar{x}) \dots\dots\dots(6)$$

Where, δg and δph are the genotypic and phenotypic standard deviations, respectively and \bar{x} is the grand mean for the trait under consideration.

$$\text{Heritability (Broad-sense)} = \delta^2g / (\delta^2g + \delta^2e) \dots\dots\dots(7)$$

Where, δ^2g is the estimate of genotypic variance, δ^2e is the estimate of environmental variance.

$$\text{Genetic advance} = \text{heritability} \times k \times \delta ph \dots\dots\dots(8)$$

Where, K and δph are the selection differential and phenotypic standard deviations, respectively.

III. Results and Discussion

The analysis of variance revealed highly significant differences among genotypes for all the characters indicating presence of considerable variability for the characters under study among the test genotypes ([Table 02](#)). This suggests that there was genetic diversity in these characters among the accessions studied and further suggests prospects for meaningful selection for *Corchorus* improvement. This agree with the reports of [Dar and Sharma \(2011\)](#), who reported significant variation in quantitative characters in 60 tomatoes genotypes, [Kitila et al. \(2011\)](#) reported significant variation in quantitative traits in coffee; [Singh et al. \(2011\)](#) reported significant variations quantitative characters in field pea, [Nwangburuka et al. \(2012\)](#) reported significant variations in nine yield related characters in twenty-nine accessions of okra. [Bhandari et al. \(2017\)](#) reported significant variations in ten yield related characters in 66 genotypes of tomato.

The different genetic parameters like range, mean, phenotypic variance, genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as a percentage of mean are presented in [table 03](#). The range was the maximum for green weight (g)/plant 400.00 (550.00-150.00) followed by stick weight (g)/plant 67.60 (92.00-24.40) and fibre weight (g)/plant (22.00). The maximum coefficient of range was reported for green

weight (g)/plant (0.57) and stick weight (g)/plant (0.57) followed by fibre weight (g)/plant (0.52), green bark thickness (mm) (0.48) and core diameter (mm) (0.42) indicating existence of sufficient variability among the test genotypes for the characters. The PCV value was found slightly higher than the GCV value for all the characters. This may suggest that slight environmental effect on the phenotype of all the other characters. This report corresponds to the report of Denton and Nwangburuka (2011), Nwangburuka *et al.* (2012), Mohammed *et al.* (2012), Yadav *et al.* (2011) and Ayalneh *et al.* (2012) who observed slight differences between PCV and GCV in characters studied in *Solanum anguivi*, okra, Ethiopian Duram wheat, Rice and in Tef, respectively.

Table 02. Analysis of variance for different yield related characters of forty-seven tossa jute (*Corchorus olitorius*) Genotypes

Source of variation	Df	Plant height (m)	Base diameter (mm)	Core diameter (mm)	Green bark thickness (mm)	Green weight (g)/plant	Fibre weight (g)/plant	Stick weight (g)/plant
Replication	2	0.009	5.58	8.06	0.06	1587.94	2.68	28.25
Genotypes	46	0.17**	9.12**	7.49**	0.25**	17615.20**	56.57**	471.55**
Error	92	0.04	3.72	2.96	0.14	369.82	0.97	7.43
CV%		5.68	11.60	13.50	19.52	6.63	5.36	5.99

** Significant at 1% level of probability

Table 03. Genetic parameters of different yield related characters

Parameter / character	Mean	Range	Coefficient of range	Phenotypic variance	Genotypic variance	PCV	GCV	h^2 (bs)	Genetic Advance	Genetic Advance as % of mean
Plant height (m)	3.38	2.70-4.20	0.22	0.06	0.04	7.25	5.92	80.00	0.40	11.83
Base diameter (mm)	16.63	11.40-24.60	0.36	3.04	1.80	10.48	8.07	59.21	2.12	12.75
Core diameter (mm)	12.76	8.00-19.80	0.42	2.50	1.51	12.39	9.63	60.40	1.95	15.28
Green bark thickness (mm)	1.94	1.00-2.90	0.48	0.08	0.03	14.58	8.93	37.50	0.22	11.34
Green weight (g)/plant	289.93	150.00-550.00	0.57	5871.73	5748.46	26.43	26.15	97.90	154.53	53.29
Fibre weight (g)/plant	18.38	10.00-32.00	0.52	18.86	18.53	23.63	23.42	98.30	8.79	47.82
Stick weight (g)/plant	45.50	24.40-92.00	0.57	157.18	154.71	27.55	27.33	98.42	25.41	55.85

The PCV ranged from (7.25) for plant height (m) to (27.55) for stick weight (g)/plant. Similarly, GCV ranged from (5.92) for plant height (m) to (27.33) for Stick weight (g)/plant. The high PCV and GCV values recorded in stick weight (g)/plant suggests that this character accounts for most of the variation recorded in *C. olitorius*. The phenotypic and genotypic variance was the highest in green weight (g)/plant (5871.73 and 5748.46) but the lowest in the plant height (m) (0.06) and green bark thickness (mm) (0.03), respectively. High genotypic variance facilitates selection for the improvement and widens the probability for heritability of traits from parents to offspring (Ayalneh *et al.* 2012). Broad-sense heritability estimates varied from low to high. Dabholkar (1992) categorized heritability estimates as low (5-10%), medium (11-30%) and high (>30%). Maximum estimates of broad-sense heritability was recorded in stick weight (g)/plant (98.42) followed by fibre weight (g)/plant (98.30), green weight (g)/plant (97.90) and plant height (m) (80.00) This suggests the effect of additive genes in the inheritance of these characters. This further indicates that any selection in *C. olitorius* based on the phenotypic of these characters will be effective in the improvement of *C. olitorius* yield. According to Ghandi *et al.* (1964) and Ibrahim and Hussein (2006), prediction of the response of an individual to selection are more reliable when GCV, estimates of broad-sense heritability and genetic advance is

combined instead of relying on the estimates of broad-sense heritability estimates alone. When the GA is high the heritability is mainly due to additive gene effect (Percy and Turcotte, 1991). Hence selection based on characters such as green weight (g)/plant (26.15, 97.90 and 53.29), fibre weight (g)/plant (23.42, 98.30 and 47.82) and stick weight (g)/plant (27.33, 98.42 and 55.85) combining high GCV, heritability and GA, respectively are under additive gene effect and will be effective in accurate prediction of yield (Bello et al., 2006). This agree with the reports of Mohammed et al. (2012) in their work with wheat; Yadav et al. (2011) in their report on rice. High heritability and genetic advance is an indication of how much selection to improve a character can be based of phenotypic performance (Johnson et al., 1995).

IV. Conclusion

The study leads to the conclusion that there is significant genetic variability among the accessions studied. It further concludes that characters such as Green weight (g)/plant, Fibre weight (g)/plant and Stick weight (g)/plant combining high GCV, heritability and GA, should considered during selections for yield in *C. olitorius*.

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