

Phenotypic variation and the relationships among jute (*Corchorus* species) genotypes using morpho-agronomic traits and multivariate analysis

Ranjit Kumar Ghosh¹, Tanee Sreewongchai¹, Sutkhet Nakasathien¹ and Chalernpol Phumichai^{1*}

¹Department of Agronomy, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand

* Corresponding author: chalernpol.ph@gmail.com, agrcpp@ku.ac.th

Abstract

Twenty-five morpho-agronomic traits of 63 jute genotypes, including 2 varieties with 37 accessions of *C. capsularis* and 1 variety with 23 accessions of *C. olitorius*, were evaluated to assess the extent and patterns of variability and their relationships. Seed traits exhibited a wider range of variation than fiber traits and the genotypes in *C. olitorius* varied the most than those in *C. capsularis*. Qualitative traits were also the most informative. Significant positive correlations were recorded of fiber yield with days to 50% flowering (0.60), plant height at average flowering (0.72), plant base diameter (0.74) and fresh weight (0.90), whereas, leaf angle was negatively (-0.52) correlated. Seed yield was significantly positively correlated with pod length (0.72) and seeds per pod (0.79). The clustering patterns suggested that the two jute species are distantly related. The highest diversity (0.69) was observed between clusters IX and IV, whereas clusters III and IV showed the greatest similarity (0.14). Principal component (PC) analysis revealed that the first five PCs having eigenvalues >1 explained 75.93% of the total variation. The variance explained by PC1 was mostly due to traits related to fiber and seed yield, whereas PC II was mostly related to color traits. Two-dimensional scatter plots supported the grouping patterns of cluster analysis. The accessions BRA/4792 and BRA/4794 and variety O-9897 of *C. olitorius* were identified as the most promising genotypes, based on their phenotypic variability and high yield performance, for use as genetic material for future jute breeding programs and for germplasm conservation.

Keywords: cluster analysis; correlation; eigenvalue; principal component; qualitative traits; quantitative traits; scatter plot.

Abbreviations: CV - coefficient of variation; DF - days to 50% flowering; DPM - difference as percent of minimum value; FY - fiber yield; PBD - plant base diameter; PCA - principal component analysis; PL₁ - petiole length; PL₂ - pod length; SY - seed yield.

Introduction

Jute (*Corchorus* spp.) is a natural fiber crop and is second in the world after cotton in terms of global production, consumption and availability. It is a completely biodegradable, recyclable and eco-friendly lingo-cellulose fiber (Kundu, 1951; Mir et al., 2008). The jute fibers are derived from the bark of the plant. The genus *Corchorus* belongs to the family Malvaceae, which is composed of approximately 100 species (Saunders, 2001). Of these, two species (*Corchorus capsularis* L. and *Corchorus olitorius* L.) are widely cultivated for natural fiber in areas distributed throughout the tropical and sub-tropical regions of the world, particularly in Asia, Africa and Latin America (Kundu, 1951; Edmonds, 1990; Hossain et al., 2002). The most common use of jute fiber is in packaging materials such as hessian, sacking and ropes. A variety of products, such as floor coverings, home textiles, agro-textiles, blankets, handicrafts and fashion accessories, are also made from jute. In recent years, jute has been used for making pulp and papers in the paper industry (Mohiuddin et al., 2005). The fiber yield of jute in Bangladesh, the second largest producer in the world, has slightly increased from 1.74 t ha⁻¹ in 1999-2000 to 2.22 t ha⁻¹ in 2009-2010 (BBS, 2010), despite the expanding global demand for natural fiber. In addition, seed is a basic input for any crop production program, which leads inevitably for agricultural change of a country but Bangladesh has been facing an acute shortage of quality jute seed every year (Hossen et al., 2008), due to the lack of work on breeding

new superior varieties based on fiber and seed yield. Furthermore, the two cultivated species of jute are different in terms of growth habitat, disease and pest resistance and characteristics related to fiber and seed yield (Kundu, 1951; Edmonds, 1990). For example, *C. olitorius* is relatively tolerant to diseases and pests and produces a stronger fiber than *C. capsularis*, whereas *C. capsularis* is more resistant to water logging and drought (Roy et al., 2006). Combining the desirable traits of the two species would be advantageous; however, these species cannot be crossbred, possibly because of the presence of a strong sexual incompatibility barrier between them (Patel and Datta, 1960). Nevertheless, Islam and Rashid (1960) and Choudhuri and Mia (1962) have succeeded in producing hybrids. Moreover, advanced technologies such as somatic hybridization, chromosome doubling, embryo rescue and genetic transformation could be used to overcome the sexual incompatibility problems (Saha et al., 2001; Ghosh et al., 2002). If jute is to be genetically improved, the divergent genotypes must first be identified, the genetic variability characterized and the degree and nature of the associations of various traits with yield determined. The gene bank of the Bangladesh Jute Research Institute has 5,936 accessions of jute and allied fiber crops (Haque et al., 2007) that could be used to accomplish this goal. Although some diversity studies were carried out with molecular markers to evaluate the genetic variation in jute (Basu et al., 2004; Roy et al., 2006; Akter et al., 2008; Benor

Table 1. List of accessions and varieties of the two cultivated species of jute used in the study.

No	<i>C. capsularis</i>	Status	Country/ Origin	No	<i>C. olitorius</i>	Status	Country/Origin
1	CVL-1	V	Bangladesh	40	O-9897	V	Bangladesh
2	C-83	V	Bangladesh	41	KEN/3705	A	Kenya
3	BAN/2596	A	Bangladesh	42	KEN/3727	A	Kenya
4	BAN/2749	A	Bangladesh	43	KEN/3728	A	Kenya
5	BAN/2753	A	Bangladesh	44	KEN/3732	A	Kenya
6	BAN/2761	A	Bangladesh	45	KEN/3784	A	Kenya
7	BAN/3465	A	Bangladesh	46	KEN/3835	A	Kenya
8	BAN/3466	A	Bangladesh	47	TAN/4177	A	Tanzania
9	BAN/3473	A	Bangladesh	48	TAN/4178	A	Tanzania
10	TAI/4374	A	Taiwan	49	TAN/4189	A	Tanzania
11	THA/4467	A	Thailand	50	TAN/4191	A	Tanzania
12	THA/4520	A	Thailand	51	TAN/4231	A	Tanzania
13	NEP/4588	A	Nepal	52	THA/4461	A	Thailand
14	TAN/4617	A	Tanzania	53	THA/4466	A	Thailand
15	BRA/4619	A	Brazil	54	IND/4546	A	Indonesia
16	BRA/4620	A	Brazil	55	NEP/4566	A	Nepal
17	BRA/4621	A	Brazil	56	NEP/4574	A	Nepal
18	THA/4683	A	Thailand	57	NEP/4579	A	Nepal
19	NEP/4701	A	Nepal	58	NEP/4580	A	Nepal
20	NEP/4705	A	Nepal	59	CHI/4739	A	China
21	NEP/4711	A	Nepal	60	CHI/4740	A	China
22	CHI/4724	A	China	61	BRA/4792	A	Brazil
23	CHI/4727	A	China	62	BRA/4794	A	Brazil
24	CHI /4731	A	China	63	NIG/4796	A	Niger
25	NEP/4879	A	Nepal				
26	CHI/4937	A	China				
27	CHI/4939	A	China				
28	CHI/4955	A	China				
29	CHI/4958	A	China				
30	CHI/4964	A	China				
31	CHI/4965	A	China				
32	CHI/4988	A	China				
33	CHI/4995	A	China				
34	CHI/5000	A	China				
35	CHI/5002	A	China				
36	NEP/5062	A	Nepal				
37	NEP/5063	A	Nepal				
38	NEP/5064	A	Nepal				
39	NEP/5065	A	Nepal				

V and A indicate variety and accession, respectively. Except for the varieties, the first three letters prior to each accession number designate the country of origin

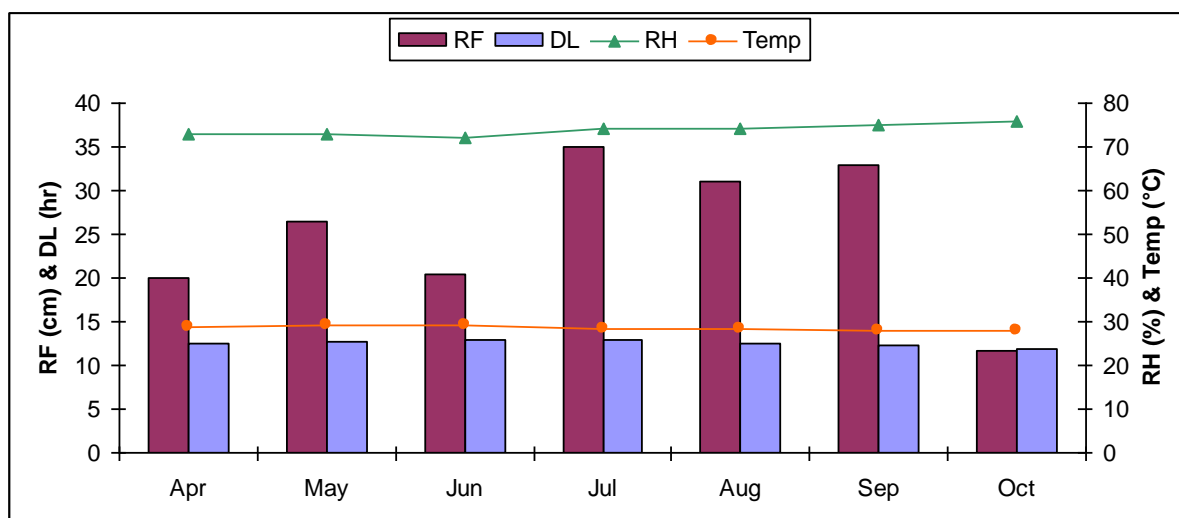


Fig 1. Meteorological data on monthly average temperature (°C), rainfall (cm), relative humidity (%) and day length (hr) during the jute-growing season.

et al., 2012), phenotypic descriptors are necessary for evaluating the genetic variation of a crop species (Franco et al., 2005; Laurentin, 2009). Phenotypic evaluation is used for thorough investigation of the genetic variability in germplasm collections and contributes valuable information to conservation efforts and breeding programs (Gupta et al., 1991). To the best of our knowledge, there has been very little research on the phenotypic diversity and relationships of jute with diverse geographical origins. In the past, Palit et al. (1996) studied germplasm diversity and genetic advance in *C. olitorius* accessions focusing on 4 morpho-physiological traits; Palve and Sinha (2005) used 6 accessions of *C. capsularis* and 7 accessions of *C. olitorius* for their study. Recently, Benor et al. (2012) used only *C. olitorius* species to study genetic diversity and relationships inferred from molecular and morphological data. Multivariate methods such as principal component analysis (PCA) have proven to be useful for characterizing, evaluating and classifying germplasm when a large number of accessions are assessed for several characteristics of agronomic importance (Peeters & Martinelli, 1989; Badenes et al. 2000). Therefore, the present study was planned with the objectives i) to evaluate the most discriminating and essential morpho-agronomic traits, ii) to determine the important associations among 17 quantitative traits and iii) to identify the most divergent genotypes in jute in terms of phenotypic diversity for use in germplasm conservation and efficient breeding programs.

Results and discussion

Variation in quantitative traits

To evaluate the extent of variability of the genotypes of *C. capsularis*, *C. olitorius* and overall accessions and varieties, as well as variability within the species listed in Table 1, data for 17 quantitative traits were subjected to separate analysis of variance using IRRISTAT software, version 5.0. The ANOVA results (Table 3) showed that the mean square values were highly significant ($P < 0.01$) for all traits of the genotypes of *C. capsularis*, *C. olitorius* and their accessions and with the exception of the leaf length-width ratio (NS) of varieties, implying that the genotypes were highly variable. The coefficient of variation was ranged from 1.73- 7.78%, 1.12-8.14%, 1.57-7.45% and 0.53-5.44% for the genotypes of *C. capsularis*, *C. olitorius*, overall accessions and varieties, respectively demonstrating the accuracy of the study.

Variation between species in quantitative traits

The mean, range, difference as percent of minimum values (DPM) and mean squares for each of the 17 quantitative traits of the genotypes of *C. capsularis* and *C. olitorius* are summarized in Table 3. The table showed that the mean values of the genotypes of each species generally displayed considerable differences between the minimal and maximal values for all the traits evaluated. In *C. capsularis*, the mean fiber yield was 7.36 g plant⁻¹ with a range of 5.99-10.20 g plant⁻¹ and the seed yield varied from 2.22-14.86 g plant⁻¹ with a mean of 6.06 g plant⁻¹. In *C. olitorius*, the fiber yield ranged from 8.16-15.56 g plant⁻¹ with a mean value of 12.45 g plant⁻¹ and the seed yield varied from 3.10-23.06 g plant⁻¹ with a mean value of 11.08 g plant⁻¹. Among fiber traits, the highest range of variation was observed in days to 50% flowering for both the species (141% for *C. capsularis* and 262% for *C. olitorius*) suggesting the genotypes were highly distinct in respect their flowering behavior. The lowest variation was in the leaf width (43%) and leaf length-width

ratio (40%) for the genotypes of *C. capsularis* and *C. olitorius*, respectively. In seed traits, the highest (569% and 644%) and lowest (29% and 41%) ranges of variations were found in seed yield and 1,000-seed weight of the genotypes of *C. capsularis* and *C. olitorius*, respectively. The mean DPM values of the fiber traits of *C. capsularis* and *C. olitorius* were 82.36% and 90.64%, respectively, with a range of 43-141% and 40-262%, respectively. In seed traits, the mean DPM values were 168.33% and 211.67% with a range of 29-569% and 41-644%, respectively, indicating wider genotypic variation in the seed traits than in the fiber traits and wider variation in the genotypes of *C. olitorius* compared with those of *C. capsularis*. For example, for pod length, the maximal values exceeded the corresponding minimum values by 182% in the genotypes of *C. olitorius* but by only 55% in the genotypes of *C. capsularis*. The higher phenotypic variability in *C. olitorius* compared to *C. capsularis* may be associated with a higher level of natural outcrossing in *C. olitorius* compared to *C. capsularis*. Ghose and Gupta (1945) previously reported relatively higher percentages (8-12%) of natural cross pollination within *C. olitorius* than *C. capsularis* (3-4%). Many of the observed variations for seed traits in jute are in agreement with the findings of Benor et al. (2012) for *C. olitorius* and those of Edmonds (1990) for cultivated species of jute. The broad variations in seed traits among the jute genotypes could provide ample opportunity for the genetic improvement of the crop through selection, intra-specific, inter-specific and somatic hybridization (Saha et al., 2001) or genetic transformation techniques (Ghosh et al., 2002).

Variation between accessions and varieties in quantitative traits

According to the analysis of variance (Table 3), the accessions differed significantly ($P < 0.01$) for all traits examined. In the fiber traits, the range of variation for the accessions was highest for fresh weight (75.44-225.52 g plant⁻¹) with a mean of 145.03 g plant⁻¹; the DPM value for fresh weight was 199%. The lowest variation (62%) was observed in plant base diameters. In seed traits, seeds per pod exhibited the maximum range of variation (19.70-212.42) with a mean of 76.97; the DPM value for when the maximal value exceeded the corresponding minimal values was 978%. Among seed traits, the 1,000-seed weight had the lowest variation (82%). Regarding varieties, the highest range of variation among the fiber traits was recorded for fiber yield (7.30-15.36 g plant⁻¹) with a mean of 10.95 g plant⁻¹; the DPM value for fiber yield was 110%. The lowest range of variation was measured for leaf angle (8%). In seed traits, the highest range of variation encountered was for pod length (1.23-7.21 cm) with a mean of 3.35 cm and the DPM values was 486%. The lowest range of variation among seed traits was for 1,000-seed weight (55%). A higher variation was observed for all traits in the accessions compared to the varieties (Table 3). For example, the plant height at 120 days in the accessions was in the range of 176.33-327.33 cm with a DPM value of 86%; in the varieties, the plant height ranged from 263.33-324.00 cm with a DPM value of 23%. Moreover, the mean and range of DPM values of the accessions were higher than those of the varieties for both fiber and seed traits. For instance, the mean DPM values of the accessions and varieties in seed traits were 563.50% and 232.83% with ranges of 82-978% and 55-486%, respectively, suggesting that the accessions were more highly variable than the varieties. This differentiation of the varieties from the accessions could be because fewer numbers of the varieties

Table 2. Morpho-agronomic traits recorded, together with their codes and descriptions.

No	Traits	Code	Description
Quantitative traits			
a) Fiber traits			
1.	Days to 50% flowering	DF	Number of days from seed germination to 50% flowering
2.	Plant height at average flowering	PH ₁	Height of the plant at first flowering (cm)
3.	Plant height at 120 days of plant age	PH ₂	Height of the plant at 120 days from seed germination for fiber yield (cm)
4.	Plant base diameter	PBD	Diameter of plant base at soil level at 120 days (mm)
5.	Fresh weight	FW	Weight of a fresh plant (without leaves) immediately after harvest (g)
6.	Fiber yield	FY	Weight of the dried fiber of a plant (g)
7.	Petiole length	PL ₁	Length of the leaf stalk (cm)
8.	Leaf length	LL	Length of a matured lamina from the proximal end of the mid-vein to the distal end (cm)
9.	Leaf width	LW	Width of the matured leaf at the widest-point (cm)
10.	Leaf angle	LA	The angle between the stem and the line connecting the base of the center of the midrib of the matured leaf (degree)
11.	Leaf length-width ratio	LL/LW	The ratio of the leaf blade length to the leaf width derived by LL/LW
b) Seed traits			
12.	Pods per plant	PP	Total number of matured pods of a plant
13.	Pod length	PL ₂	Length of the pod (cm), excluding the pedicel
14.	Pod diameter	PD	Diameter of the pod at widest-point (mm)
15.	Seeds per pod	SP	Total number of matured seeds in a pod
16.	1,000-seed weight	TSW	Weight of 1,000 dry seeds (g)
17.	Seed yield	SY	Dry seed weight of the individual plant (g)
Qualitative traits			
18.	Stem color	SC	Light green (1), dark green (2), light red (3), dark red (4)
19.	Branching habit	BH	Non-branching (0), leaf auxiliary buds in rudimentary form but do not grow into well-developed branches (3)
20.	Leaf shape	LS	Ovate (1), ovate-lanceolate (2), lanceolate (3)
21.	Stipule color	SC	Green (1), green stipules with dark red base (2), green stipules with red tip (3)
22.	Leaf vein color	LVC	Green (1), red (2)
23.	Petiole color	PC	Green (1), red (2)
24.	Leaf lamina color	LLC	Light green (1), dark green (2), red (3)
25.	Seed color	SC	Dark brown (1), greenish blue (2), blackish blue (3), brownish black (4) and grayish black (5)

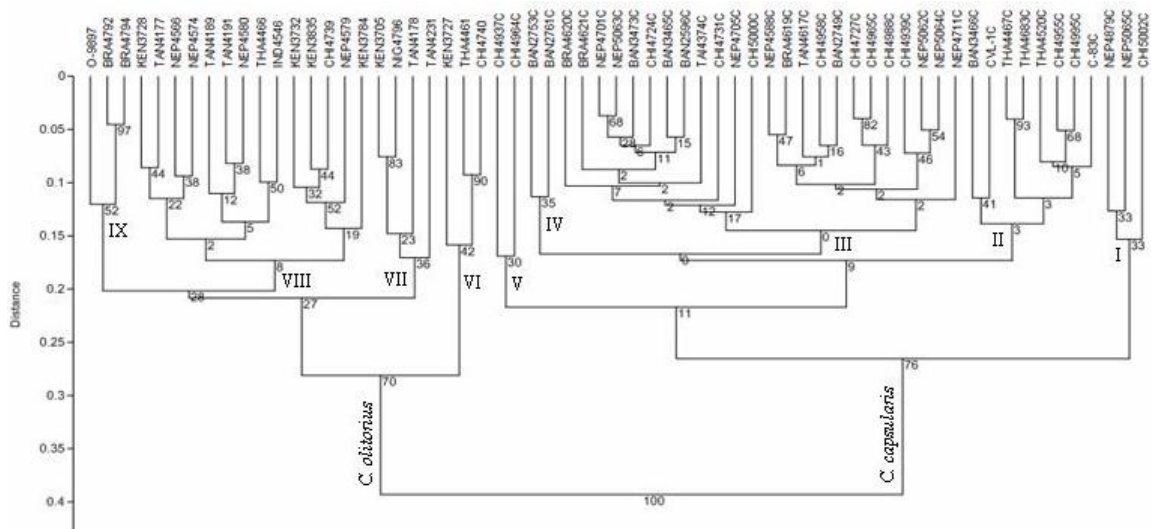


Fig 2. Cluster analysis showing the relationships among 63 genotypes of jute based on 25 morpho-agronomic traits (scale: Gower distance). The letter C on the right side of the genotype label indicates *C. capsularis*.

than the accessions were used in our study and the varieties were selected after cross hybridization with specific objective. In general, the success of any breeding program is principally dependent on genetic variation availability in the breeding materials. In the present study, we observed considerable genetic variation among accessions that could be useful for widening the genetic base of this neglected crop.

Variation within species in quantitative traits

Differences in mean fiber yield and seed yield and their contributing traits in each species of jute are separately presented in Table 4. The table showed that among the accessions of *C. capsularis*, accession BAN/3466 produced the highest fiber yield (9.77 g plant⁻¹), followed by accession CHI/4995 (9.57 g plant⁻¹). The highest plant height at average flowering was recorded for accession THA/4467 (244.33 cm), followed by accession THA/4683 (231.33 cm). For seed yield, accession BAN/3466 produced the highest seed yield (11.81 g plant⁻¹), followed by accession CHI/4995 (10.20 g plant⁻¹). Accessions NEP/4701, BAN/2753 and NEP/4705 produced the lowest fiber yield (5.99 g plant⁻¹), plant height at average flowering (123.00 cm) and seed yield (2.22 g plant⁻¹), respectively, which suggests that there is significant variation among the accessions. The variation in the morpho-agronomic traits of *C. capsularis* has been previously reported by Palit et al. (1996). The significant phenotypic variation among accessions may represent a useful source for improving the character of interest in either of the directions depending upon the objectives to be met. Although some of the accessions in *C. capsularis* performed better than the cheek variety C-83 (moderate yielder), none of the accessions performed better in fiber and seed yield than the high yielding cheek variety CVL-1, while judging by their respective LSD values. In *C. olitorius*, significant variations were also found among the accessions for all of the quantitative traits. For example, accession BRA/4792 had the highest plant height at average flowering (315.33 cm), fresh weight (225.52 g plant⁻¹) and fiber yield (15.56 g plant⁻¹). The accession THA/4461 produced the lowest plant height at average flowering (164.00 cm), fresh weight (84.15 g plant⁻¹) and fiber yield (8.16 g plant⁻¹). Comparing the performance of the accessions in *C. olitorius* with the performance of the check variety (O-9897), accessions BRA/4792 and BRA/4794 had the highest fiber yield (15.56 and 15.54 g plant⁻¹, respectively), which was not significantly different from the yield of the popular check variety O-9897 (15.36 g plant⁻¹). However, these accessions produced significantly higher seed yields (23.06 and 21.49 g plant⁻¹, respectively) than the cheek variety (15.51 g plant⁻¹). Higher seed yield is an important criterion for selecting genotypes. These high yielding accessions could be incorporated into jute seed production program in Bangladesh to overcome the acute jute seed shortages every year and could also be useful for genetic improvement of existing varieties of jute. Moreover, the higher seed yield accessions could be used for diversified uses of jute because jute seed having 7.9-12.9% of valuable oil (Hossen, 2008).

Variation in qualitative traits

Morpho-agronomic characterization of the 63 genotypes of the two cultivated species of jute revealed considerable variation in qualitative traits. The most commonly recorded stem color and leaf lamina color were dark green; the most

common leaf vein color and petiole color were green and the leaf shape was of the ovate-lanceolate type in both species (Table 5). Among the traits, the variation was highest in seed color (5 types) followed by stem color (4 types); the lowest variation was in leaf vein color, petiole color, branching habit and leaf lamina color (only 2 types).

Variation between species in qualitative traits

Of 8 qualitative traits, *C. olitorius* showed more variation than *C. capsularis* in 5 of the traits, namely stem color, petiole color, stipule color, leaf shape and seed color (Table 5). Though the number of genotypes of *C. capsularis* was higher (39) than that of *C. olitorius* (24), we observed higher variation in *C. olitorius* than in *C. capsularis*. For example, only dark brown seed color (100%) was found in the genotypes of *C. capsularis*, whereas four different types were found in those of *C. olitorius* [greenish blue (4%), blackish blue (71%), brownish black (17%) and grayish black (8%)]. The higher phenotypic variations in qualitative traits in *C. olitorius* compared to *C. capsularis* are in accordance with the results of quantitative traits in this study. Variations in seed color, stem color, leaf shape and stipule color are the most informative phenotypic variables in jute, especially in the genotypes of *C. olitorius*. These quality traits could be used for characterization and classification of jute genotypes. Benor et al. (2012) reported similar findings for *C. olitorius* jute; they reported that variations in branching habit, stipule color and leaf morphology, especially leaf shape, leaf base, leaf apex and leaf margin, are the most informative qualitative traits in *C. olitorius*. Examples of morphological variation in leaf shape and seed color are shown in Fig 4.

Variation between accessions and varieties in qualitative traits

Accessions showed more variation than the varieties for all the qualitative traits (Table 5). For instance, only dark green stem color (100%) was found in the varieties, but the stem colors of the accessions included light green (10%), dark green (73%), light red (10%) and dark red (7%). The higher variation in accessions compared with varieties might be due to the higher number of accessions (60) than varieties (3) used in this study.

Correlation analysis

Pearson correlation coefficients between different pairs of characteristics are shown in Table 6. The correlation coefficients of the fiber yield traits showed that fiber yield was positively and significantly correlated ($P < 0.01$) with days to 50% flowering, plant height at average flowering, plant height at 120 days, plant base diameter, fresh weight, leaf length and leaf width. Similar associations in jute were also found by Palve and Sinha (2005), Islam et al. (2001) and Khatun (1998), who reported that taller and thicker plants gave a higher fiber yield. Moreover, days to 50% flowering, plant height at average flowering, plant height at 120 days, plant base diameter, fresh weight and fiber yield were positively and significantly correlated with each other. These relationships suggest an increase in the general vigor of the plants. The significant positive correlation of days to 50% flowering with fiber yield is an important association because late flowering produces a non-branching, taller plant with more vegetative growth and a higher fiber yield. In contrast, leaf angle had significant negative correlations with days to

Table 3. Range, mean, mean squares and difference as a percent of minimum value (DPM) of 17 quantitative traits of jute as observed between two species and between accessions and varieties.

Traits code	<i>Corchorus capsularis</i>					<i>Corchorus olitorius</i>					Accession					Variety					
	Range	Mean	DPM (%)	Mean Squares	CV (%)	Range	Mean	DPM (%)	Mean Squares	CV (%)	Range	Mean	DPM (%)	Mean Squares	CV (%)	Range	Mean	DPM (%)	Mean Squares	CV (%)	
a) Fiber traits																					
DF	47.33 - 114.00	69.79	141	447.78**	2.80	42.33 - 153.33	78.81	262	1431.79**	1.72	42.33 - 108.67	71.14	157	482.77**	1.91	77.67 - 153.33	115.00	97	4296.33**	0.71	
PH ₁	123.00 - 245.67	186.87	100	2420.03**	7.78	164.00 - 336.00	232.36	105	6155.01**	3.92	123.00 - 315.33	201.27	156	4524.13**	4.75	206.67 - 336.00	262.78	62	13204.11**	5.27	
PH ₂	176.33 - 314.00	244.13	78	3555.61**	6.18	210.00 - 327.33	299.93	56	2740.61**	2.72	176.33 - 327.33	263.56	86	5389.17**	3.64	263.33 - 324.00	300.44	23	3173.78**	0.83	
PBD	9.99 - 15.27	12.30	53	7.06**	4.18	10.72 - 16.22	14.10	51	7.02**	3.79	9.99 - 16.22	12.90	62	8.98**	4.15	12.66 - 16.03	14.65	27	9.35**	1.47	
FW	75.44 - 181.39	119.41	140	1687.58**	5.06	84.15 - 225.52	188.73	168	3491.54**	8.14	75.44 - 225.52	145.03	199	5726.69**	7.45	112.47 - 221.49	161.60	97	9174.52**	2.89	
FY	5.99 - 10.20	7.36	70	3.81**	3.00	8.16 - 15.56	12.45	91	16.92**	2.47	5.99 - 15.54	9.22	159	26.25**	2.78	7.30 - 15.36	10.95	110	49.10**	2.67	
PL ₁	3.39 - 7.31	6.07	116	1.58**	3.94	4.47 - 7.18	5.55	61	1.44**	3.50	3.39 - 7.31	5.87	116	1.74**	3.79	5.16 - 6.35	5.88	23	1.19**	2.96	
LL	8.74 - 13.46	11.27	54	5.01**	2.26	12.13 - 17.83	14.82	47	7.26**	1.67	8.74 - 17.83	12.58	104	14.93**	2.01	11.60 - 16.05	13.43	38	16.28**	2.15	
LW	4.12 - 5.91	4.92	43	0.87**	1.73	4.15 - 7.20	5.89	73	1.90**	1.38	4.12 - 7.20	5.29	75	1.91**	1.57	4.48 - 6.37	5.23	42	3.03**	1.87	
LA	47.12 - 72.05	58.92	53	138.98**	2.72	41.33 - 59.12	51.39	43	58.09**	1.12	41.33 - 72.05	56.33	74	149.77**	3.24	48.48 - 52.15	50.54	8	10.57**	0.78	
LL/LW	1.83 - 2.90	2.30	58	0.18**	3.24	2.13 - 2.99	2.53	40	0.14**	2.44	1.83 - 2.99	2.38	63	0.21**	2.89	2.40 - 2.82	2.58	18	0.14 NS	3.83	
Mean		82.36					90.64					113.73					49.55				
Range		43-141					40-262					62-199					8-110				
b) Seed traits																					
PP	33.35 - 90.84	53.72	172	513.17**	4.17	17.42 - 44.53	32.73	156	206.49**	4.29	17.42 - 81.75	44.75	369	599.71**	4.21	34.17 - 90.84	65.13	166	2470.63**	5.44	
PL ₂	1.04 - 1.61	1.19	55	0.03**	3.19	2.87 - 8.08	6.19	182	5.66**	2.13	1.04 - 8.08	3.08	677	19.93**	2.86	1.23 - 7.21	3.35	486	33.65**	1.78	
PD	10.65 - 15.24	12.19	43	3.70**	2.75	3.27 - 6.04	4.89	85	1.69**	3.41	3.27 - 14.27	9.34	336	40.45**	3.17	5.56 - 15.24	10.91	174	72.66**	3.48	
SP	19.70 - 47.69	35.83	142	121.88**	3.63	81.03 - 212.42	146.39	162	5568.77**	2.85	19.70 - 212.42	76.97	978	10539.08**	3.64	40.20 - 205.07	97.65	410	26004.34**	0.53	
TSW	2.66 - 3.43	3.04	29	0.11**	2.12	1.85 - 2.60	2.17	41	0.13**	2.93	1.85 - 3.37	2.70	82	0.64**	2.36	2.21 - 3.43	2.77	55	1.14**	2.44	
SY	2.22 - 14.86	6.06	569	19.97**	5.73	3.10 - 23.06	11.08	644	94.65**	5.90	2.22 - 23.06	7.74	939	63.33**	6.19	7.52 - 15.51	12.63	106	59.05**	2.89	
Mean		168.33					211.66					563.50					232.83				
Range		29-569					41-644					82-978					55-486				

DF = Days to 50% flowering, PH₁= Plant height at average flowering (cm), PH₂ = Plant height at 120 days (cm), PBD = Plant base diameter (mm), FW = Fresh weight (g plant⁻¹), FY = Fiber yield (g plant⁻¹), PL₁ = Petiole length (cm), LL = Leaf length (cm), LW = Leaf width (cm), LA = Leaf angle (Degree), LL/LW = Leaf length-width ratio, PP = Pods per plant, PL₂= Pod length (cm), PD = Pod diameter (mm), SP = Seeds per pod, TSW = 1000-seed weight (g), SY = Seed yield (g plant⁻¹)
 **significant at p<0.01, NS = Not significant

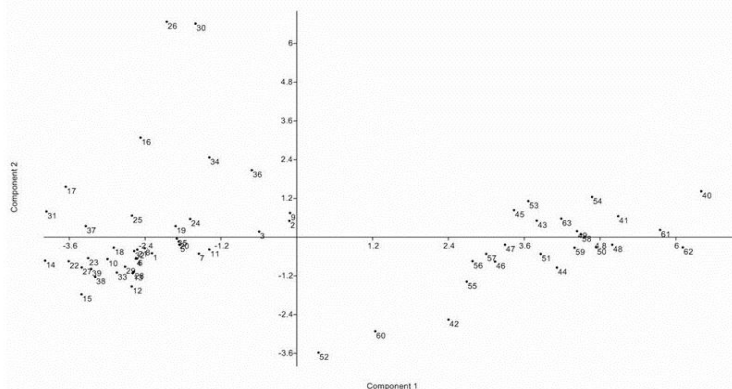


Fig 3. Two-dimensional scatter plot of 63 jute genotypes for the first two principal components accounting for 55.76% (PC I = 44.59% and PC II = 11.17%) of the total variance. The numbers on the scatter plot indicate the serial numbers of each genotype as listed in Table 1. *C. olitorius* genotypes are on the right side of the plot, and *C. capsularis* genotypes are on the left side of the plot for both positive and negative loading.

50% flowering, plant height at average flowering, plant height at 120 days, plant base diameter, fresh weight, fiber yield, leaf length and leaf width, possibly because a lower leaf angle made the jute leaf more active photosynthetically, resulting in higher growth and fiber yield. The negative association between leaf angle and internodal length was found by Kabi and Bhaduri (1981) in jute. They also concluded that leaf angle in jute is an important criterion that may be exploited in a recombination breeding program. Among seed traits, seed yield had highly significant positive correlations with days to 50% flowering, plant height at average flowering, plant height at 120 days, plant base diameter, fresh weight, fiber yield, leaf length, leaf width, leaf length-width ratio, pod length and seeds per pod. The major seed-yield components, including plant height at average flowering, pod length and seeds per pod, showed highly significant positive correlations with seed yield, as was demonstrated in the findings by Khan (1995). Seed yield was negatively correlated with pod diameter and 1,000 seed weight. Ali and Sasmal (2006) also found a negative correlation between seed yield and 1,000 seed weight in an F₂ generation of tossa jute (*C. olitorius*) but did not find a negative association between pod diameter and seed yield, suggesting that this quantitative trait may be influenced by genetic factors as well as the environment.

Cluster analysis

The dendrogram for the 63 genotypes representing two species of jute over 25 morpho-agronomic traits shows that the genotypes were broadly divided into two groups (Gower distance = 0.39 and supported by a bootstrap P value of 100%), which were further subdivided into nine clusters according to Gower distance, using PAST software (Fig 2). The first major group (clusters I to V) comprised 39 genotypes of *C. capsularis*. Values for the petiole length, leaf angle, pods per plant, pod diameter and 1,000-seed weight were higher for this group, but the values for plant height, fiber yield, pod length, seeds per pod and seed yield were lower. In contrast, the genotypes of *C. olitorius* in the second group (clusters VI to IX) had higher values for most of the fiber yield components along with pod length, seeds per pod and seed yield (Table 7). The most discriminating traits between species were pod length, seeds per pod, pod diameter, seed yield and fiber yield. The discrepancy between the two species of jute is in agreement with the previous morpho-physiological findings of Kundu (1951) and Palit et al. (1996) and with the molecular data of Basu et al. (2004) and Roy et al. (2006). The cophenetic matrix value was high ($r = 0.90$), indicating that the data set was reliable. Among the nine clusters, cluster I comprised 3 genotypes having high values for leaf angle and leaf length-width ratio but low values for pod length and seed yield per plant. Genotypes in this cluster had the highest pod diameter. Cluster II comprised eight genotypes, including two varieties that originated from China, Thailand and Bangladesh. This cluster had the highest values for pods per plant and 1,000-seed weight but mid-range mean values for plant height at 120 days, fresh weight and fiber yield. The third cluster had the largest number of genotypes (24), which originated from five countries. The genotypes in this cluster were characterized by early flowering, short plant height and lowest seed yield. The two genotypes in cluster IV had very short plant height and the shortest pod length but the highest values for petiole length and leaf angle. Cluster V had the lowest values for fresh weight, fiber yield, leaf length and leaf length-width ratio. Cluster VI, comprising three genotypes from three

countries, showed early flowering and had the narrowest leaves and the lowest values for base diameter, petiole length, pods per plant and pod diameter. Cluster VII genotypes had the smallest seeds and the largest leaf size. The 14 members of cluster VIII, which originated from six Asian and African countries, showed high values for all the traits except leaf angle, pods per plant, pod diameter and 1,000-seed weight. Finally, cluster IX, comprising three genotypes (one variety and two accessions) originating from Bangladesh and Brazil, showed the highest values for fiber yield, fresh weight, pod length, seeds per pod and seed yield but the lowest value for leaf angle. In jute, early flowering, strong branching and short plant height are undesirable characteristics that are usually linked to lower fiber yield. In our experiment, early flowering, shorter plants and a branching tendency were observed in the genotypes of cluster IV, V and VI, respectively. By contrast, the genotypes O-9897, BRA/4792 and BRA/4794 in cluster IX had the highest fiber yield (15.49 g plant⁻¹) and seed yield (20.02 g plant⁻¹), followed by those in cluster VII; both groups showed similar trends with regard to the major characteristics contributing to yield. The genotypes in clusters I, II and VIII were identified as moderate to high performers on agronomic traits related to fiber yield. On the basis of high yield performance as well as phenotypic distinctness, the genotypes O-9897, BRA/4792 and BRA/4794 in cluster IX were identified as the most promising parental materials for genetic improvement of jute. To evaluate the genetic variability or similarity of the genotypes among the clusters, the inter-cluster Gower distance and relationships were calculated using PAST software (Table 8). The highest distance (0.69) was between cluster IX and IV, which suggested that the members of these clusters diverge on most of the studied traits and could be used in breeding programs, especially in programs using advanced breeding technologies to avoid crossbred barriers. The lowest distance (0.14) was between cluster III and cluster IV, suggesting that their maternal origin may be very closely related.

Principal component analysis

We used principal component analysis (PCA), a multivariate statistical technique, to extract the important information from the data table and simplify the description of the data set. The results (Table 9) indicated that the first five components of the total of 25 accounted for 75.93% of the total variation, whereas the remaining 20 components accounted for only 24.07% of the morpho-agronomic diversity. PC I explained the most variability (44.59%), followed by PC II (11.17%), PC III (9.28%), PC IV (5.89%) and PC V (5%). PC I was mainly characterized by plant height, plant base diameter, fresh weight, fiber yield, leaf length, leaf width, pod length, seeds per pod, seed yield and seed color with the largest positive correlations, whereas leaf angle, pods per plant, pod diameter, 1,000-seed weight and branching habit had negative correlations. These results of PC I are in agreement with the results of the correlation analysis. PC II was positively associated with color traits such as stem color, leaf vein color, petiole color and stipule color. The PC II results support with the findings of Benor et al. (2012) that qualitative characteristics alone can help discriminate among jute accessions. A scatter plot of the first two components (PC I on the X-axis and PC II on the Y-axis) accounting for 55.76 % of the total variation in 63 jute genotypes showed the presence of two distinct groups (Fig 3), which is in accordance with the results of the cluster

Table 4. Mean performance of the genotypes of *C. capsularis* and *C. olitorius* of jute in 17 quantitative traits [genotypes arranged according to their descending order of fiber yield (g plant⁻¹)].

Genotype	DF	PH ₁	PH ₂	PBD	FW	FY	PL ₁	LL	LW	LA	LL/LW	PP	PL ₂	PD	SPP	TSW	SY
<i>C. capsularis</i>																	
BAN/3466	86.67	219.00	302.67	14.92	133.81	9.77	6.53	12.32	4.83	50.01	2.55	81.75	1.13	12.51	43.92	3.29	11.81
CHI/4995	81.67	189.00	227.00	13.81	146.49	9.57	6.34	13.05	5.34	54.16	2.44	77.87	1.26	12.75	40.48	3.23	10.20
THA/4683	82.33	231.33	309.33	14.06	165.67	9.07	6.06	13.00	5.64	53.06	2.30	52.66	1.19	11.18	31.87	3.16	5.30
THA/4520	77.33	219.33	255.00	13.91	147.82	9.04	6.52	13.39	5.80	47.12	2.31	50.84	1.12	11.12	31.75	2.86	4.64
THA/4467	77.00	244.33	290.00	14.50	167.02	8.61	5.89	12.25	5.65	51.81	2.17	42.51	1.18	11.95	36.13	3.01	4.64
NEP/5065	71.00	222.00	294.33	13.66	124.64	8.20	6.20	11.76	4.75	53.81	2.47	49.71	1.21	14.33	34.20	2.76	4.68
TAN/4617	76.33	213.33	259.33	13.33	133.40	8.15	5.71	9.02	4.62	52.04	1.95	33.35	1.04	11.55	27.47	3.02	2.77
NEP/4705	77.33	173.33	264.00	13.99	126.28	8.11	7.31	12.91	5.22	54.34	2.47	37.63	1.15	12.73	19.70	2.99	2.22
NEP/4588	67.33	197.67	229.00	10.49	101.16	7.65	5.87	11.48	5.91	58.89	1.94	42.31	1.38	12.86	39.06	3.16	5.21
TAI/4374	74.67	174.00	284.33	14.00	110.35	7.64	5.20	9.60	4.48	59.10	2.14	53.58	1.20	10.77	36.84	3.08	6.08
BAN/2753	74.67	123.00	190.33	12.16	103.90	7.61	6.14	9.81	4.13	66.53	2.37	69.46	1.13	12.28	41.68	2.80	8.13
BAN/2596	66.67	179.00	231.67	11.33	122.64	7.58	6.14	9.31	4.14	68.32	2.25	45.00	1.21	12.03	41.73	2.99	5.61
BRA/4621	73.67	203.67	267.67	12.33	130.76	7.56	6.86	11.04	5.45	62.87	2.03	45.77	1.17	11.93	34.75	3.37	5.35
CHI/4955	64.33	207.33	250.67	13.73	119.43	7.45	6.51	13.46	5.27	54.88	2.55	71.15	1.27	12.68	40.98	3.36	9.78
CHI/5000	80.67	178.67	221.67	10.76	134.89	7.43	6.01	11.04	4.95	58.56	2.23	67.58	1.12	11.80	37.59	3.26	8.31
BAN/3465	57.33	152.67	217.00	10.82	119.34	7.37	6.70	11.34	4.64	63.82	2.44	49.49	1.20	11.84	37.70	2.99	5.61
BAN/2761	79.33	136.00	190.00	11.83	129.66	7.33	6.67	11.65	5.03	64.84	2.32	51.92	1.09	10.74	39.31	3.18	6.47
NEP/5064	63.00	161.33	223.00	10.99	104.15	7.25	6.62	11.63	4.22	61.50	2.76	34.36	1.14	11.34	28.87	2.93	2.91
CHI/5002	71.33	187.00	271.67	12.66	181.39	7.15	5.65	10.70	4.28	67.69	2.50	61.49	1.24	14.72	44.03	2.94	8.03
CHI/4958	73.33	202.00	260.67	13.66	121.73	7.01	6.18	11.44	5.11	58.37	2.24	34.56	1.07	10.99	20.92	3.25	2.35
CHI/4988	67.67	162.33	238.67	10.99	112.76	6.95	5.23	9.94	4.46	69.14	2.23	45.50	1.10	11.10	38.08	3.36	5.84
CHI/4724	57.67	195.33	235.00	10.49	113.29	6.90	6.08	12.24	5.77	57.87	2.12	53.97	1.23	12.87	24.98	2.85	3.84
BAN/2749	55.33	191.67	258.33	11.83	121.89	6.83	5.80	10.86	4.68	61.03	2.32	58.48	1.11	10.99	36.60	3.01	6.45
CHI/4965	75.67	167.33	231.33	10.58	81.86	6.74	5.04	9.00	4.51	71.62	2.00	49.81	1.13	12.17	39.69	2.84	5.64
NEP/4879	71.00	209.33	276.33	11.99	114.95	6.73	6.15	11.32	4.58	66.06	2.47	45.50	1.25	12.13	30.76	2.91	4.07
BAN/3473	72.33	165.00	216.33	9.99	107.71	6.72	6.80	12.04	5.22	53.18	2.31	57.65	1.23	11.75	37.25	2.95	6.33
NEP/5062	47.33	156.00	222.00	10.91	128.70	6.71	6.01	12.05	4.16	55.82	2.90	45.15	1.14	10.93	35.42	3.03	4.84
CHI/4727	54.33	162.33	245.00	10.33	95.54	6.65	5.74	8.74	4.43	72.05	1.97	63.70	1.28	12.32	39.70	2.81	7.11
NEP/5063	55.67	164.33	228.00	11.49	105.39	6.65	6.51	11.24	5.02	65.79	2.24	61.85	1.21	12.81	41.98	3.03	7.86
CHI/4964	72.00	201.33	206.67	13.65	78.46	6.59	4.23	9.29	4.23	56.15	2.20	58.93	1.42	14.22	41.87	3.08	7.60
CHI/4939	62.33	202.33	236.33	12.66	86.76	6.18	6.44	11.25	4.12	66.22	2.73	48.16	1.07	12.88	34.54	2.98	4.95
BRA/4619	66.00	193.33	255.00	10.83	119.29	6.12	5.85	10.16	5.56	58.14	1.83	44.75	1.08	10.65	35.47	2.98	4.72
NEP/4711	50.67	161.67	191.33	10.89	120.65	6.11	3.39	11.16	5.06	51.04	2.20	46.93	1.23	11.99	30.82	2.88	4.17
BRA/4620	66.67	194.33	249.00	14.82	122.45	6.08	6.63	12.71	5.83	47.59	2.18	48.98	1.06	10.79	32.85	3.16	5.08
CHI/4731	47.67	143.67	176.33	10.49	90.56	6.07	6.73	12.01	5.38	60.58	2.23	48.80	1.16	12.92	24.64	2.71	3.26
CHI/4937	63.33	170.00	187.33	11.33	75.44	6.05	5.78	9.54	4.93	63.86	1.94	42.79	1.23	12.90	33.52	2.99	4.31
NEP/4701	68.67	181.33	251.33	11.49	93.55	5.99	6.81	11.42	5.12	59.43	2.23	59.76	1.19	12.92	42.54	3.02	7.67
C-83 (Ck₁)	77.67	206.67	263.33	12.66	112.47	7.30	6.35	11.60	4.83	48.48	2.40	70.36	1.23	11.94	40.20	2.66	7.52
CVL-1 (Ck₂)	114.00	245.67	314.00	15.27	150.84	10.20	6.12	12.63	4.48	52.15	2.82	90.84	1.61	15.24	47.69	3.43	14.86
Mean	69.79	186.87	244.13	12.30	119.41	7.36	6.07	11.27	4.92	58.92	2.30	53.72	1.19	12.19	35.83	3.04	6.06
LSD (0.05)	3.16	23.51	24.40	1.18	13.70	0.52	0.52	0.58	0.19	2.12	0.17	5.12	0.08	0.76	2.95	0.14	0.79
CV (%)	2.81	7.78	6.18	5.96	7.10	4.36	5.32	3.20	2.45	2.22	4.60	5.90	4.46	3.85	5.10	2.97	8.12
<i>C. olitorius</i>																	
BRA/4792	108.67	315.33	326.00	16.20	225.52	15.56	5.53	15.20	5.83	48.05	2.61	44.53	8.08	5.55	212.42	2.44	23.06
BRA/4794	92.67	313.33	327.33	16.22	220.76	15.54	4.76	15.28	5.91	49.44	2.59	43.15	8.05	5.62	209.13	2.38	21.49
NEP/4580	87.33	274.00	305.33	15.07	205.37	15.32	5.75	13.93	5.35	45.15	2.61	41.52	5.95	5.85	129.60	2.01	10.83
IND/4546	97.33	201.33	298.33	15.21	202.26	15.26	4.71	15.82	6.16	56.49	2.57	42.64	7.72	5.11	167.70	2.41	16.69
TAN/4191	64.67	226.67	318.33	15.24	210.01	14.74	5.76	15.48	6.04	48.81	2.56	37.98	7.45	5.45	189.92	2.28	16.48
THA/4466	85.33	192.67	325.67	14.10	212.07	14.31	4.76	15.40	5.98	53.92	2.57	40.46	6.66	5.40	127.26	2.56	13.18
TAN/4178	88.00	248.33	317.00	15.25	199.01	13.95	5.24	14.08	5.95	47.81	2.37	28.81	6.11	5.54	114.60	1.95	6.50
KEN/3705	76.67	280.00	316.33	13.67	206.80	13.37	5.78	16.70	6.87	55.87	2.43	41.92	7.33	5.78	200.81	1.85	15.63
TAN/4231	91.00	222.33	306.67	15.16	191.53	13.33	6.54	15.12	6.14	51.05	2.46	44.14	6.77	6.04	161.08	1.99	14.17
NEP/4579	72.00	224.33	305.67	14.61	168.63	13.30	7.18	14.47	5.99	54.26	2.42	24.43	4.91	3.73	100.48	2.03	4.98
CHI/4739	82.33	257.00	302.33	14.26	196.09	12.97	5.81	17.83	7.15	56.23	2.49	26.63	4.97	4.68	110.53	1.99	5.86
TAN/4189	82.00	225.00	315.00	13.16	206.11	12.81	5.77	14.98	5.24	53.01	2.86	29.71	7.61	5.32	201.92	2.36	14.19
KEN/3732	63.33	208.67	317.67	14.49	199.74	12.71	5.28	17.22	6.08	55.04	2.83	19.00	3.62	3.27	87.79	2.04	3.42
NEP/4566	65.67	178.00	265.33	11.66	182.57	11.79	5.67	13.90	5.62	55.70	2.48	35.05	6.47	4.48	141.25	1.96	9.71
KEN/3728	67.33	219.00	310.33	14.49	191.90	11.48	5.34	13.17	5.58	47.80	2.36	29.41	6.14	4.49	161.97	2.15	10.24
TAN/4177	64.67	190.33	307.67	13.99	206.91	10.95	5.64	12.79	5.87	43.95	2.18	33.13	6.74	4.93	137.93	2.19	10.02
KEN/3835	56.33	260.67	306.00	13.99	203.40	10.63	5.92	15.33	7.20	59.12	2.13	17.42	2.87	3.93	81.03	2.18	3.10
NIG/4796	77.33	234.67	305.00	14.89	175.57	10.24	6.68	16.72	6.83	54.19	2.45	37.91	6.83	5.00	188.91	2.21	15.84
KEN/3784	81.67	218.00	298.00	14.49	188.41	9.87	6.45	15.40	6.77	53.37	2.27	27.04	5.32	4.32	116.96	2.60	8.23
NEP/4574	68.00	205.67	273.00	11.84	158.59	9.53	5.50	13.90	4.97	41.33	2.80	29.63	6.29	4.69	140.36	2.23	9.29
KEN/3727	68.00	188.00	293.33	12.22	171.06	9.30	4.90	12.13	5.06	48.31	2.40	24.64	6.15	4.83	148.11	2.01	7.31
CHI/4740	55.33	193.33	219.33	10.72	101.48	8.36	4.56	12.28	4.24	50.65	2.90	20.46	4.32	3.95	90.64	1.98	3.67
THA/4461	42.33	164.00	210.00	11.49	84.15	8.16	4.47	12.44	4.15	52.84	2.99	31.70	4.92	4.03	87.88	2.10	5.85
O-9897 (Ck_{3</}																	



Fig 4. Representative samples of variation in (a) leaf shape, (b) jute fiber, (c) pod shape and size, and (d) seed morphology. (a) Leaf shape a₁: ovate; a₂: ovate-lanceolate; and a₃: lanceolate. (b) Fiber color b₁: whitish, soft fiber in *C. capsularis*; b₂: golden, strong fiber in *C. olitorius*. (c) Pod shape and size c₁: capsule shape with higher diameter; and c₂: elongated pod. (d) The seeds above the green line are the dark brown, large seeds of *C. capsularis* (1-39), whereas the smaller, variously colored seeds below the line are *C. olitorius* (40-63).

analysis (Fig 2). PC III was positively dominated by the effect of days to 50% flowering and negatively by stipule color. PC IV and PC V were depicted mainly the patterns of variation in petiole length (positively) and leaf lamina color (negatively), respectively. In our experiment, the PC analysis ultimately showed the amount of variability for the traits among the genotypes that could be used for the improvement of jute.

Materials and methods

Plant materials

The plant materials of the two cultivated species of jute were selected to ensure the diversity of the geographical locations of their sources (Table 1). Two varieties (C-83 and CVL-1) with 37 accessions of *C. capsularis* and one variety (O-9897) with 23 accessions of *C. olitorius* were evaluated. The varieties C-83 (moderate yielder) and CVL-1 (high yielder) for *C. capsularis* and O-9897 (high yielder) for *C. olitorius* were used in this experiment to compare the phenotypic performance of the accessions with varieties. The materials were obtained from the Bangladesh Jute Research Institute (BJRI).

Experimental design

The experiment was conducted in 2011 in the net house at the department of Agronomy, Kasetsart University, Thailand. A randomized, complete block design with three replications was used. The seeds of the sixty-three jute genotypes described in Table 1 were sown randomly in each block on April 20. Each plot consisted of a single row 4 m in length with 30 cm between the rows and a plant-to-plant distance of 10 cm, with 41 plants per row. Two border rows surrounded each block to prevent border effects. Plots were kept free from weeds, diseases and insects throughout the growing season. Soil fertility and moisture content were sufficient for normal crop growth. The monthly average temperature,

rainfall, humidity and day length during the growing season are shown in Fig 1.

Data collection

All of the genotypes were characterized for different morphological and agronomic traits (Table 2) from the seedling stage up to the crop harvest. Trait selection and measurement techniques were based on International Jute Organization (IJO, 1989) descriptors for *Corchorus capsularis* and *C. olitorius*. Ten plants in each genotype were randomly selected and their quantitative and qualitative traits were measured. At 120 days, fiber-yield traits including plant height (PH₂), plant base diameter, fresh weight and fiber yield were measured as shown in Table 2. The pods per plant, pod length, pod diameter and seeds per pod were recorded at the full-maturity stage of the pod for each genotype. Ten pods from each plant were selected randomly and the pod length and diameter were measured using a digital scale.

Statistical analysis

An analysis of variance (ANOVA) for 17 quantitative traits was carried out using IRRISTAT software version 5.0. Correlations of the quantitative traits were determined using the Pearson correlation coefficient to identify the relationships between the traits. All quantitative and qualitative data were used for principal component analysis (PCA) and cluster analysis for all of the genotypes. The mean data were standardized prior to multivariate analysis to eliminate the effects resulting from using different scales. To separate the 63 genotypes into groups and to evaluate the patterns of similarity and dissimilarity, the data were subjected to cluster analysis according to Gower distance (Gower 1971), using PAST software version 2.15 (Hammer et al., 2001). Principal component analysis (PCA) of the correlation matrix was performed with the same software to determine the sources of variation among genotypes. Bootstrapping over the data set with 1,000 replications was used to assess the strength of the evidence for the branching

Table 5. Frequency (F) distribution between the genotypes of *C. capsularis* and *C. olitorius* and the accessions and varieties in 8 qualitative traits of jute.

Traits	Type	<i>C. capsularis</i>		<i>C. olitorius</i>		Accession		Variety	
		F	%	F	%	F	%	F	%
Stem color	1) Light green	0	0	6	25	6	10	0	0
	2) Dark green	35	90	12	50	44	73	3	100
	3) Light red	0	0	6	25	6	10	0	0
	4) Dark red	4	10	0	0	4	7	0	0
Leaf vein color	1) Green	37	95	24	100	58	97	3	100
	2) Red	2	5	0	0	2	3	0	0
Petiole color	1) Green	36	92	20	83	53	88	3	100
	2) Red	3	8	4	17	7	12	0	0
Stipule color	1) Green	36	92	11	46	44	73	3	100
	2) Green with dark red base	0	0	13	54	13	22	0	0
	3) Green with tip red	3	8	0	0	3	5	0	0
Leaf shape	1) Ovate	0	0	2	8	2	3	0	0
	2) Ovate-lanceolate	35	90	12	50	45	75	2	67
	3) Lanceolate	4	10	10	42	13	22	1	33
Branching habit	1) Non-branching	3	8	23	96	25	42	1	33
	2) Branching	36	92	1	4	35	58	2	67
Leaf lamina color	1) Light green	13	33	7	29	20	33	0	0
	2) Dark green	26	67	17	71	40	67	3	100
Seed color	1) Dark brown	39	100	0	0	37	62	2	67
	2) Greenish blue	0	0	1	4	0	0	1	33
	3) Blackish blue	0	0	17	71	17	28	0	0
	4) Brownish black	0	0	4	17	4	7	0	0
	5) Grayish black	0	0	2	8	2	3	0	0

Table 6. Pearson correlation coefficients for 17 quantitative traits of 63 genotypes of jute.

Traits code	DF	PH ₁	PH ₂	PBD	FW	FY	PL ₁	LL	LW	LA	LL/LW	PP	PL ₂	PD	SP	TSW	SY
DF	1.00																
PH ₁	0.67**	1.00															
PH ₂	0.56**	0.78**	1.00														
PBD	0.65**	0.75**	0.79**	1.00													
FW	0.54**	0.70**	0.84**	0.72**	1.00												
FY	0.60**	0.72**	0.79**	0.74**	0.90**	1.00											
PL ₁	-0.03	-0.13	-0.07	-0.03	-0.16	-0.23	1.00										
LL	0.39**	0.63**	0.68**	0.64**	0.80**	0.80**	-0.01	1.00									
LW	0.33**	0.58**	0.59**	0.53**	0.70**	0.62**	0.08	0.81**	1.00								
LA	-0.28*	-0.51**	-0.50**	-0.56**	-0.53**	-0.52**	0.17	-0.54**	-0.40**	1.00							
LL/LW	0.13	0.20	0.26*	0.26*	0.30*	0.40*	-0.11	0.49**	-0.11	-0.33**	1.00						
PP	0.10	-0.24	-0.30**	-0.13	-0.41**	-0.39**	0.25*	-0.43**	-0.42**	0.25*	-0.13	1.00					
PL ₂	0.39**	0.57**	0.66**	0.54**	0.80**	0.87**	-0.34**	0.75**	0.56**	-0.54**	0.42**	-0.53**	1.00				
PD	-0.16	-0.44**	-0.58**	-0.42**	-0.72**	-0.75**	0.32*	-0.74**	-0.59**	0.50**	-0.39**	0.75**	-0.87**	1.00			
SP	0.44**	0.63**	0.67**	0.56**	0.80**	0.85**	-0.31*	0.74**	0.56**	-0.49**	0.39**	-0.46**	0.98**	-0.82**	1.00		
TSW	-0.09	-0.42**	-0.49**	-0.33**	-0.62**	-0.69**	0.31**	-0.66**	-0.50**	0.45**	-0.37**	0.68**	-0.83**	0.88**	-0.77**	1.00	
SY	0.59**	0.57**	0.55**	0.57**	0.63**	0.70**	-0.19	0.53**	0.34**	-0.35**	0.34**	0.13	0.72**	-0.39**	0.79**	-0.33**	1.00

DF = Days to 50% flowering, PH₁ = Plant height at average flowering (cm), PH₂ = Plant height at 120 days (cm), PBD = Plant base diameter (mm), FW = Fresh weight (g plant⁻¹), FY = Fiber yield (g plant⁻¹), PL₁ = Petiole length (cm), LL = Leaf length (cm), LW = Leaf width (cm), LA = Leaf angle (Degree), LL/LW = Leaf length-width ratio, PP = Pods per plant, PL₂ = Pod length (cm), PD = Pod diameter (mm), SP = Seeds per pod, TSW = 1,000-seed weight (g), SY = Seed yield (g plant⁻¹); *significant at p<0.05, ** significant at p<0.01

Table 7. Average value per cluster and between species for 17 morpho-agronomic traits of 63 genotypes of jute.

Traits Code	Clusters									Between species	
	I (3)	II (8)	III (24)	IV (2)	V (2)	VI (3)	VII (4)	VIII (14)	IX (3)	C. Capsularis(39)	C. Olitorius(24)
DF	71.11	81.38	64.93	77.00	67.67	55.22	83.25	74.14	118.22	69.79	78.81
PH ₁	206.11	220.33	178.19	129.50	185.67	181.78	246.33	220.10	321.56	186.87	232.36
PH ₂	208.78	276.50	237.18	190.17	197.00	240.89	311.25	303.48	325.78	244.13	299.74
PBD	12.77	14.11	11.64	11.99	12.49	11.47	14.74	14.12	16.15	12.30	14.10
FW	140.33	142.94	112.71	116.78	76.95	118.90	193.23	195.15	222.59	119.41	188.73
FY	7.36	8.88	6.94	7.47	6.32	8.61	12.73	12.55	15.49	7.36	12.45
PL ₁	6.00	6.29	6.07	6.41	5.00	4.64	6.06	5.68	5.15	6.07	5.55
LL	11.26	12.71	10.99	10.73	9.41	12.28	15.66	14.79	15.51	11.27	14.82
LW	4.54	5.23	4.92	4.58	4.58	4.48	6.45	6.00	6.04	4.92	5.89
LA	62.52	51.46	60.31	65.69	60.01	50.60	52.23	51.73	49.50	58.92	51.39
LL/LW	2.48	2.44	2.25	2.35	2.07	2.76	2.43	2.49	2.57	2.30	2.53
PP	52.24	67.25	49.10	60.69	50.86	25.60	38.19	31.00	40.62	53.72	32.73
PL ₂	1.23	1.25	1.17	1.11	1.33	5.13	6.76	5.91	7.78	1.19	6.19
PD	13.73	12.42	11.87	11.51	13.56	4.27	5.59	4.69	5.57	12.19	4.89
SP	36.33	39.13	34.14	40.50	37.70	108.88	166.35	135.34	208.87	35.83	146.39
TSW	2.87	3.13	3.03	2.99	3.04	2.03	2.00	2.21	2.35	3.04	2.17
SY	5.59	8.59	5.18	7.30	5.96	5.61	13.04	9.77	20.02	6.06	11.05

Numbers in parentheses indicate the number of genotypes in each cluster

Table 8. Gower distance and similarities among nine clusters of 63 genotypes of jute using PAST software.

	Clusters								
	I	II	III	IV	V	VI	VII	VIII	IX
I	0								
II	0.30	0							
III	0.28	0.20	0						
IV	0.26	0.24	0.14	0					
V	0.27	0.30	0.20	0.23	0				
VI	0.55	0.44	0.37	0.47	0.42	0			
VII	0.60	0.44	0.52	0.60	0.63	0.37	0		
VIII	0.50	0.34	0.45	0.53	0.48	0.30	0.19	0	
IX	0.68	0.48	0.61	0.69	0.62	0.42	0.28	0.23	0

Table 9. Eigenvalues, proportion of variability and morpho-agronomic traits that contributed to the first five principal components of jute genotypes.

Traits	PC I	PC II	PC III	PC IV	PC V
Eigenvalue	11.15	2.79	2.32	1.47	1.25
% of total variance	44.59	11.17	9.28	5.89	5.00
Cumulative variance %	44.59	55.76	65.04	70.93	75.93
Eigen vectors					
Days to 50% flowering	0.50	0.46	0.51	-0.08	0.04
Plant height at average flowering	0.75	0.26	0.35	0.04	-0.16
Plant height at 120 days	0.81	0.30	0.17	0.11	-0.13
Plant base diameter	0.72	0.35	0.36	0.03	-0.08
Fresh weight	0.91	0.19	0.06	0.09	-0.07
Fiber yield	0.94	0.10	0.12	-0.07	-0.01
Petiole length	-0.28	0.18	0.29	0.60	0.28
Leaf length	0.87	0.01	0.07	0.22	0.08
Leaf width	0.69	-0.02	0.16	0.47	-0.20
Leaf angle	-0.63	0.09	-0.18	0.05	-0.05
Leaf length-width ratio	0.42	0.01	-0.14	-0.45	0.43
Pods per plant	-0.53	0.43	0.44	-0.26	0.28
Pod length	0.94	-0.10	-0.13	-0.11	0.11
Pod diameter	-0.87	0.35	0.24	-0.03	0.06
Seeds per pod	0.93	-0.03	-0.06	-0.11	0.14
1,000-seed weight	-0.80	0.28	0.38	-0.04	-0.04
Seed yield	0.67	0.28	0.27	-0.32	0.28
Stem color	-0.12	0.65	-0.48	0.27	-0.11
Leaf vein color	-0.10	0.67	-0.48	0.00	0.05
Petiole color	-0.28	0.63	-0.35	-0.06	0.05
Stipule color	0.29	0.51	-0.54	0.13	0.23
Leaf shape	0.34	-0.01	0.04	0.20	0.38
Branching habit	-0.80	0.06	0.40	0.12	0.11
Leaf lamina color	0.14	0.36	0.04	-0.39	-0.67
Seed color	0.87	-0.23	-0.25	-0.02	0.03

patterns of the dendrogram. The difference as percent of minimum value (DPM) for each trait was calculated using the following equation: $DPM (\%) = [(difference\ between\ maximum\ and\ minimum\ values) / minimum\ value] \times 100$.

Conclusion

Our study demonstrates that the studied genotypes were highly variable for all of the morpho-agronomic traits and the genotypes of *C. olitorius* showed higher variation than those in *C. capsularis*. As the fiber of *C. olitorius* has higher economic value than *C. capsularis*, it is important to exploit this species for further improvement. The traits that diverse the most in *C. olitorius* were seed yield per plant, days to 50% flowering and pod length and in *C. capsularis*, seed yield per plant, pod per plant and seeds per pod were the most variation. Seed traits varied more than fiber traits for both species. Qualitative traits could be used to characterize jute genotypes. Fiber yield was positively correlated with days to 50% flowering, plant height at average flowering, plant height at 120 days, plant base diameter, fresh weight, leaf length and leaf width, but it had a negative association with some traits, including 1,000 seed weight, pod diameter and leaf angle. Cluster analysis separated the two species into two distinct groups for all the morpho-agronomic traits. The genotypes in cluster IX, accessions BRA/4792 and BRA/4794, which originated from Brazil, and a Bangladeshi popular variety (O-9897), showed the highest fiber and seed yield and maximum phenotypic diversity for most of the studied traits. Therefore, from the breeding point of view, these genotypes appear to be good candidates for jute-breeding programs focusing on fiber and seed yield. Principal component analysis summarized maximum diversity among the genotypes in 5 components. Moreover, our analysis shows for the first time that the results of principal component analysis, which reduces the number of traits, are in accordance with the results of cluster analysis and correlation analysis of the characteristics of jute. We recommend further investigation of the traits in PC1 (such as days to 50% flowering, plant height at average flowering, plant height at 120 days, plant base diameter, fresh weight, fiber yield, leaf length leaf width, pod length, seeds per pod and seed yield), focusing on molecular diversity and multilocal evaluation.

Acknowledgments

The authors are thankful to the Bangladesh Jute Research Institute for supplying jute seeds for this research. The financial support from the National Agricultural Technology Project, Phase-1, Bangladesh Agricultural Research Council, Government of Bangladesh, is gratefully acknowledged.

References

Akter J, Islam MS, Sajib AA, Ashraf N, Haque S, Khan H (2008) Microsatellite markers for determining genetic identities and genetic diversity among jute cultivars. *Aust J Crop Sci.* 1:97-107

Ali MN, Sasmal BG (2006) Association of seed yield and its components in segregating population of tossa jute (*Corchorus olitorius*). *Agric Sci Digest.* 26:206-208

Badenes ML, Martinez-Calvo J, Llacer G (2000) Analysis of a germplasm collection of loquat (*Eriobotrya japonica* Lindl.). *Euphytica.* 114:187-194

Basu A, Ghosh M, Meyer R, Powell W, Basak SL, Sen SK (2004) Analysis of genetic diversity in cultivated jute determined by means of SSR markers and AFLP profiling. *Crop Sci.* 44:678-685

BBS (2010) Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics. Ministry of Planning and Statistics Division, Govt. of People's Republic of Bangladesh, Dhaka. Website: <http://www.bbs.gov.bd>

Benor S, Demissew S, Hammer K, Blattner FR (2012) Genetic diversity and relationships in *Corchorus olitorius* (Malvaceae s.l.) inferred from molecular and morphological data. *Genet Resour Crop Evol.* 59:1125-1146

Choudhuri SD, Mia AJ (1962) Species crosses in the genus *Corchorus* (jute plant). *Euphytica.* 11:61-64

Edmonds JM (1990) Herbarium survey of African *Corchorus* species. Systematic and Ecogeographic Studies on Crop Genepools 4. International Board for Plant Genetic Resources, Rome

Franco J, Crossa J, Taba S, Shands H (2005) A sampling strategy for conserving genetic diversity when forming core subsets. *Crop Sci.* 45:1035-1044

Ghose RLM, Gupta BD (1945). Floral biology, anthesis and natural crossing in jute. *Indian J Genet.* 4:80-84

Ghosh M, Saha T, Nayak P, Sen SK (2002) Genetic transformation by particle bombardment of cultivated jute, *Corchorus capsularis* L. *Plant Cell Rep.* 20:936-942

Gower JC (1971) A general coefficient of similarity and some of its properties. *Biometrics.* 27: 857-871

Gupta VP, Sekhon MS, Satija DR (1991) Studies on genetic diversity, heterosis and combining ability in Indian mustard (*Brassica juncea* L.). *Indian J Genet.* 51:448-453

Hammer Ø, Harper DAT, Ryan PD (2001) PAST: paleontological statistics software package for education and data analysis (version 2.15). *Palaeontologia Electronica.* 4:9

Haque S, Begum S, Sarker RH, Khan H (2007) Determining genetic diversity of some jute varieties and accessions using RAPD markers. *Plant Tissue Cult Biotech.* 14:143-148

Hossain MB, Haque S, Khan H (2002) DNA Fingerprinting of jute germplasm by RAPD. *J Biochem Mol Biol.* 35:414-419

Hossen M, Ali MS, Begum M, Khatton A, Halim A (2008) Study on high yield of quality jute seed production for diversified uses. *J Innov Dev Strategy.* 2:71-73

IJO (1989) Descriptors and Descriptor Stayes for Characterization and Preliminary Evaluation of *Corchorus olitorius* and *C. capsularis*. International Jute Organization, Dhaka, pp.1-22

Islam AS, Rashid A (1960) First successful hybrid between the two jute yielding species, *Corchorus olitorius* L. (Tossa) × *C. capsularis* L. (White). *Nature.* 185:258-259

Islam MS, Uddin MN, Haque MM, Islam MN (2001) Path coefficient analysis for some fiber yield related traits in white jute (*Corchorus capsularis* L.). *Pak J Biol Sci.* 4:47-49

Kabi T, Bhaduri PN (1981) Genetic variability for leaf orientation in jute. *Indian J Genet.* 41:285-291

Khan MA (1995) Effect of sowing date and genotype on *C. olitorius* jute seed production. M.S. Thesis, Dept. Agron., Bangladesh Agr. Univ., Mymensingh

Khatun R (1998) Genetic behavior of yield and other characters of kenaf (*Hibiscus cannabinus* L.). *Bangladesh J Plant Breed Genet.* 11:65-68

Kundu BC (1951) Origin of jute. *Indian J Genet Pl Br.* 11:95-99

- Laurentin H (2009) Data analysis for molecular characterization of plant genetic resources. *Genet Resour Crop Evol.* 56:277-292
- Mir RR, Rustgi S, Sharma S, Singh R, Goyal A, Kumar J, Gaur A, Tyagi AK, Khan H, Sinha MK, Balyan HS, Gupta PK (2008) A preliminary genetic analysis of fiber traits and the use of new genomic SSRs for genetic diversity in jute. *Euphytica.* 161:413-427
- Mohiuddin G, Rashid M, Rahman M, Hasib SA, Razzaque A (2005) Biopulping of whole jute plant in soda-anthraquinone and kraft processes. *TAPPI J.* 4:23-27
- Palit P, Sasmal BC, Bhattacharyya AC (1996) Germplasm diversity and estimate of genetic advance of four morpho-physiological traits in a world collection of jute. *Euphytica.* 90:49-58
- Palve SM, Sinha MK (2005) Genetic variation and interrelationships among fiber yield attributes in secondary gene pool of *Corchorus* spp. *SABRAO J Breed Genet.* 37:55- 64
- Patel GI, Datta RM (1960) Interspecific hybridization between *Corchorus olitorius* and *C. capsularis* and the cytogenetical basis of incompatibility between them. *Euphytica.* 9:89-110
- Peeters JP, Martinelli JA (1989) Hierarchical cluster analysis as a tool to manage variation in germplasm collections. *Theor Appl Genet.* 78:42-48
- Roy A, Bandyopadhyay A, Mahapatra AK, Ghosh SK, Singh NK, Bansal KC, Koundal KR, Mohapatra T (2006) Evaluation of genetic diversity in jute (*Corchorous* species.) using STMS, ISSR and RAPD markers. *Plant Breeding.* 125:292-297
- Saha T, Majumdar S, Banerjee NS, Sen SK (2001) Development of interspecific somatic hybrid cell lines in cultivated jute and their early characterization using jute chloroplast RFLP marker. *Plant Breeding.* 120:439-444
- Saunders M (2001) Recovery plan for the endangered native jute species, *Corchorus cunninghamii* F. Muell in Queensland (2001-2006). Natural Heritage Trust, Australia, pp. 1-29