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RESEARCH ARTICLE

# Genetic Diversity in *Corchorus olitorius* Genotypes Using Jute SSRs

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**Abstract** Tossa jute (*Corchorus olitorius* L.) is an important lingo-cellulosic bast fibre-crop. It provides biodegradable and environment friendly fibre next to cotton, in terms of usage, global consumption, production, and availability. Narrow genetic diversity of the crop is the major hurdle, which is a demand at priority for any crop improvement programme. In the current investigation 138 jute genotypes of *C. olitorius* were characterized with ten jute specific SSR markers. A total of 23 alleles were amplified with an average of 2.3 alleles per locus and the PIC value ranged from 0.13 to 0.76 with an average of 0.455. The un-weighted pair-group method with arithmetic average cluster analysis of the 138 jute genotypes depicted a dendrogram using DARWIN, which divided the genetic resource into three major clusters. The study indicated the utility of SSR primers for providing useful and high levels of polymorphism for individual plant genotypes even with a narrow genetic base. Based on cluster analysis the most divergent genotypes identified were OIJ 167 (from Indonesia), OIM 058 and OIM 059 (India), however based on the agronomic traits as maximum plant height, basal diameter and fibre weight they were OIJ 245, OIJ (153 and 161) and OIJ 040, respectively.

**Keywords** Genetic diversity · Jute · *Corchorus olitorius* · SSR · Polymorphism · Agronomic traits

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## Introduction

Jute (*Corchorus* L.) commonly known as "Golden fibre" is one of the most important natural lingo-cellulosic bast fibre crop, next to cotton [1, 2] with respect to production and economic turn over globally. It is a principal coarse fiber crop grown for commercial purposes in many south Asian countries [3], predominately in India and Bangladesh. At the interface of discernible global climatic change, which demands utilization of biodegradable or eco-friendly products for better survival and perpetuation, jute offers best option owing to its biodegradable and non-eco-offensive nature [4]. It is a cash crop with marketable significance for generation of diversified value-added industrial products, in addition to its immense potential for packaging material [5].

Initially jute was classified in the family Tiliaceae [6], which was successively merged with the family Malvaceae based on certain molecular evidences of the chloroplast genome [7, 8]. Recently the genus has been reclassified within the family Sparrmanniaceae [9]. It has been reported to originate from Indo-Burma and Africa [10] and is natural inhabitant of the tropical and subtropical regions of the world. The genus *Corchorus*, is endowed with about 215 species, subspecies, varieties and land races (Global Biodiversity Information Facility 2008),[1] out of which only 50–60 species are important [11, 12]. The genus consists of annual or short-lived perennials [13], distributed in tropical, sub-tropical and warm temperate regions of the world, majority of the species being confined to Africa [1, 14]. It is represented by two cultivated jute species, viz., *C. capsularis* L. (the white jute) and *C. olitorius* L. (the tossa jute) which evolved through conventional breeding and pure line

[1] http://www.gbif.org

selection based on their yield and agronomic performances [15]. Both the cultivated species have haploid number of seven ($n = 14$) chromosomes, a few tetraploid ($2n = 28$) are also known [16].

It is a self-pollinated crop bearing very limited genetic variation [17]. Jute cultivars are currently distinguished by morpho-physiological characters such as pigmentation pattern in plant, leaf shape, stipule, seed coat colour of mature field-grown plants [18]. This method is slow and unreliable [19] and phenotypic identification based on morphological traits is subjected to environmental variation [20]. Information generated on the genetic diversity within and among closely related crop species is essential for crop improvement and to meet the diverse goals like producing cultivars with increased yield [21], wider adaptability, desirable quality, pest and disease resistance [22]. Cultivars that are closely related or have low genetic variability cannot be readily distinguished by morphological indices [23, 24], whereas molecular tools are the better alternatives for such studies.

PCR based molecular markers, such as randomly amplified polymorphic DNA (RAPD), simple sequence repeats (SSRs) and amplified fragment length polymorphisms (AFLPs) have an apparent advantage as cultivar descriptors as they are unaffected by environmental or physiological factors [25]. Among different molecular markers, SSRs are more abundant, ubiquitous in presence, hyper variable in nature and have high polymorphic information content [26]. They have been proven as an excellent tool for cultivar identification, evaluation of genetic diversity, pedigree analysis etc. in many plant species [27]. These have been reported to detect high level of polymorphism even amongst closely related plant germplasms [28]. These markers are almost twice as informative as dominant markers (RAPD and AFLP)and more informative than RFLP in soybean [29] and six times more informative than RAPD and nine times more informative than allozymes in poplar [30], emphasizing these markers as ideal for discriminating individuals and for parentage determinations.

Jute genetic diversity has been reported using SSRs [31, 32], RAPD [33–35], STMS, ISSR and RAPD [36]. Wild jute species have been classified [37] and cold-tolerant and cold-sensitive jute germplasms were characterized using inter simple sequence repeat marker [38]. Recently, the utility of studying genetic variability for different traits in jute genotypes using jute specific SSR markers has been reported [39, 40]. A comprehensive analysis of genetic diversity of *C. olitorius* germplasm is inadequate. The current research is focused on the analysis of genetic diversity in a diverse set of *C. olitorius* germplasm for studying genetic association of cultivars of different geographical origin and for identifying diverse genotypic combinations to aid genetic improvement of jute.

## Material and Methods

### Plant Materials

Leaf sample from 138 genotypes of cultivated *C. olitorius*, were collected from CRIJAF field, for the present analysis. The geographical distribution of these genotypes is presented in Table 1.

### DNA Extraction

Fresh young leaves (200–300 mg) from 60 day old field grown plants from each genotype were crushed in 1.0 ml CTAB extraction buffer (100 mM Tris HCl, 10 mM EDTA, pH 8.0; 1.4 M NaCl and 2 % CTAB) for DNA isolation following the CTAB procedure, with some modifications [41]. The samples (isolated DNA) were treated with RNase enzyme at 37 °C for 30 min to remove RNA contamination. RNase contamination was removed by adding an equal volume of dichloromethane and centrifugation at 14,000 rpm for 5 min at room temperature. To the supernatant isoproponal was added and centrifuged at 13,000 rpm for 5 min. To precipitate the DNA, a double volume of absolute ethanol was added and was mixed gently by inverting the tube. After centrifugation, the DNA pellet was washed with 70 % ethanol, air-dried and finally the purified DNA pellet was dissolved in 80 µl of TE buffer.

**Table 1** *C. olitorius* genotypes and their geographical distribution

| S. no. | Country of origin | Accession no. |
|---|---|---|
| 1 | Tanzania | OEX 002 to 004; OIJ 109, 138, 142, 143 (7) |
| 2 | Kenya | OIJ 014, 035, 038, 042, 055, 202, 257 (7) |
| 3 | Thailand | OIJ 153, 161, 177, 198, 267 (5) |
| 4 | Indonesia | OIJ 167, 175 (2) |
| 5 | Nepal | OIJ 206, 210, 227, 228, 243, 245, 246, 251, 273, 274, 277 (11) |
| 6 | Brazil | OIJ 253 (1) |
| 7 | India | OIM 001, 002, 004–061 (60) |
| | | OIN 004, 051, 071, 099, 105, 132, 181, 193, 198, 205, 207, 208, 211, 224, 231, 266, 271, 288, 289, 302, 339, 348, 359, 366, 371, 376, 387, 389, 397, 499, 604, 622, 664, 672, 681 711, 715, 744, 759 (39) |
| | | **Varieties** |
| | | BIDHAN RUPALI, JRO 128, JRO 066, JRO 8432, KOM 062, TJ 040 (6). |

### SSR Profiling

PCR was performed in GeneAmp® PCR system 9700 (Applied Biosystem, *Cat. No.* 4359659). Each of the 20 µl reaction mixture containing 50 ng of jute genomic DNA, 1× reaction buffer (2.0 µl PCR buffer, 15 mM $MgCl_2$), 2.5 mM $MgCl_2$, 0.2 mM dNTPs 1.0 unit of Taq DNA polymerase (QIAquick PCR Purification Kit (50), Qiagen, Cat. No. 28104) and 10 pmol of each primer. The thermal cycler was performed as follows: preheating for 5 min at 94 °C; followed by 30 cycles of 1.00 min at 94 °C (denaturation), 1 min at 56–57 °C (annealing) based on the primer Tm and 1 min at 72 °C (extension), and one cycle of final extension at 72 °C for 8 min followed by cooling to 4 °C for infinite period.

### Separation and Staining of PCR Products

Before loading on to gels, PCR products were denatured by adding equal volume of tracking dye (95 % formamide, 10 mM EDTA, 0.23 % bromophenol blue and 0.23 % xylene cyanol) and heating at 94 °C for 5 min. Amplified products were separated in 6 % denaturing polyacrylamide (38:2 acrylamide: bisacrylamide, SRL) gel in 1 × TBE buffer adjusted to pH 8.3 at 180 V for 1 h, using sequencing gel apparatus (Hoefer, USA). Silver staining of the gels was performed according to the procedure given by Sanguinetti et al. [42] and fragment size was documented by gel documentation system (Alpha Innotech) and calculated using the computer programme Gene Profiler 4.05 Software by comparing with the fragments of 100 bp DNA ladder (Gene Rular, Fermentas).

### Agronomical Study

One hundred and thirty three genotypes, (excluding six varieties) were evaluated for different agronomical traits in a randomized complete block design at CRIJAF. The data on various agronomical traits viz, plant height (m), basal, middle, top, core diameter (cm), number of nodes, fibre weight (g), stick weight (g), branching habit, number of days required to 50 % flowering from sowing, 1000 seed weight (g) and harvest index from each replication was recorded (Data not presented), among which plant height, basal diameter and fibre weight were the important parameters for which mean and standard deviation was calculated.

### Performance of Genotypes

Performance of 133 genortypes was studied based on the agronomical data generated for plant height, basal diameter and fibre weight for different groups of germplasm. For plant height (m) the accessions were grouped into four classes: number of accessions in the height class below 1.00, class 1.01–2.00, class 2.01–3.00 and above 3.00. Similarly for basal diameter (cm): number of accessions in the basal diameter class below 1.00, class 1.01–2.00 and class 2.01–3.00 was recorded. For fibre weight (g): number of accessions under class below 1.00, class between 1.01 and 6.00, class between 6.01 and 12.00 and class 12.01–17.00 was recorded. Range, mean and standard deviation for plant height, basal diameter and fibre weight in each group of accessions was calculated.

### Data Analysis

The amplified products were scored to generate binary matrix. During scoring, only intense and clearly resolved amplified products that were reproducible in multiple runs were considered for further analysis. The DNA fragments that were amplified by a given primer were scored as '1' for presence or '0' for absence of a particular locus for all of the genotypes that were studied. PIC was calculated for each SSR [43] using following formula.

$$\mathrm{PIC} = 1 - \sum (\mathrm{Pi})$$

where, Pi, is the frequency of the ith allele for marker.

A dendrogram was generated for identification of genetic relatedness among the genotypes based on the distance matrix by applying the UPGMA cluster analysis using the software DARWIN version 5.0 software.

## Results and Discussion

Simple sequence repeats markers used in the current investigation were developed at Molecular Biology Laboratory, Department of Genetics and Plant Breeding of Ch. Charan Singh University, Meerut, UP, India. Based on the initial studies [44] using these SSR markers, ten highly polymorphic SSR (Table 2) markers were employed to study genetic diversity among 138 different jute samples. The number of alleles per locus generated by each marker varied from 2 to 3, with an average of 2.3 alleles per locus, which differed as $4.61 \pm 1.92$, 3.04 and $6.33 \pm 2.04$ alleles per locus [31, 32, 39], respectively. The difference in the average number of alleles may be due to the different genotypes utilized in the study. The highest number of allele was 3 (SSR 489,SSR 566 and SSR 714) and lowest was 2 (SSR 487, SSR 536, SSR 554, SSR 569, SSR 639, SSR 666 and SSR 740). Banding pattern of 138 genotypes using SSR 639 is presented in Fig. 1. The polymorphism information content (PIC) value is a measure of polymorphism among varieties for a marker locus used. PIC value is indicative of the effectiveness of SSR loci information and measure the information of a given marker locus for the pool of genotype [45]. The PIC value of each marker

**Table 2** PIC value for SSR primer used for jute genetic diversity study

| S. no. | Primer code/name | | | Expected base pairs (bp) | Observed base pairs (bp) | NA[a] | PP[b] | PIC[c] | $R_p^d$ | Mean $R_p$ |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | SSR/MJM 566 | F | GGGTTTGCATCATAGTAGCCA | 320 | 320–208 | 3 | 33 | 0.63 | 1.98 | 0.66 |
| | | R | TAGGTCACGAGAAGAGCGAAG | | | | | | | |
| 2 | SSR/MJM 666 | F | GTAGCCAAGTCTGCTTCCTGA | 218 | 218–200 | 2 | 50 | 0.29 | 0.71 | 0.35 |
| | | R | TAGGTCACGAGAAGAGCGAAG | | | | | | | |
| 3 | SSR/MJM 569 | F | GTAGCCAAGTCTGCTTCCTGA | 386 | 398–325 | 2 | 50 | 0.30 | 0.68 | 0.34 |
| | | R | TAGGTCACGAGAAGAGCGAAG | | | | | | | |
| 4 | SSR/MJM 639 | F | CTGGTAAGGAGCTGCCTCTCT | 233 | 283–244 | 2 | 50 | 0.69 | 1.17 | 0.58 |
| | | R | TGCCTGTAAACCAACTTCTGG | | | | | | | |
| 5 | SSR/MJM 714 | F | TGCCTGTAAACCAACTTCTGG | 309 | 356–280 | 3 | 33 | 0.58 | 1.02 | 0.34 |
| | | R | CTGGTAAGGAGCTGCCTCTCT | | | | | | | |
| 6 | SSR/MJM 740 | F | CGCCAGAGAAGCAAATGTAAC | 315 | 286–250 | 2 | 50 | 0.76 | 1.02 | 0.51 |
| | | R | TAGAGCTCACCAGAGACTGCC | | | | | | | |
| 7 | SSR/MJM 554 | F | CTATCAGACTGCAGGTCAGCC | 312 | 370–318 | 2 | 100 | 0.34 | 0.75 | 0.37 |
| | | R | ACCTGATTTGCACACCAGAAC | | | | | | | |
| 8 | SSR/MJM 489 | F | TTGGTGTGGACCTTACAGGAG | 310 | 300–230 | 3 | 33 | 0.38 | 1.34 | 0.44 |
| | | R | ATTAGTGGCGACTCCTCCATT | | | | | | | |
| 9 | SSR/MJM 487 | F | ATTGGAAGAGGATATTTGCGA | 309 | 310–260 | 2 | 50 | 0.13 | 0.27 | 0.13 |
| | | R | GCATTCCCAATGACCAAGTTA | | | | | | | |
| 10 | SSR/MJM 536 | F | TAGGTTGCAGATGTTTGGTCC | 316 | 300–280 | 2 | 100 | 0.41 | 0.98 | 0.49 |
| | | R | GCAGACACTTGTACATAGTCAGG | | | | | | | |
| | | | | | | 23 | | 0.455 | | |

[a] *NA* number of alleles

[b] *PP* percent of polymorphism

[c] *PIC* polymorphic information content

[d] $R_p$ resolving power

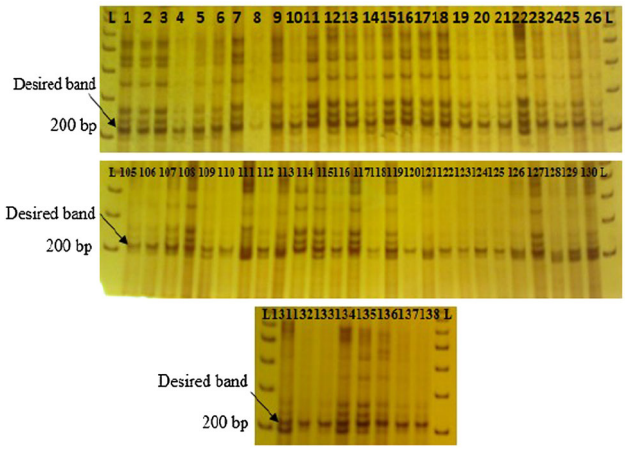


**Fig. 1** Polymorphism of *C. olitorius* genotypes with SSR 639 on 6 % polyacrylamide gel Legends: L- 100 bp DNA ladder, lane 1-138- jute genotypes

evaluated on the basis of its alleles, varied greatly among the tested SSR loci from 0.13 (SSR 487) to 0.76 (SSR 740) with an average value of 0.455 (Table 2), which was higher than the average PIC of 0.135 as reported by Das et al. [44] using 140 *C. olitorious* genotypes and 30 SSR. Four SSR markers (566, 639, 714 and 740) were highly informative and polymorphic as evident from its PIC value. The resolving power of the primers used in this experiment showed highest value (1.98) expressed by SSR 566 and the lowest value expressed (0.27) by SSR 487.

The UPGMA-based dendrogram was obtained from the binary data deduced from the DNA profiles of the samples analyzed where the genotypes that are derivatives of genetically similar types clustered together. A dendrogram based on UPGMA analysis grouped the 138 jute genotypes into three major clusters (Fig. 2), indicating that the genotypes have been grouped into three separate genetic groups. Cluster I carried the largest number of genotypes (94) followed by cluster II (37) and cluster III (7). The minimum similarity (0.11) was observed between OIN 397 and OIM 055 and maximum similarity (1.00) between OEX 002 and OIJ 243, OIJ 273, OIM 018, OIM 031, OIM 035. The major clusters I, II and III were sub divided into two minor clusters each with 77 and 17; 31 and 6; and 1 and 6 genotypes, respectively. Sub-group of cluster I carried improved, Indian and exotic germplasm.

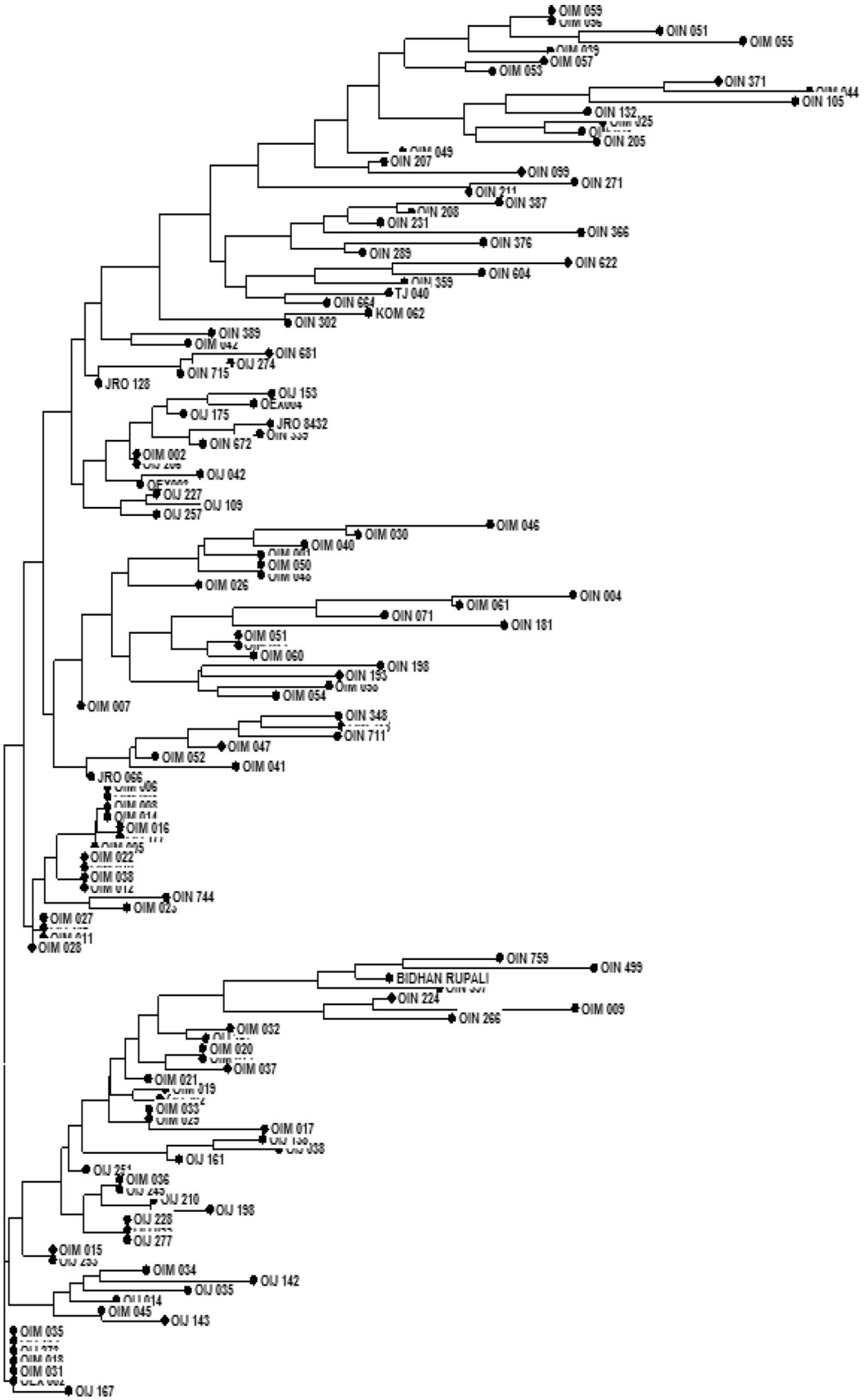


**Fig. 2** A dendrogram generated for 138 jute genotypes using SSR data

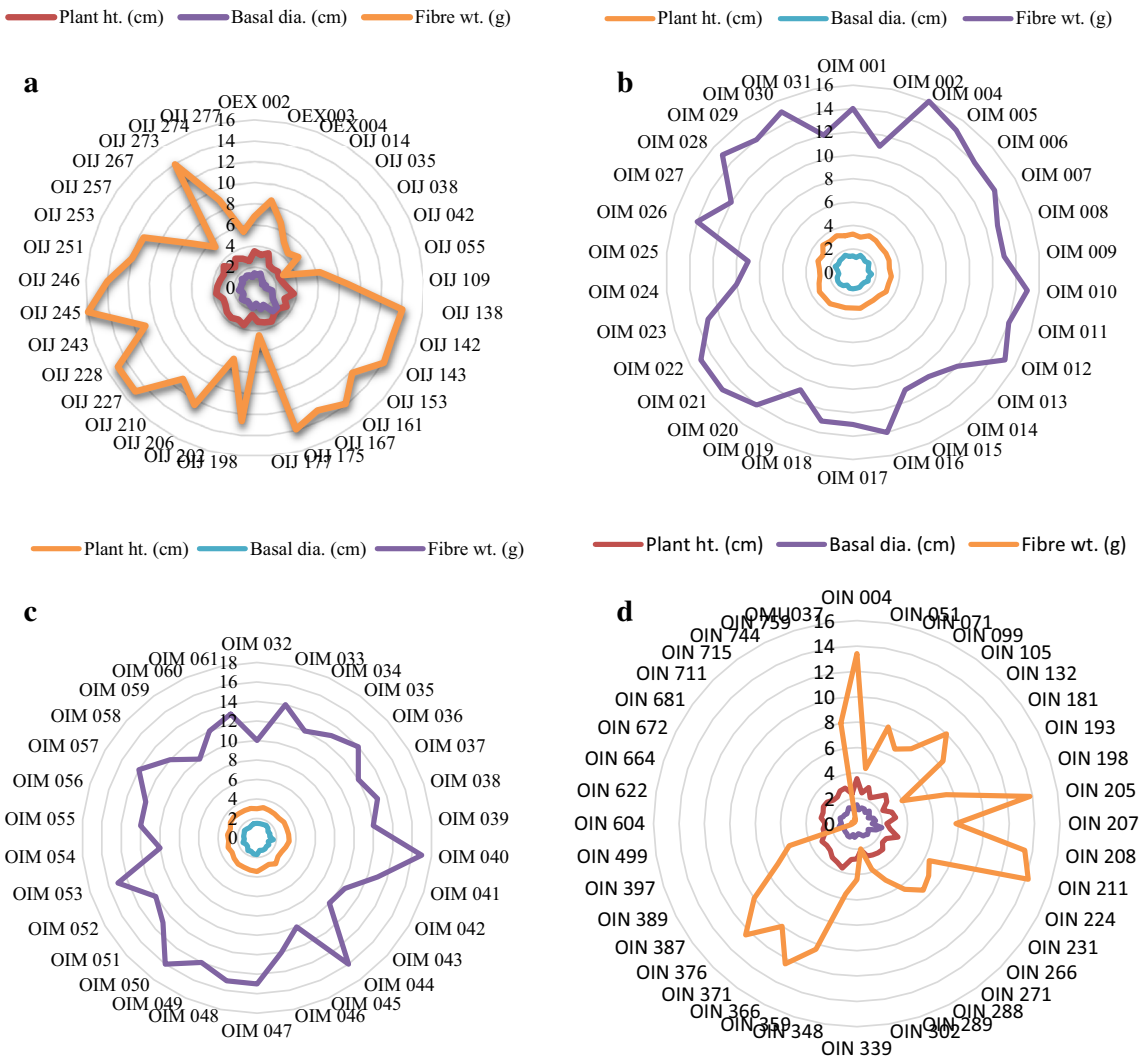


**Fig. 3** Performance of jute accession for plant height, basal diameter and fibre weight. **a** Representing OEX and OIJ accessions; **b, c** representing OIM accessions; **d** representing OIN and OMU accessions

The maximum number of OIM (improved types), OIN (indigenous collection) genotypes were grouped into the major cluster I and some of them in cluster II and III. OIJ genotypes were present among all the three clusters, whereas in OEX except OEX002 (cluster III) all others were grouped into cluster I. The varieties JRO 128, JRO 8432, TJ 040, KOM 062 were grouped in cluster I along with other genotypes showing some relationship with them, but BIDHAN RUPALI and JRO 66 deviated from this cluster and grouped into major cluster II and III, respectively indicating some variations at molecular level from other varieties grouped under cluster I. It is seen from the dendrogram that a few indigenous genotypes of Indian origin were deviated from cluster I (maximum grouped) and grouped into cluster II (20) and cluster III (3), which indicates similarity at genomic level with the other members of the cluster, which was represented by markers. Jute is self-pollinating and highly incompatible for inter-specific cross hybridization, which results in a narrow genetic base, however results of the current investigation showed good percent of polymorphism, similar results were reported in jute [31, 32, 39] and in many other plant species [30].

Though SSRs are generally believed to be locus specific and expected to amplify single or twin bands with a single SSR primer, in the present study multiple alleles were observed and similar results were also reported [46], which may arise from amplification of more than one homeolocus as suggested by Holton et al. [47]. The observed allele size ranged between 208 and 398 bp. The amplification percentage of the primers used in the investigation fell between 33.33 and 100 %. The average PIC value was found to be greater than the calculated PIC value

**Table 3** Performance of genotypes for plant height, basal diameter and fibre weight

| plant height (m) | Total number of accessions in different groups of germplasm | | | | |
|---|---|---|---|---|---|
| | Exotic (OEX) 3 | Exotic (OIJ) 30 | Indigenous (OIN) 39 | Mutant (OMU) 1 | Improved (OIM) 60 |
| Accessions for plant height in different groups of germplasm | | | | | |
| Number of accessions in the height class below 1.00 | 0 | 0 | 0 | 0 | 0 |
| Number of accessions in the height class 1.01–2.00 | 0 | 0 | 0 | 0 | 0 |
| Number of accessions in the height class 2.01–3.00 | 0 | 9 | 30 | 1 | 12 |
| Number of accessions in the height class above 3.00 | 3 | 21 | 9 | 0 | 48 |
| Range | 3.22–3.57 | 2.52–3.68 | 2.11–3.67 | 2.39 | 2.83–3.46 |
| Mean | 3.40 | 3.15 | 2.83 | 2.39 | 3.15 |
| SD ± | 0.19 | 0.39 | 0.34 | | 0.16 |
| Basal diameter (cm) | Total number of accessions in different groups of germplasm | | | | |
| | Exotic (OEX) 3 | Exotic (OIJ) 30 | Indigenous (OIN) 39 | Mutant (OMU) 1 | Improved (OIM) 60 |
| Accessions for basal diameter in different groups of germplasm | | | | | |
| Number of accessions in the basal diameter class below 1.00 | 0 | 3 | 5 | 0 | 0 |
| Number of accessions in the basal diameter class 1.01–2.00 | 3 | 24 | 33 | 1 | 60 |
| Number of accessions in the basal diameter class 2.01–3.00 | 0 | 3 | 1 | 0 | 0 |
| Range | 1.3–1.5 | 0.8–2.80 | 0.8–2.00 | 1.00 | 1.2–1.7 |
| Mean | 1.40 | 1.49 | 1.21 | 1.00 | 1.43 |
| SD ± | 0.1 | 0.47 | 0.12 | | 0.22 |
| Fibre weight (g) | Total number of accessions in different groups of germplasm | | | | |
| | Exotic (OEX) 3 | Exotic (OIJ) 30 | Indigenous (OIN) 39 | Mutant (OMU) 1 | Improved (OIM) 60 |
| Accessions for fibre weight in different groups of germplasm | | | | | |
| Number of accessions in the fibre weight class below 1.00 | 0 | 0 | 0 | 0 | 0 |
| Number of accessions in the fibre weight class 1.01–6.00 | 0 | 7 | 12 | 0 | 0 |
| Number of accessions in the fibre weight class 6.01–12.00 | 1 | 9 | 26 | 1 | 25 |
| Number of accessions in the fibre weight class 12.01–17.00 | 2 | 14 | 1 | 0 | 35 |
| Range | 11.2–15.5 | 03.0–16.0 | 03.9–19.6 | 08.0 | 09.0–16.0 |
| Mean | 14.06 | 10.41 | 7.40 | 08.0 | 13.01 |
| SD ± | 2.48 | 3.99 | 1.84 | | 2.81 |

0.13 of *C. olitorious* [36] and 0.41 and 0.47 with SSR and AFLP markers, respectively [48] with 63 jute genotypes of both the cultivated species. Similarly, the genetic diversity, using SSR loci information, was also relatively high, ranging from 0.32 to 0.88, with a mean value of 0.68 ± 0.16 [31]. High genetic diversity (0.76 ± 0.15) as reported among *C. olitorius* genotypes [49], whereas a mean value of 0.81 ± 0.06 was reported using SSR in *Corchorus* sp. [39], which is higher in comparison to the results observed in the current study.

## Agronomical Study

Among the 133 genotypes plant height ranged from 2.11 [OIN 302 (India, Karnataka)] to 3.68 m [OIJ 245 (Nepal)], whereas the basal diameter ranged from 0.8 [OIJ 042

(Kenya) and OIN 302 (India, Karnataka)] to 2.80 cm [OIJ 153 and 161 (Thailand)]. Accordingly number of nodes ranged from 50 [OIM 025 (India)] to 101 [OIJ 245 (Nepal)], which did not show any effect on flowering as seen in other crops. Days to 50 % flowering ranged from 51 [OIJ 175 (Indonesia)] to 170 days [OIJ 206 (Nepal)]. The fibre weight ranged from 03.0 g [OIJ 042 (Kenya)] to 17.0 g [OIM 040 (India)], however stick weight was recorded between 04.8 [OIN 289 (India, Karnataka)] and 84.5 g [OIJ 198 (Thailand)]. The number of branches ranged from 0 to 9, maximum number of accessions showed single branching, which is a plus point for jute crop. The maximum seed weight for 1000 seeds was recorded as 12 g [OIJ 035 (Kenya)], whereas the minimum was found as 0.9 g [OIN 208 (India, UP)]. Middle, top and core diameter was calculated for OIJ and OIM accessions, where middle diameter ranged from 0.5 [OIJ 042 (Kenya)] to 1.60 cm [OIJ 153 (Thailand)]; top diameter ranged between 0.2 [OIJ 038, 042, 055 and 277] to 0.6 cm [OIJ 161 (Thailand) and 167 (Nepal)], whereas core diameter ranged from 0.6 [OIJ 042 (India)] to 2.50 cm [OIJ 161 (Thailand)]. The harvest index percentage for OEX and OIN accession, ranged from 12.0 [OIN 266] to 53.0 % [OIN 289 (India, Karnataka)].

### Performance of Genotypes

Based on the agronomical data performance of genotypes in different groups of accessions in terms of plant height, basal diameter and fibre weight was studied. Under plant height category the number of accessions grouped under plant height class above 3.00 was 3 (OEX), 21 (OIJ), 9 (OIN) and 48 (OIM), whereas the number of accession under height class 2.01-3.00 from each group was 9 (OIJ), 30 (OIN), 1 (OMU) and 12 (OIM). Overall 81 accessions grouped under height class above 3.00, followed by 52 accessions under class 2.01–3.00. Number of accession from each group under the basal diameter category was recorded as 3 (OIJ) and 5 (OIN) under basal diameter class below 1.00, whereas number of accessions under class 1.01–2.00 was 3 (OEX), 24 (OIJ), 33 (OIN) and 1 (OMU), followed by OIJ (3) and OIN (1) under basal diameter 2.01-3.00. The maximum number (118) of accessions was found in the basal diameter class 1.01–2.00, whereas class below 1.00 grouped eight accessions followed by four accessions in class 2.01–3.00. In the category of fibre weight, the number of accessions from each group was found to be 7 (OIJ) and 12 (OIN) respectively under the fibre weight class 1.01–6.00 and under the fibre weight class 6.01–12.00, number of accessions grouped in each group of germplasm was 1 (OEX), 9 (OIJ), 26 (OIN), 1 (OMU) and 25 (OIM), whereas under the fibre weight class 12.01–17.00, number of germplasm in each group was 2 (OEX), 14 (OIJ), 1 (OIN) and 35 (OIM). Performance of germplasm with respect to height, basal diameter and fibre weight is presented in Fig. 3a–d showing the maximum and minimum values and standard deviation calculated for each group of accession as presented in Table 3.

From the agronomic data, OIJ accessions performed best for maximum traits, whereas from the dendrogram (molecular data) 3 accessions of OIJ {245 (highest plant height), 161 (maximum basal diameter) and 035} were grouped together in one cluster. Based on cluster analysis genotypes named, OIJ 167 (from Indonesia, cluster I), OIM 058 and OIM 059 (from India, cluster III) were found highly diverse. A minimum value of 0.80, 0.50, 0.20, 0.60 cm and 03.0 g for basal, middle, top, core diameter and fibre weight, respectively were recorded for accession OIJ 042 (Kenya), indicating not a good source for fibre generation. The accession OIJ 245 with maximum plant height (3.68 m) and highest number of nodes (OIJ 245), followed by OIM 040 (3.33 m) with highest fibre weight (17.0 g) performed better. These accessions can be considered best and incorporated in the breeding programme in near future for better yield (in terms of fibre). In nutshell based on agronomy and molecular data the accessions OIJ 153 (cluster III), OIJ 161 (cluster I), OIM 040 (cluster III) and OIJ 245 (cluster II) can be utilized in jute improvement programme. The best combination could be OIJ 245 (maximum plant height) from cluster II and OIM 040 (maximum fibre weight) from cluster III.

## Conclusion

Narrow genetic diversity need to be broaden by under taking hybridization programs involving diverge genotypes of jute. Other biotechnological tools such as somatic hybridization, chromosome doubling, embryo rescue and genetic transformation etc. can be employed to overcome the sexual incompatibility barrier between the two cultivated species of jute to enhance the diversity. The ease of detection with SSR markers to elucidate the diversity among 138 genotypes from different regions may encourage the use of SSR markers to characterize all the jute material (germplasm, genotypes, varieties, cultivars, breeding material etc.), which will certainly reduce duplication if any, in the collection. These SSR markers in near future may help plant breeders and geneticists to locate gene/s (agronomically significant) at particular region of the genome, which can be introgressed into appropriate material by either through development of transgenic or by breeding methodologies (map based cloning or marker assisted selection (MAS)). The diverse genotype identified based on molecular and agronomical data can be used for breeding programme of jute.

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