GMR
The Original

Assessment of Genetic Structure and Diversity of *Corchorus olitorius* L. Germplasm in Saudi Arabia

Widad S. ALJuhani[1]* and Ashwaq Yousef ALjohani[2]

[1]Department of Biology, Faculty of Science, Umm Al-Qura University, 24381 Makkah, Saudi Arabia
[2]Research Laboratories Centre, Faculty of Science, Umm Al-Qura University, 24381 Makkah, Saudi Arabia

Corresponding author: Widad S. ALJuhani
E-mail: wsjuhani@uqu.edu.sa
rosmary_flow@hotmail.com

Genet. Mol. Res. 23 (2): gmr2326
Received May 18, 2024
Accepted June 25, 2024
Published June 28, 2024
DOI http://dx.doi.org/10.4238/gmr2326

ABSTRACT. Jute, scientifically referred to as *Corchorus olitorius* is a plant that used both as a food source and Fibers, in addition it had health benefits. There is limitation in jute genetic foundation and recommendations for cultivating jute. Thes main goal for this work to evaluate the genetic diversity of jute germplasm in Saudi Arabia, their relationship with worldwide varieties using a molecular marker simple sequence repeat SSR (Microsatellite). The research involved 24 jute cultivars totaling 72 samples, including 8 cultivars (24 samples) from Saudi Arabia and 16 cultivars (48 samples), from Southeast Asia, Southwest Asia, North Africa, and the United States. The analysis was conducted using eight microsatellite markers. The results revealed that the markers used showed an amount of variation between jute cultivars, were observed 56 alleles. The polymorphic information content (PIC) value for SSR was in mean 0.763. By utilizing Structure and discriminant analysis of components (DAPC) and SSR markers data the *C. olitorius* genotypes were categorized into three groups. Moreover, the local species were divided into two groups well. These findings have implications for those involved in jute production as it helps in mapping crop, selecting cultivars optimizing reproduction processes expanding genetic diversity improving crop traits such as yield

and adaptability to different environments and enhancing disease resistance capabilities. This the first time of study diversity of local jute in KSA used SSR markers, analysis, and comparison with international crops.
Key words: Crops; Genetic; Diversity; Identification; Microsatellite; Molecular

INTRODUCTION

The plant genus known as Corchorus is commonly called 'jute' or 'molokhia', in Arabic (Ahmed, 2021). Corchorus belongs to the Malvaceae Juss. family. *Corchorus capsularis and Corchorus olitorius* species hold the highest value.

Jute is globally recognized for its indispensability and economic importance as it stands out as one of the leading fibers. Moreover *C. olitorius* serves as a food (Zhang et al., 2019) also contains flavonoids, phenols, amino acids, and minerals (Adebo et al., 2015; Do et al., 2021). It contents proteins, several of vitamins beside the fibre (Adebo et al., 2015; Zakaria & Shuranjan, 2022).

Corchorus cultivation is widespread across subtropical regions in Africa, America, Australia, and Asia (Benor, 2018). However, the precise origins of the species remain insufficiently documented. Based on the range of varieties and their extensive diversity it is highly likely that *C. olitorius* originated in Africa (Fawzi, 2018).

Jute is usually with self-pollination, subjected to several environmental biotic and abiotic stresses (Zhang et al., 2019). In addition, there is lack in information of *C. olitorius* varieties. Most of the original *C. olitorius* germplasm have not yet been fully characterized, which prevents their use in breeding programs, thus limited genetic diversity among germplasms (Mukul and Akter, 2021).

Numerous morphological characteristics were employed in order to differentiate between different types of molokhia, and the presence of morphological heterogeneity among these varieties was verified. However, the quantity of these characteristics is limited, and their expression can be influenced by environmental factors. Consequently, breeders turned to the utilization of genetic markers to explore the variations within jute genotypes (Helaly et al., 2017). These molecular markers, unlike their morphological counterparts, are unlimited in number and remain unaffected by environmental conditions.

Different genotypes of jute were analysed using several types of molecular techniques. (Youssef et al., 2019) conducted research, on *C. olitorius* from Egypt employing Random Amplified Polymorphic DNA (RAPD) and Sequence related polymorphism (SRAP) markers. Their findings confirmed a clear variation in jute accession. On the hand (Haque et al., 2007) investigated around 18 accessions of *C. capsularis and C. olitorius* species using RAPD markers. This study reflected low level of variations between the samples. (Basu, 2004) used 10 AFLP markers to assess diversity among 49 cultivars of *Corchorus olitorius* and *Corchorus capsularis*.

(Roy et al., 2006) examined the variations in jute using ISSR primers, their studies showed a polymorphism rate of 98.44% across all species, with diversity observed within individual species. On the hand, in their study (Nag et al., 2018) examined the differences, in *Corchorus* plants by analysing ISSR and SSR data from 33 samples of *C. olitorius* and 65 samples of C. Capsularis collected from India, Kenya and Sudan. The findings indicated that there was variation, among the *Corchorus olitorius* accessions in compared to the *Corchorus capsularis* ones.

Several works were preformed to evaluate the jute diversity using SSR markers and have proven effective in verifying cultivar identity and analysing population structure. These markers are

known for their co-dominance, polymorphism, and abundance in plant genomes (Adeyemo et al., 2021). (Ghosh et al., 2015) employed 10 SSR primers to analyse the diversity in 138 *C. olitorius* cultivars from Indonesia and India. Their findings confirmed that SSR markers exhibit levels of polymorphism and variation among the genotypes.

Furthermore, (Ngomuo, 2017) investigated the diversity between 83 jute samples using 25 microsatellite loci. The author observed that each marker produced a number of alleles with mean 2.63 alleles. In another study (Yang et al., 2018) screened variation among 453 genotypes of *C. olitorius* sourced from Kenya, Nepal, and China. The cultivars that were examined showed an amount of variation.

As, per (Mujahid, 1989) three types of *Corchorus* plants, *C. olitorius, C. Tridens* and *C. depressus* widely distributed among wild of Saudi Arabia. Cultivation of Jute was extended across regions in the KSA (Emad, 2012; Yusuf, 2014). Currently, there is not enough knowledge about genetic diversity in jute cultivars in Saudi Arabia and the phenotypic have not been adequately described. The cultivation of this crop faces challenges such as salinity, water scarcity and soil depletion. Efforts are currently being made to preserve jute germplasms in the seed repository managed by the Ministry of Agriculture and Water in the KSA. However, conservation and improvement of these germplasms requires comprehensive information and evaluation their genetic diversity.

The purpose of this study is to assess the genetic variation, in jute germplasm conserved within the Saudi Seed Bank using microsatellite markers. Additionally, a comparative analysis will be conducted between germplasm and those obtained from seed repositories.

METHODS

The Plant Material

A 24 jute " (*Corchorus olitorius*) cultivars have been used in this study, seven of these cultivars were obtained from the seed repository of the Ministry of Environment, Water and Agriculture in Saudi Arabia. In addition to six jute germplasms had been obtained of commercial stores in Saudi Arabia. They represent the best local jute cultivars and preferred by consumers. While the remaining eleven cultivars were sourced from regions, around the world including Southeast Asia, Southwest Asia, North Africa, and the United States. We obtained these cultivars from the seed repository located in IPK Gatersleben, Germany. Table (1) presents information related to cultivars under this study (Table 1).

Germination of Seeds

The seeds were cultivated using sterilized soil, which comprised a combination of agricultural soil with a sandy texture and pitmos. The cultivation process involved maintaining temperature conditions that ranged from 30°C to 180°C, with the seeds being irrigated twice daily. After 60 days of cultivation, the fresh young leaves were carefully collected from *C. olitorius* accessions. Specifically, the leaves were collected from the sixth leaf from the top. It is important to note that three replicates were utilized for each cultivar, ensuring different seedlings were represented. Subsequently, the leaf samples were divided into smaller fragments, and the DNA of the plant was extracted from these fresh young leaves.

Table 1. Showcasing the *corchorus olitorius* accessions that were utilized in the molecular investigations.

No	Samples Codes	Country of origin	Source of collection
1	S.A(Giz)	Saudi Arabia (Gizan)	Ministry of Environment, Water and Agriculture, Riyadh
2	S.A(Raf)	Saudi Arabia (Rafha)	
2	S.A(Mad)	Saudi Arabia (Madina)	
4	S.A(Tai)	Saudi Arabia (Taif)	
5	S.A(Qat)	Saudi Arabia (Al-Qateef)	
6	S.A-M-(Muz)	Saudi Arabia [Mecca (Al-Muzaiq)]	
7	SA-M-Yam	Saudi Arabia [Mecca (Al-Yamania)]	
8	SA-Lay	Saudi Arabia (allayth)	Saudi Arabia commercial Store
9	Egypt2	Egypt - Giza (Saidy)	
10	Egypt3	Egypt (Saidy)	
11	USA	Origin:U.S.A -(Saidy)	
12	Egypt4	Egypt (Saidy)	
13	Egypt5	Egypt	
14	India	India	IPK Gatersleben, Germany
15	China	China	
16	Libya1	Libyan Arab Jamahiriya	
17	Libya2	Libyan Arab Jamahiriya	
18	Libya3	Libyan Arab Jamahiriya	
19	Libya4	Libyan Arab Jamahiriya	
20	Tunisia1	Tunisia	
21	Tunisia2	Tunisia	
22	Tunisia3	Tunisia	
23	Egypt1	Egypt	
24	Japan	Japan	

DNA Extraction

The method used to extract DNA was the hexadecyltrimethylammonium bromide (CTAB) technique, which was described by (Doyle and Doyle, 1987). To determine the amount of extracted DNA we employed the NanoDrop Lite Spectrophotometer, from Thermo Scientific/Germany. Additionally, the quality of the DNA has been checked in gel agarose 1%. Visualized it by exposing the gel to UV light using the UVITIC Cambridge Images System (FIREREADER V10, France).

Screening the Microsatellite Primer Pairs

In the beginning we chose 16 sets of primers (SSR) that were developed by (Adeyemo et al., 2021). They were specifically selected because they have a level of polymorphism as mentioned in the literature by (Mir *et al*., 2008; Das *et al*., 2012; Adeyemo *et al*., 2021). We then tested these sets with the samples, in our study to confirm their ability to amplify DNA. After this evaluation we narrowed down our selection to eight pairs of primers (SSR78, SSR569, SSR688, J179, J188a, DQ108572, MJM1030 and J139) which successfully amplified DNA from all the samples tested. These details are provided in Table 2.

Preparation for the Polymerase Chain Reaction (PCR)

The current study used PCR protocol that mentioned by (Adeyemo et al., 2021) to gain PCR products. The PCR process involved a volume of 25µl comprising of 12.5 µl of Master Mix

Table 2. Displays the primers information used in *corchorus olitorius* cultivars.

S/N	Marker name	Sequences		Optimal Ta(°C)	References
1	SSR78	Forward (5`-3`)	GCTCACCGGTGGAAGTTAGAAGCA	65.8	(Adeyemo et al., 2021)
		Reverse (3`-5`)	GTGGCGGAGACGGTGGTGTG		
2	SSR569	Forward (5`-3`)	TGAATGCATATGTGATATGTGTTAAGTC	64	(Adeyemo et al., 2021)
		Reverse (3`-5`)	GAAGGCTCAAGTTTGAACTTTGAATA		
3	SSR688	Forward (5`-3`)	TGTGTTCCATAGGACCATTATTCA	59	(Adeyemo et al., 2021)
		Reverse (3`-5`)	CCTTTCACTATTGCATGAACACAA		
4	J179	Forward (5`-3`)	GACGCCATTTTGACCCAAGC	60	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	GGGATCATCGAAGGGTGAAGC		
5	J188a	Forward (5`-3`)	GCTTTGCCGTTTCAAAGCAG	59	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	TGGGAAGCATCGGCAAAGAG		
6	DQ108572	Forward (5`-3`)	GGGTATTTTGATTCATTTCTTGTAGG	59	(Adeyemo et al., 2021)
		Reverse (3`-5`)	CAAAAAGACCATGGCTATCTAGGTATAA		
7	MJM 1030	Forward (5`-3`)	ATTGGTGGGAGTTTGGTTGA	59	(Das et al., 2012; Adeyemo et al., 2021)
		Reverse (3`-5`)	TGGAGCAATAAACTTATAAAAGAATG		
8	J139	Forward (5`-3`)	CCCAAGACCGAAAGAGGACG	59	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	ACCGTGGAAGACTCCGGTG		
9	J15	Forward (5`-3`)	ACTCACTCATGAATTGAGTAAGCATC	55	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	TCAGCCCTTAAAACGTCCTAG		
10	J57	Forward (5`-3`)	ACCCAATTTCCTTTCCCACC	59	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	CGAATTGCTTTGCTGAAAGATGG		
11	J142b	Forward (5`-3`)	TTGCCAAAGGGATGAGGTTG	57	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	GTTTATGGTGGTGGTGGTGG		
12	J143	Forward (5`-3`)	CGGCGTTCCCACCTTCATCAG	64	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	GGTCCTCGCATGGCGTGTATTC		
13	J150	Forward (5`-3`)	TCTCCCACCAAGTCCAACACC	58	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	CGTGCAATAACGAAGGCTTG		
14	J174	Forward (5`-3`)	CCATGATGCAAAGAATGGATGC	60	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	TTGTCCTCCAGCCTCTTGTTGTTCC		
15	MJM 1133	Forward (5`-3`)	CACGAGGCTCCTAAAGTTGC	59	(Das et al., 2012; Adeyemo et al., 2021)
		Reverse (3`-5`)	TCAGACGGAGCATATGATGG		
16	J191a	Forward (5`-3`)	CGTTGTCGGTTCGTCCAGTG	59	(Mir et al., 2008; Adeyemo et al., 2021)
		Reverse (3`-5`)	TCTTTTTCTTGGCTGTCTGTTTGG		

ThermoScientific™ (ThermoFisher in Lithuania) 8.5 µL of nuclease free water 2 µl of DNA and 0.1 µl each of Forward and Reverse primers. For the PCR profile they employed the Thermal Cycler GeneTouch 96 Well Fast manufactured by Bioer Technology in China. The temperature and time settings were used as described by (Adeyemo et al., 2021). The procedure commenced a 95°C for a and 5 minutes for denaturation stage, reaction performed in 35 cycles and 94°C for 15 seconds. While temperature increasing gradually have been increased from 55°C to 60°C for a period of 20 in annealing stage. The extension stage conducted in 72°C for 30 seconds. Finally, a final extension step at 72°C fora period of 7 minutes.

Fragment Analysis

The PCR products of each amplification were sent to Macrogene Genome Centre, Korea, to perform fragment analysis (https://dna.macrogen.com/, Seoul, South Korea).

Data Analyses

Data of fragment analysis obtained from Macrogene company have been used in molecular data analysis. To determine the number of alleles and genotypes per marker well as the average number of markers. We used established methods described by (Botstein et al., 1980) and Powermarker V. 3.25 software (Liu and Muse, 2005) to calculate the polymorphic information content (PIC).

Genetic dissimilarity (GD) between samples was calculated by using DARWIN software version 6.0.021.2029 (Perrier et al., 2009). To illustrate the variation within and between cultivars a heat map was preformed in GraphPad Prism program V. 9.5.1 (March 2023) based on a matrix of dissimilarity.

There is not enough information available about the origin and genetic structure of jute germplasms in Saudi Arabia, so we used the Structure v. 2.3.3 (Pritchard et al., 2000) to screen number of clusters (populations). This analysis was conducted to classify individuals into sub-populations and identify admixed individuals using the SSR dataset without knowledge of the number of populations (K). This process determined whether a sample belonged to one or more subgroups or if it had a structure that was a combination or admixture of populations (Ojango et al., 2011). Monte Carlo Markov Chain (MCMC) analysis, in burn length of 50,000 and 100,000 iterations. it has been used number of clusters of 1, to 10.

Additionally, we performed analysis of components (DAPC) to detect number of sub-clusters, for both local and international jute varieties. DAPC analysis helps in detect the relationships between the individuals (convergence), grouping individuals into clusters according to similarity. We carried out this analysis using data and the Adegenet package 1.4 2 (Jombart and Ahmed, 2011) in combination, with R program V. 3.0.2 (2013).

RESULTS

Eight out of sixteen pairs of SSR primers that successfully showed amplification with all study samples were selected (SSR78, SSR569, SSR688, J179, j188a, DQ108572, MJM1030, and J139). The remaining markers were excluded because they did not amplify a clear band or yielded a weak band.

The eight selected SSR loci exhibited high polymorphism (Table 3) and produced 56 alleles, with mean 7 alleles. Less number of alleles was 4 alleles in SSR78 locus, while MJM1030 and SSR688 loci exhibited the highest number of alleles at 10. The mean PIC was 0.763, and lowest PIC value 0.633 in DQ108572 locus and highest one is 0.881 in SSR78 locus. The total number of genotypes was 29, with a mean of 4, ranging from 2 in J179 to 5 in MJM1030 and J188a loci. We notice that three SSR loci MJM1030, SSR688, and J188a), had each the highest number of alleles and genotypes (Table 3).

Genetic dissimilarities are presented in a heat map in Figure 1, it is apparent that the extent of variation between the different cultivars spans from 0.00 to 0.750. The highest genetic dissimilarity was 0.750, which was recorded between the cultivars of Egypt (Egypt3) and China. On the other hand, the lowest variation of 0.063 was found between the cultivars of Tunisia (Tunisia2) and India (India), Japan and Libya (Libya2), and Saudi (SA-M-Yam) and Egypt (Egypt2). No variation or ‘0’ variation was recorded between samples of the same cultivars collected from the same regions.

The findings of the structural examination are exhibited in K-values in Figure 2 and bar graphs in Figure 3 as shown in (figure 3) jute samples distributed into three sub-clusters. The first

Table 3. Presents an overview of the genetic diversity observed in a sample of 72 *c. Olitorius* accessions cultivated in saudi arabia, using a set of 8 ssr markers. The polymorphism information content (pic).

SSR Markers	Allele No	Genotype No	PIC
MJM1030	10	5	0.830
SSR688	10	4	0.749
J188a	8	5	0.845
SSR569	7	3	0.666
DQ108572	6	3	0.633
J179	6	2	0.675
SSR78	4	3	0.881
J139	5	4	0.822
Total	56	29	
Mean	7	4	0.763

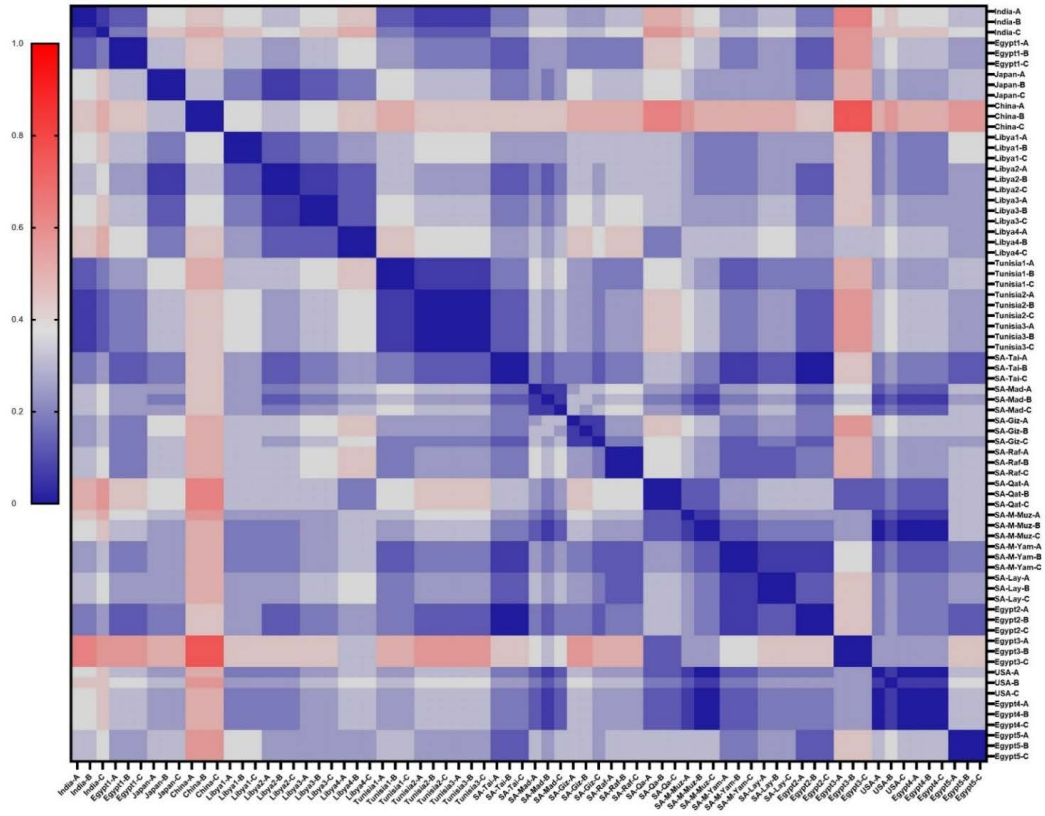

Figure 1. The heat-map showing the percentage of dissimilarity among *corchorus olitorius* cultivars based on ssr marker data.

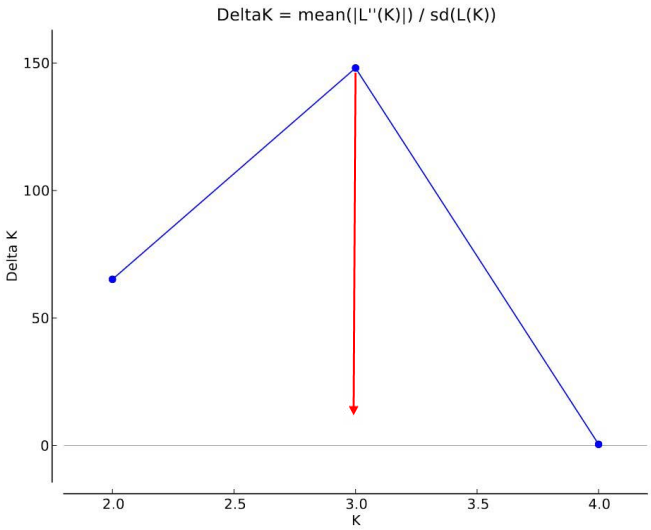

Figure 2. Presents determine the number of clusters denoted as k, through the utilization of structure software, and analysis of ssr in a set of 72 samples of *c. Olitorius* cultivars. The data (δ k) is calculated for values of k, and the process is repeated 10 times. The findings suggest that the ideal number of clusters is three.

cluster (red bar) consist of the Indian samples, most samples of Egypt (Egypt1, Egypt2, and Egypt5), Tunisia (Tunisia1 and Tunisia2), and local cultivars of Saudi (Gizan, Rafha, Allayth, Taif, and Mecca-Al-Yamania). The second cluster (green bar) includes a mix of all samples from the US and a few cultivars of Egypt (Egypt3 and Egypt4), local cultivars from Saudi Arabia (Madina, Mecca-Al-Muzaiq, Al-Qateef), and Tunisia (Tunisia3). The third sub-group (blue bar) includes only international cultivars—samples from Asia (China and Japan) and Africa (Libya) (Figures 4). According to SSR markers, most of the jute samples in this study were pure and clearly belonged to one of the three sub-groups. There were no admixed samples or those with a genetic structure that was a combination of more than one population. The local jute cultivars from the KSA were included in the first and second groups (red and green).

The DAPC of 72 jute cultivars were divided into three groups, as depicted in Figure 4. The principal component (PC) 1 and PC 2 Highly have discrimination power. PC1 interpreted 67% of the variations and PC2 interpreted 33% of the variations between samples. Of the 72 samples, 18% were assigned to cluster 1 “blue” and cluster 2 “green.” In contrast, 36% of the cultivars were included in cluster 3, “red,” which had the highest density. The results obtained in the DAPC analysis was similar to the structure analyses in terms of the contents of cluster 1, which included only international cultivars that is, samples from Asia (China and Japan) and Africa (Libya). Local cultivars of Saudi Arabia were distributed in clusters 2 and 3 and mixed with international samples from Egypt, Tunisia, and the US.

Overall, the group of cultivars from China, Japan, and Libya appears distinct, occupies the cluster itself, and indicates a clear genetic distance from the remaining cultivars. Furthermore, it was evident from the results of the analyses that the local cultivars of Saudi Arabia are distributed in two groups—S.A-Giz, S.A-Raf, S.A-lay, S.A-Tai, and S.A-M-Yam in one group and S.A-Mad, S.A-M-Muz, and S.A-Qat in the other group. Geographic origin had no clear effect on the distribution of samples within clusters.

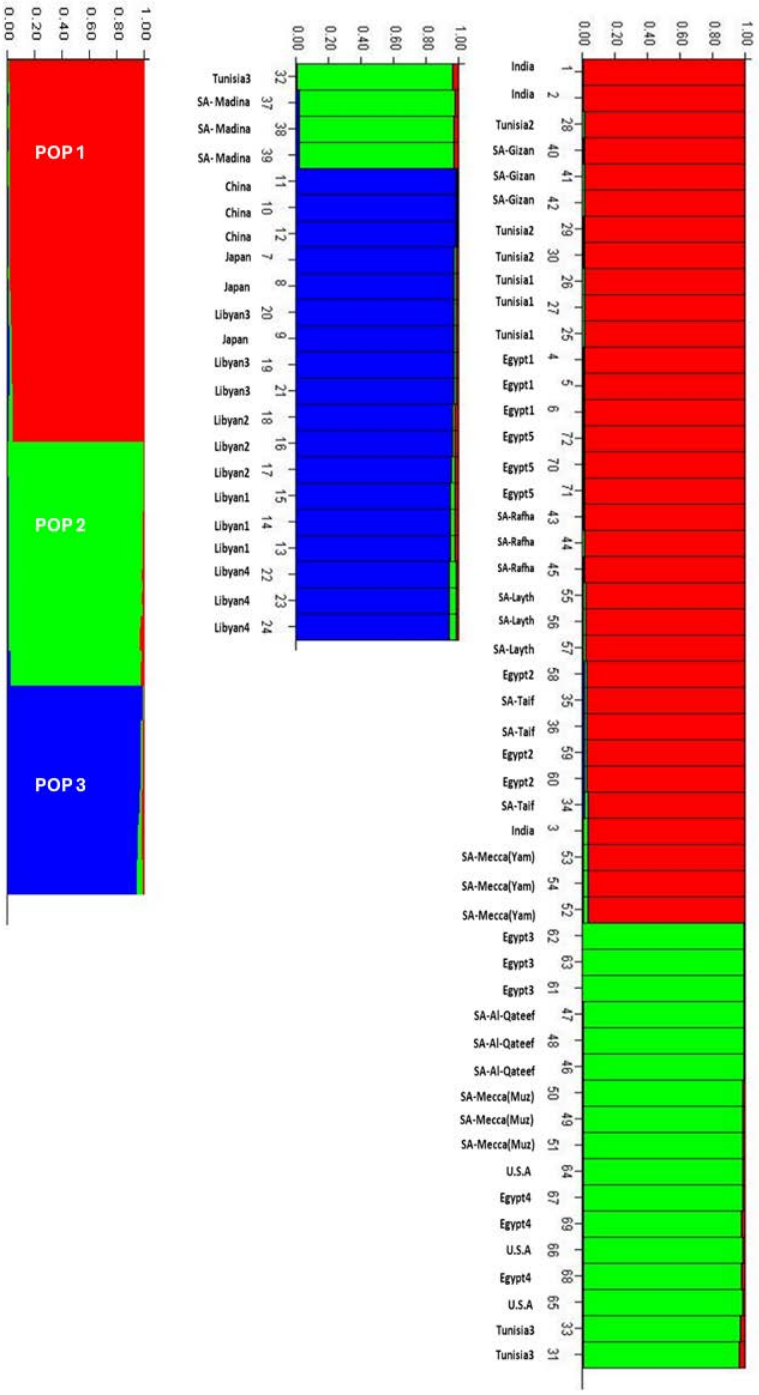

Figure 3. Inferred clusters in the *corchorus olitorius* cultivars and 8 ssr markers, using structure, the analysis showed that there are three bars(k), each bar within the figure represents a distinct individual genotype. Local jute genotypes from saudi arabia can be classified into two subgroups.

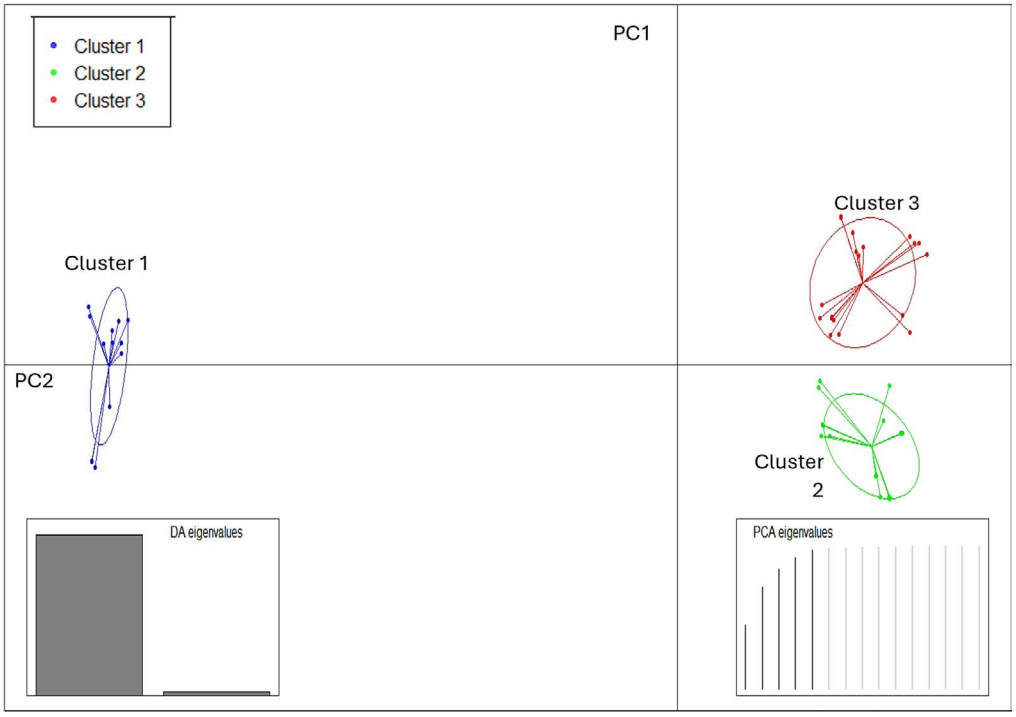

Figure 4. The dapc analysis of local and international *corchorus olitorius* genotypes using ssr loci.

DISCUSSION

In the current study 56 alleles have been detected in the screening of 24 cultivars (72 samples) using 8 SSR markers, with mean 7 alleles. We observed high number of alleles compared to that mentioned in study of (Adeyemo et al., 2021) which utilized 16 SSR primer pairs and 16 cultivars of Nigeria, 41 alleles have been recorded within samples. This may be due to use of local and international jute accessions in this study.

Furthermore, our findings can be contrasted with the study by (Kiebre et al., 2019), where 53 alleles were identified in 16 variety of *C. olitorius var ilicifolius* and 80 of *C. olitorius var olitorius* from Burkina Faso using 17 SSR markers. However, this study recorded a smaller number of alleles compared to the research conducted by (Haque et al., 2007), which reported 171 alleles in 16 *C. olitorius* genotypes from India and Bangladesh using 27 SSR markers. This discrepancy can be attributed to the utilization of samples with high genetic diversity and a wide hybridization background (Al-Mamari, 2013).

Overview, as presented in the curent results the average of PIC value was 0.763, according to (Sharma et al., 2009) microsatellite loci are significant when the PIC value ≥0.5, as well the PIC values for all eight SSR loci ranged from 0.633 to 0.881 indicating that the markers used in this study informative. Although we only used eight SSR markers in this study it was enough to identify and distinguish between the 72 samples. It's worth noting that this number is relatively low compared to studies, like (Kiebre et al., 2019) research where they analysed 96 jute accessions using 17 SSR markers.

An array of genetic differences was observed among the types of *C. olitorius* plants with variations ranging from GD=0.00, to 0.750. Our findings align with (Huq et al., 2007) research, which also highlighted a level of diversity within *C. olitorius* varieties. Similarly, (Ghosh et al., 2015) study analysed the diversity within 138 types of *C. olitorius*. Found that SSR markers show substantial levels of variation and genetic differences among different genotypes even when the genetic foundation is limited. In contrast to (Yuan et al., 2015) investigation that used 63 SSR markers to explore population structure and relationships in a sample of 159 accessions of *C. olitorius* and *C. Capsularis*, the outcomes shown that 81% of the variance were between species while 19% was found within subgroups.

All analysis conducted using DAPC and structure techniques revealed that the samples of *C. olitorius* cultivars can be classified into three clusters. Thus, methods were sufficient to determine the genetic diversity between samples study, and able to be grouped cultivars according to similarity within three clusters, which represented three genotype patterns. (Adeyemo *et al*., 2021) also reported results when studying 16 jute cultivars in Nigeria, where the SSR data divided the samples into three groups indicating variations and relationships.

The results obtained from the DAPC, and structure analyses were consistent, in terms of that specific local and international germplasms were grouped together in all three analyses. This suggests that geographic location does not play a role, in their distribution. Our findings align with those of (Yuan et al., 2015) who investigated 159 jute accessions and confirmed that geographic location does not affect their distribution.

Since structure analysis is useful in knowing the number of population groups within local germplasm into which species are divided according to their genetic structure and helps in understanding the origins of local species. The results of Structure analyses suggest that the native plant varieties in Saudi Arabia can be divided into two genotypes. The population 1 contents cultivars of (Gizan, Rafha, Taif, Mecca-Al-Yamania), and population 2 consist of cultivars (Madina, Mecca-Al-Muzaiq, Al-Qateef), supporting the idea that there are two genetic populations within the local jute variants in Saudi Arabia. While, the group of varieties, from China, Japan and Libya shows another different pattern of genotype. All local jute germplasms were pure and there were no combination or admixture of populations in cultivars under the current study.

Currently, several available jute cultivars narrow genetic base and used limited number of cultivars because of lack morphological and molecular characterized, need to more genetic variation is required to Improvement the cultivars, in addition to used wild species of Corchorus in crop. The varieties used in this study show three different genotypes, and these different patterns can be used in improving programs, which helps in expanding the range of genetic diversity between the cultivars and producing germplasm resistant to biotic and abiotic stress, that pose a challenge to the growth of the cultivars in arid environments, such as salinity and drought in jute varieties.

To effectively utilize the preserved germplasms in gene banks it is crucial to evaluate their genetic diversity level simplify their identification process facilitate their exchange, between countries and use them to improve plant varieties. To achieve this goal, it is better to use a low number of primers for distinguishing between samples. Therefore, we recommend using the SSR markers used this study to screen jute germplasms, especially loci (MJM1030, SSR688, and J188a), which had the highest number of alleles and genotypes. As well, these SSR loci could be useful to evaluate the extent resistance of breeds to harsh environmental conditions. (Ojango et al., 2011) mentioned high heterozygote content in microsatellite loci indicates a diversity, and may also suggest a high adaptation, to environmental conditions.

ACKNOWLEDGMENT

We would like to thank Ministry of Environment, Water and Agriculture, Riyadh, KSA. As well we thank the IPK Gatersleben, Germany, for help in provide us with samples.

REFERENCES

Adebo HO, Ahoton LE, Quenum F, Ezin V, (2015). Agro-morphological Characterization of Corchorus olitoriusCultivars of Benin. *ARRB.* 7: 229-240.

Adeyemo OA, Ayodele OO, Ajisafe MO, Okinedo UE, et al. (2021). Evaluation of dark jute SSR markers and morphological traits in genetic diversity assessment of jute mallow (Corchorus olitorius L.) cultivars. *S. AFR. J. BOT.* 137: 290-297.

Ahmed F (2021). Nutraceutical potential of molokhia (Corchorus olitorius L.): A versatile green leafy vegetable. *Pharmacogn. Res*. 13: 01-12.

Al-Mamari AGH (2013). Application of genomics and molecular genetics in date palm (Phoenix dactylifera L.). PhD thesis. University of Nottingham.

Basu AG, Meyer MR, Powell W, Asak BSL, et al. (2004). Analysis of genetic diversity in cultivated jute determined by means of SSR markers and AFLP profiling. *Crop. Sci.* 44: 678–685.

Benor S (2018). Molecular phylogeny of the genus Corchorus (Grewioideae, Malvaceae s.l.) based on nuclear rDNA ITS sequences. *Crop. J.* 6: 552-563.

Botstein D, White RL, Skolnick M, Davis RW, (1980). Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *AJHG*. 32: 314–331.

Das M, Banerjee S, Dhariwa R, Vyas S, et al. (2012). Development of SSR markers and construction of a linkage map in jute. *J. Genet.* 91: 21-31.

Do MH, Lee HHL, Kim Y, Lee HB, et al. (2021). Corchorus olitorius L. ameliorates alcoholic liver disease by regulating gut-liver axis. *J. Funct. Foods.* 85: 104648.

Doyle JJ, Doyle JL (1987). A Rapid DNA Isolation Procedure For Small Quantities of Fresh Leaf Tissue. *Phytochem. Bull.* 19: 11-15.

Emad AA, Ahmad MA, Ayed SA, Sayed MR (2012). Exploration of wild plants wealth with economic importance tolerant to difficult conditions in Khulais Governorate, Saudi Arabia. *SRE.* 7: 3903-3913.

Excoffier L, Smouse PE, Quattro JM (1992). Analysis of Molecular Variance Inferred From Metric Distances Among DNA Haplotypes: Application to Human Mitochondrial DNA Restriction Data. *Genet.* 131: 479-491.

Fawzi NM (2018). Seed morphology and its implication in classification of some selected species of genus Corchorus L. (Malvaceae). Middle. East. *J. Agric. Res.* 7(1): 1-11.

Ghosh S. Meena K, Sinha MK, Karmakar PG, (2015). Genetic Diversity in Corchorus olitorius Genotypes Using Jute SSRs. *Proc. Natl. Acad. Sci. India Sect. B Biol. Sci.* 87: 917-926.

Graphpad Prism 10. Available at: [https://www.graphpad.com/features/ 21/ 3/2023]

Haque S, Begum S, Sarker RH, Khan AH, (2007). Determining Genetic Diversity of Some Jute Varieties and Accessions Using RAPD Markers. *PCTOC.* 17: 183-191.

Helaly A, Alkharpotly A, Mady E, Craker LE, (2017). Characterization of Four Molokhia (Corchorus olitorius) Landraces by Morphology and Chemistry. *JMAP.* 2: 1-6.

Jombart T, Ahmed I, (2011). Adegenet 1.3-1: new tools for the analysis of genome-wide SNP data. *Bioinform.* 27: 3070-3071.

Kiebre M, Sawadogo B, Kiebre Z, Sawadogo N, (2019). Molecular Characterization of Corchorus olitorius L. of Burkina Faso. *J. Exp. Agric. Int.* 32: 1-9.

Liu K, Muse SV (2005). PowerMarker: an integrated analysis environment for genetic marker analysis. *Bioinform.* 21: 2128-2129.

Mujahid AM (1989). Flora of Saudi Arabia. King Saud University Press, Riyadh.

Mukul MM, Akter N (2021). Morpho-anatomical variability, principal component analysis and Euclidean clustering of tossa jute (Corchorus olitorius L.). Heliyon. 7(5).

Nag S, Mitra J, Satya P, Kar CS, et al. (2018). Genetic diversity assessment in jute (Corchorus species) utilizing inter simple sequence repeat and simple sequence repeat markers§ ISSR. *IJBT.* 17: 16-326.

Ngomuo MS (2017). Genetic characterization of jute mallow (Corchorus spp.): a traditional African vegetable. PhD thesis. Nelson Mandela African Institution of Science, Arusha, Tanzania.

Ojango JN, Mpofu N, Marshall K, Andersson-Eklund L, (2011). Quantitative methods to improve the understanding and utilization of animal genetic resources. *Anim. Genet. Resour. Inf.* 3. 2025.

Perrier X, Jacquemoud-Collet JP, (2009). DARwin software. Available at: [http://darwin.cirad.fr/darwin/2/9/2010]

Pritchard JK, Stephens M, Donnelly AP (2000). Inference of population structure using multilocus genotype data. *Genet.* 155: 945-959.

Roy A, Bandyopadhyay A, Mahapatra AK, Ghosh SK, et al. (2006). Evaluation of genetic diversity in jute (Corchorus species) using STMS, ISSR and RAPD markers. *Plant Breed.* 125: 292-297.

Sharma M, Kantartzi SK, Stewart JM, (2009). Molecular Diversity and Polymorphism Information Content of Selected Gossypium hirsutum Accessions. Summaries of Arkansas Cotton Research. *AAES.* 582: 124-127.

Yang Z, Lu R, Dai Z, Yan A, et al. (2018). Analysis of genetic diversity and population structure of a worldwide collection of Corchorus olitorius L. germplasm using microsatellite markers. *Biotechnol. Biotechnol. Equip.* 32: 961-967.

Youssef AF, Younes NA, Youssef M, (2019). Genetic diversity in Corchorus olitorius L. revealed by morphophysiological and molecular analyses. *Mol. Biol. Rep.* 46: 2933-2940.

Yuan M, Zhang L, Tao A, Xu J, et al. (2015). Genetic Structure and Relationship Analysis of an Association Population in Jute (Corchorus spp.) Evaluated by SSR Markers. *PLoS One.* 10: e0128195.

Yusuf M, Al-Oqail MM, Al-Sheddr ES, Al-Rehaily AJ, et al. (2014). Diversity of medicinal plants in the flora of Saudi Arabia: an inventory of 15 plant families and their conservation management. *Int. J. Environ.* 3: 312-320.

Zakaria A, Shuranjan S, (2022). Review on jute leaf: A powerful biological tool. *IJSR.* 4: 064-085.

Zhang L, Ibrahim AK, Niyitanga S, Zhang L, et al. (2019). Jute (Corchorus spp.) Breeding. In Advances in Plant Breeding Strategies: Industrial and Food Crops. Berlin: 85-113.